

PF59083SeqList PF59083.txt

Glu Val Gln Ala Asp Arg Tyr Trp Gly Ala Gln Ala Gln Arg Ser Leu
 50 55 60
 Gly Asn Phe Lys Ile Gly Trp Glu Lys Gln Pro Ala Ser Val Val Arg
 65 70 75 80
 Ala Leu Gly Ile Val Lys Gln Ala Ala Ala Arg Ala Asn Met Ala Leu
 85 90 95
 Ala Gly Leu Asp Pro Lys Val Gly Asp Ala Ile Ile Ala Ala Ala Gln
 100 105 110
 Glu Val Ile Asp Gly Lys Leu Thr Glu His Phe Pro Leu Val Val Trp
 115 120 125
 Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu Val Ile
 130 135 140
 Ser Asn Arg Ala Ile Glu Met Leu Gly Gly Glu Met Gly Thr Lys Lys
 145 150 155 160
 Pro Val His Pro Asn Asp His Val Asn Met Ser Gln Ser Ser Asn Asp
 165 170 175
 Thr Tyr Pro Thr Ala Met His Ile Ala Cys Val Glu Glu Ile Val His
 180 185 190
 His Leu Leu Pro Ala Leu Lys His Leu His Thr Ala Leu Glu Ala Lys
 195 200 205
 Val Lys Gln Phe Glu Lys Ile Ile Lys Ile Gly Arg Thr His Thr Gln
 210 215 220
 Asp Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Ala Ala
 225 230 235 240
 Gln Val Ala Ser Ala Ile Ala Asn Ile Glu Leu Thr Leu Pro Ala Leu
 245 250 255
 Ser Lys Leu Ala Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Ala
 260 265 270
 Pro Val Gly Phe Ala Glu Lys Val Ala Glu Glu Ile Ser Glu Ile Thr
 275 280 285
 Gly Leu Ser Phe Val Thr Ala Pro Asn Lys Phe Glu Ala Leu Ala Ser
 290 295 300
 His Asp Ser Met Val Phe Ser His Gly Ala Ile Asn Ala Ala Ala Ala
 305 310 315 320
 Ala Leu Phe Lys Ile Ala Asn Asp Ile Arg Phe Leu Gly Ser Gly Pro
 325 330 335
 Arg Ala Gly Leu Gly Glu Leu Ser Leu Pro Glu Asn Glu Pro Gly Ser
 340 345 350
 Ser Ile Met Pro Gly Lys Val Asn Pro Thr Gln Ser Glu Ala Leu Thr
 355 360 365
 Gln Val Cys Ala His Ile Phe Gly Asn Asn Ala Ala Leu Ser Phe Ala
 370 375 380
 Gly Ser Gln Gly His Phe Glu Leu Asn Val Tyr Asn Pro Met Met Ala
 385 390 395 400
 Tyr Asn Phe Leu Gln Ser Val Gln Leu Leu Gly Asp Ala Ala Val Ser
 405 410 415
 Phe Thr Asp Asn Cys Val Val Gly Ile Glu Ala Arg Glu Asp Asn Ile
 420 425 430
 Arg Lys Gly Val Glu Asn Ser Leu Met Leu Val Thr Ala Leu Asn Gly
 435 440 445
 Lys Leu Gly Tyr Asp Ile Cys Ala Lys Ile Ala Lys Thr Ala His Lys
 450 455 460
 Asn Gly Thr Thr Leu Arg Glu Glu Ala Val Gly Gly Gly Tyr Leu Thr
 465 470 475 480
 Asn Glu Glu Phe Asp Gln Tyr Val Arg Pro Glu Asn Met Ile Gly Pro
 485 490 495
 Lys

<210> 9557
 <211> 1446
 <212> DNA
 <213> Agrobacterium tumefaciens str. C58

<220>
 <221> CDS
 <222> (1)..(1446)
 <223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 9557
gtg gag gaa aaa gtg agt gtg acg cgc agg gag cat gat ttg ctc ggg      48
Met Glu Glu Lys Val Ser Val Thr Arg Arg Glu His Asp Leu Leu Gly
1      5      10      15
acg aag gaa att ccg gct gat gtc tat tgg ggc gtg cac acc gcg cgc      96
Thr Lys Glu Ile Pro Ala Asp Val Tyr Trp Gly Val His Thr Ala Arg
20      25      30
gcc gtg gaa aac ttc aag atc acc ggg gta acc att ggc cat aac cct      144
Ala Val Glu Asn Phe Lys Ile Thr Gly Val Thr Ile Gly His Asn Pro
35      40      45
tat ctc gtc agg gga ctg gcc tat gtg aag gag gca gcc gca cgc gca      192
Tyr Leu Val Arg Gly Leu Ala Tyr Val Lys Glu Ala Ala Ala Arg Ala
50      55      60
aat cac gaa ctc ggc ctg ctc gac aag gag cgc atg gaa gcg atc gcg      240
Asn His Glu Leu Gly Leu Leu Asp Lys Glu Arg Met Glu Ala Ile Ala
65      70      75
gaa gcc tgc cgc gaa atc cgc gcc ggc gcg ctg cac gag caa ttc gtg      288
Glu Ala Cys Arg Glu Ile Arg Ala Gly Ala Leu His Glu Gln Phe Val
85      90      95
gtc gac gag atc cag ggg gga gcc ggc act tcc act aac atg aac gcc      336
Val Asp Glu Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala
100      105      110
aac gag gtc att tcc aac cgt gcg ctg gaa ctg ctc ggc cac gaa aaa      384
Asn Glu Val Ile Ser Asn Arg Ala Leu Glu Leu Leu Gly His Glu Lys
115      120      125
ggc gat tat tcc cgt ctt cac ccg aat gac cat gtc aat ctc agc cag      432
Gly Asp Tyr Ser Arg Leu His Pro Asn Asp His Val Asn Leu Ser Gln
130      135      140
tcc acc aac gac gcc tat cca acg gcg atc aat gtc ggg ctg atc gag      480
Ser Thr Asn Asp Ala Tyr Pro Thr Ala Ile Asn Val Gly Leu Ile Glu
145      150      155
gcg atc gac gat ctg gcg gtc tcc atg ggc gtg ctg aaa gac gct ttc      528
Ala Ile Asp Asp Leu Ala Val Ser Met Gly Val Leu Lys Asp Ala Phe
160      165      170
gac cgc aag gcg cag gaa ttt gcc ggc ttc atc aag atc ggt cgc acc      576
Asp Arg Lys Ala Gln Glu Phe Ala Gly Phe Ile Lys Ile Gly Arg Thr
175      180      185
cag ctg cag gat gcc gtg ccg atg acg ctc ggc cag gaa ttc cgc act      624
Gln Leu Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Arg Thr
190      195      200
ttc gtg gtg atg ctc ggc gaa gat cag gct cgc ctg atc gaa tcc gcc      672
Phe Val Val Met Leu Gly Glu Asp Gln Ala Arg Leu Ile Glu Ser Ala
205      210      215
gca ctg ctg cac gaa atc aat ctc ggc gcc acc gcc atc ggc acc ggt      720
Ala Leu Leu His Glu Ile Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly
220      225      230
ctc aat gcg ccg cgc ggt tat gcc gag ctt gcc tgc cag cat ctg gct      768
Leu Asn Ala Pro Arg Gly Tyr Ala Glu Leu Ala Cys Gln His Leu Ala
235      240      245
aag ctg acc gga cgg cca ctg gtg acg gca gac ctg atc gaa gcc      816
Lys Leu Thr Gly Arg Pro Leu Val Thr Ala Ala Asp Leu Ile Glu Ala
250      255      260
aca cag gat ccc ggt gcc ttc gtg cac ctt tcc ggc gtg ctg aag cgc      864
Thr Gln Asp Pro Gly Ala Phe Val His Leu Ser Gly Val Leu Lys Arg
265      270      275
gtt gcc gtc aag ctg tcc aag acc tgc aac gac ctt cgc ctg ctc tcc      912
Val Ala Val Lys Leu Ser Lys Thr Cys Asn Asp Leu Arg Leu Leu Ser
280      285      290
tcc ggt ccg cgc gcc ggc atc ggc gag atc acc ctg ccc tcc gtt cag      960
Ser Gly Pro Arg Ala Gly Ile Gly Glu Ile Thr Leu Pro Ser Val Gln
295      300      305
gcg ggt tcc agc atc atg cct ggc aag atc aac ccg gtc att ccc gaa      1008
Ala Gly Ser Ser Ile Met Pro Gly Lys Ile Asn Pro Val Ile Pro Glu
310      315      320
gtg gtc aac cag gtc gcc tat gcg gtg atc ggc aac gac atc acc atc      1056
Val Val Asn Gln Val Ala Tyr Ala Val Ile Gly Asn Asp Ile Thr Ile
325      330      335
acc atg gcg gcc gaa gcc ggg cag ctg caa ttg aac gcc ttt gaa ccc      1104
Thr Met Ala Ala Glu Ala Gly Gln Leu Gln Leu Ala Phe Glu Pro
340      345      350

```


PF59083SeqList PF59083.txt

355	360	365	
atc atc gtg cgg gca ttg tcg cag agc atc agc cag ctc agc gcc gcc			1152
Ile Ile Val Arg Ala Leu Ser Gln Ser Ile Ser Gln Leu Ser Ala Ala			
370	375	380	
tgc cgc aca ttg gcg gaa cgc tgc gtt gag ggc atc gtc gca aac ccc			1200
Cys Arg Thr Leu Ala Glu Arg Cys Val Glu Gly Ile Val Ala Asn Pro			
385	390	395	
ggc atc atg gcg cag cgc gtg gaa gaa tcg atc ggt ctc gcc acc gcg			1248
Gly Ile Met Ala Gln Arg Val Glu Glu Ser Ile Gly Leu Ala Thr Ala			
405	410	415	
ctc aat ccg ctg atc ggt tat tac gcc gcg acg gaa gtg gcg aag gaa			1296
Leu Asn Pro Leu Ile Gly Tyr Tyr Ala Ala Thr Glu Val Ala Lys Glu			
420	425	430	
gcg ctt gcc agc ggc cgc acc gtg ccg cag gtc gtt ctg gaa cgg ggt			1344
Ala Leu Ala Ser Gly Arg Thr Val Pro Gln Val Val Leu Glu Arg Gly			
435	440	445	
tat ctg acg gaa acg caa ttg cag cag gcg ctc agc ccg cgt cat ctt			1392
Tyr Leu Thr Glu Thr Gln Leu Gln Gln Ala Leu Ser Pro Arg His Leu			
450	455	460	
gcc aac ctg ccc gcg gtt acc gtt acg gct ggc gaa gcc gat ctt cgc			1440
Ala Asn Leu Pro Ala Val Thr Val Thr Ala Gly Glu Ala Asp Leu Arg			
465	470	475	
cga tga			1446
Arg			

<210> 9558

<211> 481

<212> PRT

<213> Agrobacterium tumefaciens str. C58

<400> 9558

Met Glu Glu Lys Val Ser Val Thr Arg Arg Glu His Asp Leu Leu Gly	
1 5 10 15	
Thr Lys Glu Ile Pro Ala Asp Val Tyr Trp Gly Val His Thr Ala Arg	
20 25 30	
Ala Val Glu Asn Phe Lys Ile Thr Gly Val Thr Ile Gly His Asn Pro	
35 40 45	
Tyr Leu Val Arg Gly Leu Ala Tyr Val Lys Glu Ala Ala Arg Ala	
50 55 60	
Asn His Glu Leu Gly Leu Leu Asp Lys Glu Arg Met Glu Ala Ile Ala	
65 70 75 80	
Glu Ala Cys Arg Glu Ile Arg Ala Gly Ala Leu His Glu Gln Phe Val	
85 90 95	
Val Asp Glu Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala	
100 105 110	
Asn Glu Val Ile Ser Asn Arg Ala Leu Glu Leu Leu Gly His Glu Lys	
115 120 125	
Gly Asp Tyr Ser Arg Leu His Pro Asn Asp His Val Asn Leu Ser Gln	
130 135 140	
Ser Thr Asn Asp Ala Tyr Pro Thr Ala Ile Asn Val Gly Leu Ile Glu	
145 150 155 160	
Ala Ile Asp Asp Leu Ala Val Ser Met Gly Val Leu Lys Asp Ala Phe	
165 170 175	
Asp Arg Lys Ala Gln Glu Phe Ala Gly Phe Ile Lys Ile Gly Arg Thr	
180 185 190	
Gln Leu Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Arg Thr	
195 200 205	
Phe Val Val Met Leu Gly Glu Asp Gln Ala Arg Leu Ile Glu Ser Ala	
210 215 220	
Ala Leu Leu His Glu Ile Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly	
225 230 235 240	
Leu Asn Ala Pro Arg Gly Tyr Ala Glu Leu Ala Cys Gln His Leu Ala	
245 250 255	
Lys Leu Thr Gly Arg Pro Leu Val Thr Ala Ala Asp Leu Ile Glu Ala	
260 265 270	
Thr Gln Asp Pro Gly Ala Phe Val His Leu Ser Gly Val Leu Lys Arg	
275 280 285	
Val Ala Val Lys Leu Ser Lys Thr Cys Asn Asp Leu Arg Leu Leu Ser	

PF59083SeqList PF59083.txt

```

290          295          300
Ser Gly Pro Arg Ala Gly Ile Gly Glu Ile Thr Leu Pro Ser Val Gln
305 Ala Gly Ser Ser Ile Met Pro Gly Lys Ile Asn Pro Val Ile Pro Glu
310          315          320
Val Val Asn Gln Val Ala Tyr Ala Val Ile Gly Asn Asp Ile Thr Ile
325          330          335
Thr Met Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Ala Phe Glu Pro
340          345          350
Ile Ile Val Arg Ala Leu Ser Gln Ser Ile Ser Gln Leu Ser Ala Ala
355          360          365
Cys Arg Thr Leu Ala Glu Arg Cys Val Glu Gly Ile Val Ala Asn Pro
370          375          380
Gly Ile Met Ala Gln Arg Val Glu Glu Ser Ile Gly Leu Ala Thr Ala
385          390          395
Leu Asn Pro Leu Ile Gly Tyr Tyr Ala Ala Thr Glu Val Ala Lys Glu
400          405          410
Ala Leu Ala Ser Gly Arg Thr Val Pro Gln Val Val Leu Glu Arg Gly
415          420          425
Tyr Leu Thr Glu Thr Gln Leu Gln Gln Ala Leu Ser Pro Arg His Leu
430          435          440
Ala Asn Leu Pro Ala Val Thr Val Thr Ala Gly Glu Ala Asp Leu Arg
445          450          455
Arg          460          465          470          475          480

```

<210> 9559
 <211> 1374
 <212> DNA
 <213> Thermoplasma acidophilum DSM 1728

<220>
 <221> CDS
 <222> (1)..(1374)
 <223> transl_table=11

```

<400> 9559
atg agg aca gaa agg gat gtt atc ggg gag gtg cag ctg ccc gac aat      48
Met Arg Thr Glu Arg Asp Val Ile Gly Glu Val Gln Leu Pro Asp Asn
1          5          15
gta ttt tat ggc ata aac acg gca agg gca agg gag aac ttc agg atc      96
Val Phe Tyr Gly Ile Asn Thr Ala Arg Ala Arg Glu Asn Phe Arg Ile
20          25          30
acc ggg ctg acc gct gat tct gat cac atc gta tca att gcg cag gtc      144
Thr Gly Leu Thr Ala Asp Ser Asp His Ile Val Ser Ile Ala Gln Val
35          40          45
aag aag gct gca gcg ctt gca aat gcc gac gga ggc gca ctg gat aag      192
Lys Lys Ala Ala Ala Leu Ala Asn Ala Asp Gly Gly Ala Leu Asp Lys
50          55          60
gag aag gca gat tac att tca aag gca tgc gac gag ata atc ggc ggg      240
Glu Lys Ala Asp Tyr Ile Ser Lys Ala Cys Asp Glu Ile Ile Gly Gly
65          70          75
aag tac cat gac cag ttc gtg ata gac gtc tac cag gct ggc gca gga      288
Lys Tyr His Asp Gln Phe Val Ile Asp Val Tyr Gln Ala Gly Ala Gly
80          85          90
aca tcc tac aac atg aac gca aat gag gtc ata gcc aac gtt gcg ctg      336
Thr Ser Tyr Asn Met Asn Ala Asn Glu Val Ile Ala Asn Val Ala Leu
100          105          110
aca ctg atg ggc aag aat aag gga gag tac tcg gtg ata cat cca aac      384
Thr Leu Met Gly Lys Asn Lys Gly Glu Tyr Ser Val Ile His Pro Asn
115          120          125
gac cac gtg aac atg agc cag tct acg aac gat gtt tat ccg acg atg      432
Asp His Val Asn Met Ser Gln Ser Thr Asn Asp Val Tyr Pro Thr Met
130          135          140
atg cga tta aca gtc tcc aag atc agg aag ctc aag gat gca ctc      480
Met Arg Leu Thr Val Ser Lys Lys Ile Arg Lys Leu Lys Asp Ala Leu
145          150          155
aac gaa ctc ata gag agc tta gag gca aag agc agg gaa ttc agg ggg      528
Asn Glu Leu Ile Glu Ser Leu Glu Ala Lys Ser Arg Glu Phe Arg Gly

```

PF59083SeqList PF59083.txt

				165					170					175			
atc	gca	aag	ccc	ggg	agg	acc	cat	ctc	cag	gat	gct	gcg	cct	gta	acg		576
Ile	Ala	Lys	Pro	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Ala	Pro	Val	Thr		
			180					185					190				
ctt	ggg	ctt	gag	ttc	gga	gcc	tac	gcc	tac	gcc	atg	aag	aag	gac	cgt		624
Leu	Gly	Leu	Glu	Phe	Gly	Ala	Tyr	Ala	Tyr	Ala	Met	Lys	Lys	Asp	Arg		
			195				200					205					
gat	gag	ata	ata	gat	gcc	tcg	gac	tac	ata	atg	gag	ctg	aac	ata	ggg		672
Asp	Glu	Ile	Ile	Asp	Ala	Ser	Asp	Tyr	Ile	Met	Glu	Leu	Asn	Ile	Gly		
			210			215					220						
ggg	aca	gcg	gtt	ggc	acg	ggg	ata	aac	act	gcg	aag	aac	tat	cag	gaa		720
Gly	Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Thr	Ala	Lys	Asn	Tyr	Gln	Glu		
225				230						235					240		
aac	gtg	gtg	aag	cac	ata	aac	gag	ata	acg	aag	gag	aac	ttc	agg	aaa		768
Asn	Val	Val	Lys	His	Ile	Asn	Glu	Ile	Thr	Lys	Glu	Asn	Phe	Arg	Lys		
			245					250						255			
agc	acg	aat	ctg	ctc	ggc	ata	atg	cag	ttc	atg	acg	gat	ttc	tcc	agg		816
Ser	Thr	Asn	Leu	Leu	Gly	Ile	Met	Gln	Phe	Met	Thr	Asp	Phe	Ser	Arg		
			260					265					270				
gtc	atg	aat	gcg	gtc	acg	aac	ctc	gcc	ctg	gat	gtt	gag	aag	ata	gca		864
Val	Met	Asn	Ala	Val	Thr	Asn	Leu	Ala	Leu	Asp	Val	Glu	Lys	Ile	Ala		
			275				280					285					
aac	gac	ata	agg	ctg	ctt	tac	tcc	ggc	cct	ggc	gca	ggc	atc	cat	gag		912
Asn	Asp	Ile	Arg	Leu	Leu	Tyr	Ser	Gly	Pro	Gly	Ala	Gly	Ile	His	Glu		
			290			295					300						
ata	ata	att	cca	gct	gta	cag	cag	gga	tca	tcc	ata	atg	ccg	ggc	aag		960
Ile	Ile	Ile	Pro	Ala	Val	Gln	Gln	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys		
305				310						315					320		
ata	aac	ccg	tcc	atc	gcc	gag	gcc	atg	aac	atg	atc	tgc	cac	tca	gtc		1008
Ile	Asn	Pro	Ser	Ile	Ala	Glu	Ala	Met	Asn	Met	Ile	Cys	His	Ser	Val		
			325					330						335			
ata	gga	gcg	cag	cag	gcg	gtt	aat	atg	agc	gtt	cag	gca	ggg	cag	ctt		1056
Ile	Gly	Ala	Gln	Gln	Ala	Val	Asn	Met	Ser	Val	Gln	Ala	Gly	Gln	Leu		
			340					345					350				
gag	ctg	aac	gtg	atg	atg	ccc	aac	atc	gac	tac	gag	ctg	acg	aga	tcc		1104
Glu	Leu	Asn	Val	Met	Met	Pro	Asn	Ile	Asp	Tyr	Glu	Leu	Thr	Arg	Ser		
			355				360					365					
ata	gac	ata	atg	aca	aac	ggc	ctg	aag	atg	ttc	aag	cag	aaa	ctc	ata		1152
Ile	Asp	Ile	Met	Thr	Asn	Gly	Leu	Lys	Met	Phe	Lys	Gln	Lys	Leu	Ile		
			370			375					380						
gac	ggc	atc	aaa	gct	aac	gtt	cct	gta	tgc	aga	gaa	cac	ctg	gcg	aac		1200
Asp	Gly	Ile	Lys	Ala	Asn	Val	Pro	Val	Cys	Arg	Glu	His	Leu	Ala	Asn		
385				390					395					400			
agc	ttc	ggt	tca	gca	gcg	ctc	ctt	aac	ccc	tat	ctc	gga	tac	gat	aac		1248
Ser	Phe	Gly	Ser	Ala	Ala	Leu	Leu	Asn	Pro	Tyr	Leu	Gly	Tyr	Asp	Asn		
			405					410						415			
gtt	gca	aag	ata	gtg	aga	gag	gcc	gtt	gaa	act	ggg	aaa	tca	ata	aaa		1296
Val	Ala	Lys	Ile	Val	Arg	Glu	Ala	Val	Glu	Thr	Gly	Lys	Ser	Ile	Lys		
			420					425					430				
agc	cta	gta	ctc	gca	acc	gga	aaa	ctg	aca	gaa	gag	cag	tac	atg	aag		1344
Ser	Leu	Val	Leu	Ala	Thr	Gly	Lys	Leu	Thr	Glu	Glu	Gln	Tyr	Met	Lys		
			435				440					445					
ata	atg	gac	agt	ggg	gtt	cca	aag	gac	tga								1374
Ile	Met	Asp	Ser	Gly	Val	Pro	Lys	Asp									
			450			455											

<210> 9560

<211> 457

<212> PRT

<213> Thermoplasma acidophilum DSM 1728

<400> 9560

Met	Arg	Thr	Glu	Arg	Asp	Val	Ile	Gly	Glu	Val	Gln	Leu	Pro	Asp	Asn
1				5					10					15	
Val	Phe	Tyr	Gly	Ile	Asn	Thr	Ala	Arg	Ala	Arg	Glu	Asn	Phe	Arg	Ile
			20					25					30		
Thr	Gly	Leu	Thr	Ala	Asp	Ser	Asp	His	Ile	Val	Ser	Ile	Ala	Gln	Val
		35					40					45			
Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Ala	Asp	Gly	Gly	Ala	Leu	Asp	Lys

PF59083SeqList PF59083.txt

50 55 60
 Glu Lys Ala Asp Tyr Ile Ser Lys Ala Cys Asp Glu Ile Ile Gly Gly
 65 70 75 80
 Lys Tyr His Asp Gln Phe Val Ile Asp Val Tyr Gln Ala Gly Ala Gly
 85 90 95
 Thr Ser Tyr Asn Met Asn Ala Asn Glu Val Ile Ala Asn Val Ala Leu
 100 105 110
 Thr Leu Met Gly Lys Asn Lys Gly Glu Tyr Ser Val Ile His Pro Asn
 115 120 125
 Asp His Val Asn Met Ser Gln Ser Thr Asn Asp Val Tyr Pro Thr Met
 130 135 140
 Met Arg Leu Thr Val Ser Lys Lys Ile Arg Lys Leu Lys Asp Ala Leu
 145 150 155 160
 Asn Glu Leu Ile Glu Ser Leu Glu Ala Lys Ser Arg Glu Phe Arg Gly
 165 170 175
 Ile Ala Lys Pro Gly Arg Thr His Leu Gln Asp Ala Ala Pro Val Thr
 180 185 190
 Leu Gly Leu Glu Phe Gly Ala Tyr Ala Tyr Ala Met Lys Lys Asp Arg
 195 200 205
 Asp Glu Ile Ile Asp Ala Ser Asp Tyr Ile Met Glu Leu Asn Ile Gly
 210 215 220
 Gly Thr Ala Val Gly Thr Gly Ile Asn Thr Ala Lys Asn Tyr Gln Glu
 225 230 235 240
 Asn Val Val Lys His Ile Asn Glu Ile Thr Lys Glu Asn Phe Arg Lys
 245 250 255
 Ser Thr Asn Leu Gly Ile Met Gln Phe Met Thr Asp Phe Ser Arg
 260 265 270
 Val Met Asn Ala Val Thr Asn Leu Ala Leu Asp Val Glu Lys Ile Ala
 275 280 285
 Asn Asp Ile Arg Leu Leu Tyr Ser Gly Pro Gly Ala Gly Ile His Glu
 290 295 300
 Ile Ile Ile Pro Ala Val Gln Gln Gly Ser Ser Ile Met Pro Gly Lys
 305 310 315 320
 Ile Asn Pro Ser Ile Ala Glu Ala Met Asn Met Ile Cys His Ser Val
 325 330 335
 Ile Gly Ala Gln Gln Ala Val Asn Met Ser Val Gln Ala Gly Gln Leu
 340 345 350
 Glu Leu Asn Val Met Met Pro Asn Ile Asp Tyr Glu Leu Thr Arg Ser
 355 360 365
 Ile Asp Ile Met Thr Asn Gly Leu Lys Met Phe Lys Gln Lys Leu Ile
 370 375 380
 Asp Gly Ile Lys Ala Asn Val Pro Val Cys Arg Glu His Leu Ala Asn
 385 390 395 400
 Ser Phe Gly Ser Ala Leu Leu Asn Pro Tyr Leu Gly Tyr Asp Asn
 405 410 415
 Val Ala Lys Ile Val Arg Glu Ala Val Glu Thr Gly Lys Ser Ile Lys
 420 425 430
 Ser Leu Val Leu Ala Thr Gly Lys Leu Thr Glu Glu Gln Tyr Met Lys
 435 440 445
 Ile Met Asp Ser Gly Val Pro Lys Asp
 450 455

<210> 9561
 <211> 1437
 <212> DNA
 <213> Yersinia pestis C092

<220>
 <221> CDS
 <222> (1)..(1437)
 <223> transl_table=11

<400> 9561
 atg tca aat aac att cgt att gaa gaa gac ctg tta ggt aca cga gaa 48
 Met Ser Asn Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Thr Arg Glu
 1 5 10
 gtc ccc gca gag gct tac tac ggt gtt cat acc ctg cgt gcg att gaa 96
 Val Pro Ala Glu Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Ile Glu
 20 25 30

PF59083SeqList PF59083.txt

aac	ttc	tat	atc	agt	aac	agt	aaa	atc	agt	gac	gtg	ccg	gaa	ttt	gta	144
Asn	Phe	Tyr	Ile	Ser	Asn	Ser	Lys	Ile	Ser	Asp	Val	Pro	Glu	Phe	Val	
		35					40					45				
cgt	ggc	atg	gtc	atg	gta	aaa	aaa	gcg	gcg	gca	atg	gct	aac	aaa	gag	192
Arg	Gly	Met	Val	Met	Val	Lys	Lys	Ala	Ala	Ala	Met	Ala	Asn	Lys	Glu	
	50					55					60					
ttg	cat	acc	atc	ccg	cgt	aaa	att	gca	gac	atc	att	att	cag	gca	tgt	240
Leu	His	Thr	Ile	Pro	Arg	Lys	Ile	Ala	Asp	Ile	Ile	Ile	Gln	Ala	Cys	
65					70					75					80	
gat	gaa	gtt	ctg	gat	aaa	ggg	aaa	tgt	atg	gat	cag	ttc	ccc	gtt	gat	288
Asp	Glu	Val	Leu	Asp	Lys	Gly	Lys	Cys	Met	Asp	Gln	Phe	Pro	Val	Asp	
				85					90					95		
gtg	ttc	cag	ggc	ggc	gca	ggt	acc	tct	ctc	aat	atg	aac	acc	aac	gag	336
Val	Phe	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Leu	Asn	Met	Asn	Thr	Asn	Glu	
		100						105					110			
gtc	ttg	gcc	aat	att	ggc	ctg	gag	ctg	atg	ggc	cac	caa	aaa	ggg	gaa	384
Val	Leu	Ala	Asn	Ile	Gly	Leu	Glu	Leu	Met	Gly	His	Gln	Lys	Gly	Glu	
		115					120					125				
tat	cag	tac	ctt	aac	cct	aac	gac	cat	ctg	aac	aaa	tgc	cag	tcc	acc	432
Tyr	Gln	Tyr	Leu	Asn	Pro	Asn	Asp	His	Leu	Asn	Lys	Cys	Gln	Ser	Thr	
	130					135					140					
aac	gat	gcc	tac	cca	acc	ggt	ttc	cgc	att	gcg	gtc	tac	gcc	tcc	atc	480
Asn	Asp	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Ile	Ala	Val	Tyr	Ala	Ser	Ile	
145					150					155					160	
ctc	aag	ttg	atc	gat	gct	atc	aac	caa	tta	ggc	gaa	ggg	ttc	ggg	aga	528
Leu	Lys	Leu	Ile	Asp	Ala	Ile	Asn	Gln	Leu	Gly	Glu	Gly	Phe	Gly	Arg	
				165					170					175		
aaa	tct	aaa	gaa	ttc	gag	aaa	att	ctg	aaa	atg	ggc	cgt	acc	caa	tta	576
Lys	Ser	Lys	Glu	Phe	Glu	Lys	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	
		180						185					190			
cag	gat	gcc	gta	ccc	atg	act	ctg	ggc	cag	gaa	ttc	cgc	gct	ttc	cag	624
Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Arg	Ala	Phe	Gln	
		195					200					205				
gtg	tta	ttg	aat	gaa	gaa	acc	aag	aac	ctg	caa	cgg	acc	gcc	gag	ttg	672
Val	Leu	Leu	Asn	Glu	Glu	Thr	Lys	Asn	Leu	Gln	Arg	Thr	Ala	Glu	Leu	
	210					215					220					
cta	ttg	gaa	gtc	aac	ctg	ggt	gcc	act	gcc	atc	ggc	act	gcg	ctg	aat	720
Leu	Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Ala	Leu	Asn	
225					230					235					240	
aca	cca	gaa	ggt	tat	tca	caa	ctt	gcc	gtg	cag	aaa	ctg	gca	gaa	atc	768
Thr	Pro	Glu	Gly	Tyr	Ser	Gln	Leu	Ala	Val	Gln	Lys	Leu	Ala	Glu	Ile	
				245					250					255		
agc	gga	tta	gcc	tgt	gtt	cct	gcc	gaa	gat	ttg	atc	gaa	gcg	acc	tct	816
Ser	Gly	Leu	Ala	Cys	Val	Pro	Ala	Glu	Asp	Leu	Ile	Glu	Ala	Thr	Ser	
		260						265					270			
gat	tgc	ggc	gct	tac	gtg	atg	gta	cac	agc	gcc	ctg	aaa	cgc	ctg	gct	864
Asp	Cys	Gly	Ala	Tyr	Val	Met	Val	His	Ser	Ala	Leu	Lys	Arg	Leu	Ala	
		275				280						285				
gtt	aag	atg	tca	aaa	atc	tgt	aac	gac	cta	cgt	ttg	ctc	tca	tct	ggc	912
Val	Lys	Met	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	
	290					295					300					
cca	cgt	act	ggt	ttg	aat	gaa	atc	aac	ctg	cca	gaa	ttg	cag	gcg	ggc	960
Pro	Arg	Thr	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	Ala	Gly	
305					310					315					320	
tct	tct	atc	atg	cct	gca	aaa	gtg	aac	ccg	gtg	atc	cct	gaa	gtt	gta	1008
Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	
				325					330					335		
aat	cag	gtt	tgt	ttt	aag	gtg	atc	ggc	aac	gat	act	tgc	att	act	atg	1056
Asn	Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Cys	Ile	Thr	Met	
		340						345					350			
gcg	gct	gaa	gcg	ggt	cag	ctt	cag	tta	aac	ttg	atg	gaa	ccg	gta	att	1104
Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Leu	Met	Glu	Pro	Val	Ile	
		355					360					365				
ggt	cag	gcc	atg	ttt	gag	tct	atc	cat	atc	ctg	act	aat	gcg	tgt	tac	1152
Gly	Gln	Ala	Met	Phe	Glu	Ser	Ile	His	Ile	Leu	Thr	Asn	Ala	Cys	Tyr	
		370				375					380					
aac	ctg	tta	gag	aag	tgc	atc	aat	ggc	att	acc	gct	aac	aaa	gag	gtc	1200
Asn	Leu	Leu	Glu	Lys	Cys	Ile	Asn	Gly	Ile	Thr	Ala	Asn	Lys	Glu	Val	
385					390					395					400	

PF59083SeqList PF59083.txt

tgc	gag	cgc	tac	gtc	ttt	aac	tcc	ata	ggc	atc	gtc	act	tat	ctt	aac	1248
Cys	Glu	Arg	Tyr	Val	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	
			405						410					415		
ccg	ttc	att	ggc	cac	cat	aat	ggt	gac	att	gtg	ggt	aaa	atc	tgt	gcg	1296
Pro	Phe	Ile	Gly	His	His	Asn	Gly	Asp	Ile	Val	Gly	Lys	Ile	Cys	Ala	
			420					425					430			
gaa	acc	ggt	aaa	aat	gtg	cgg	gaa	gtg	gtt	ctg	gag	cgc	ggt	ttg	tta	1344
Glu	Thr	Gly	Lys	Asn	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gly	Leu	Leu	
		435				440						445				
act	gaa	gcc	gaa	ctg	gac	gac	att	ttc	tct	gtt	gaa	aac	ctg	atg	cac	1392
Thr	Glu	Ala	Glu	Leu	Asp	Asp	Ile	Phe	Ser	Val	Glu	Asn	Leu	Met	His	
	450				455						460					
cca	gcc	tat	aaa	gcg	aaa	cgt	tat	acc	gat	gaa	aat	gaa	caa	taa		1437
Pro	Ala	Tyr	Lys	Ala	Lys	Arg	Tyr	Thr	Asp	Glu	Asn	Glu	Gln			
465					470					475						

<210> 9562

<211> 478

<212> PRT

<213> Yersinia pestis C092

<400> 9562

Met	Ser	Asn	Asn	Ile	Arg	Ile	Glu	Glu	Asp	Leu	Leu	Gly	Thr	Arg	Glu	
1				5					10					15		
Val	Pro	Ala	Glu	Ala	Tyr	Tyr	Gly	Val	His	Thr	Leu	Arg	Ala	Ile	Glu	
			20					25					30			
Asn	Phe	Tyr	Ile	Ser	Asn	Ser	Lys	Ile	Ser	Asp	Val	Pro	Glu	Phe	Val	
		35					40					45				
Arg	Gly	Met	Val	Met	Val	Lys	Lys	Ala	Ala	Ala	Met	Ala	Asn	Lys	Glu	
	50					55					60					
Leu	His	Thr	Ile	Pro	Arg	Lys	Ile	Ala	Asp	Ile	Ile	Ile	Gln	Ala	Cys	
65					70				75					80		
Asp	Glu	Val	Leu	Asp	Lys	Gly	Lys	Cys	Met	Asp	Gln	Phe	Pro	Val	Asp	
			85					90					95			
Val	Phe	Gln	Gly	Ala	Gly	Thr	Ser	Leu	Asn	Met	Asn	Thr	Asn	Glu		
		100					105					110				
Val	Leu	Ala	Asn	Ile	Gly	Leu	Glu	Leu	Met	Gly	His	Gln	Lys	Gly	Glu	
	115					120					125					
Tyr	Gln	Tyr	Leu	Asn	Pro	Asn	Asp	His	Leu	Asn	Lys	Cys	Gln	Ser	Thr	
	130					135					140					
Asn	Asp	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Ile	Ala	Val	Tyr	Ala	Ser	Ile	
145					150					155					160	
Leu	Lys	Leu	Ile	Asp	Ala	Ile	Asn	Gln	Leu	Gly	Glu	Gly	Phe	Gly	Arg	
			165						170					175		
Lys	Ser	Lys	Glu	Phe	Glu	Lys	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	
		180					185						190			
Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Arg	Ala	Phe	Gln	
	195					200					205					
Val	Leu	Leu	Asn	Glu	Glu	Thr	Lys	Asn	Leu	Gln	Arg	Thr	Ala	Glu	Leu	
	210					215					220					
Leu	Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Ala	Leu	Asn	
225				230					235					240		
Thr	Pro	Glu	Gly	Tyr	Ser	Gln	Leu	Ala	Val	Gln	Lys	Leu	Ala	Glu	Ile	
			245						250					255		
Ser	Gly	Leu	Ala	Cys	Val	Pro	Ala	Glu	Asp	Leu	Ile	Glu	Ala	Thr	Ser	
		260						265					270			
Asp	Cys	Gly	Ala	Tyr	Val	Met	Val	His	Ser	Ala	Leu	Lys	Arg	Leu	Ala	
		275					280					285				
Val	Lys	Met	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Ser	Ser	Gly		
	290					295					300					
Pro	Arg	Thr	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	Ala	Gly	
305					310					315				320		
Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	
			325						330					335		
Asn	Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Cys	Ile	Thr	Met	
		340						345					350			
Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Leu	Met	Glu	Pro	Val	Ile	
	355					360						365				
Gly	Gln	Ala	Met	Phe	Glu	Ser	Ile	His	Ile	Leu	Thr	Asn	Ala	Cys	Tyr	

PF59083SeqList PF59083.txt

```

370          375          380
Asn Leu Leu Glu Lys Cys Ile Asn Gly Ile Thr Ala Asn Lys Glu Val
385          390          395
Cys Glu Arg Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn
405
Pro Phe Ile Gly His His Asn Gly Asp Ile Val Gly Lys Ile Cys Ala
420
Glu Thr Gly Lys Asn Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu
435
Thr Glu Ala Glu Leu Asp Asp Ile Phe Ser Val Glu Asn Leu Met His
450
Pro Ala Tyr Lys Ala Lys Arg Tyr Thr Asp Glu Asn Glu Gln
465          470          475

```

<210> 9563
 <211> 1488
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1488)

```

<400> 9563
atg gtg cta cca tta ttg caa cgc tcc acg ctt cgc ggc gtt caa caa      48
Met Val Leu Pro Leu Leu Gln Arg Ser Thr Leu Arg Gly Val Gln Gln
1          5          10          15
atg acg aaa ccc tgg gcc gcc att gga agt ttg cgt ctg gcc tcc cag      96
Met Thr Lys Pro Trp Ala Ala Ile Gly Ser Leu Arg Leu Ala Ser Gln
20          25          30
gag ttt cgc gtg gag agc gac acc ttt ggc gaa ctg aag gtg ccc gcg      144
Glu Phe Arg Val Glu Ser Asp Thr Phe Gly Glu Leu Lys Val Pro Ala
35          40          45
gat aag tac tat ggc gcc caa acg atg cga tcc cag atc aat ttc ccc      192
Asp Lys Tyr Tyr Gly Ala Gln Thr Met Arg Ser Gln Ile Asn Phe Pro
50          55          60
atc ggc gga gcc acc gaa cgg atg ccc aaa ccc gtg gtc cag gcc atg      240
Ile Gly Gly Ala Thr Glu Arg Met Pro Lys Pro Val Val Gln Ala Met
65          70          75          80
ggc atc ctg aag aag gcc gcc gag gtg aac gag gag ttc gga ctg      288
Gly Ile Leu Lys Lys Ala Ala Ala Glu Val Asn Lys Glu Phe Gly Leu
85          90          95
gac agc aag gtt agc gag gcg atc tcg aag gcg gcc gac gat gtg atc      336
Asp Ser Lys Val Ser Glu Ala Ile Ser Lys Ala Ala Asp Asp Val Ile
100          105          110
tct ggc aag cta tac gac gac cac ttc ccg ctg gtc atc tgg cag acg      384
Ser Gly Lys Leu Tyr Asp Asp His Phe Pro Leu Val Ile Trp Gln Thr
115          120          125
ggc tcg ggc acg cag agc aac atg aat gtg aat gag gtg atc agc aat      432
Gly Ser Gly Thr Gln Ser Asn Met Asn Val Asn Glu Val Ile Ser Asn
130          135          140
cgt gcc att gag ctg ctg ggc ggc aaa ctg ggc tcc aag acg ccc gtg      480
Arg Ala Ile Glu Leu Leu Gly Gly Lys Leu Gly Ser Lys Thr Pro Val
145          150          155          160
cat ccc aac gat cat gtg aac aaa tcg cag agc tcc aac gat acc ttc      528
His Pro Asn Asp His Val Asn Lys Ser Gln Ser Ser Asn Asp Thr Phe
165          170          175
ccc acc gcc att cac atc tcg gtg gcg ctg gag ctg aac aac aac ctt      576
Pro Thr Ala Ile His Ile Ser Val Ala Leu Glu Leu Asn Asn Asn Leu
180          185          190
aag ccg gcg att aag acg ctg cac gat gcg ctg cgt gcc aag tcg gag      624
Lys Pro Ala Ile Lys Thr Leu His Asp Ala Leu Arg Ala Lys Ser Glu
195          200          205
gag ttc aag gac att atc aag atc gga cgc acg cat acg atg gat gcg      672
Glu Phe Lys Asp Ile Ile Lys Ile Gly Arg Thr His Thr Met Asp Ala
210          215          220
gtg cca ttg acg ctg ggc caa gag ttc agc ggc tat gcc cag caa ttg      720
Val Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Ala Gln Gln Leu
225          230          235          240

```

PF59083SeqList PF59083.txt

gcc	tac	gcc	cag	gag	cg	atc	gat	gcc	tgt	ctg	ccg	cg	gtc	tat	gag	768
Ala	Tyr	Ala	Gln	Glu	Arg	Ile	Asp	Ala	Cys	Leu	Pro	Arg	Val	Tyr	Glu	
			245						250					255		
ctg	gct	ctg	ggc	ggc	act	gct	gtg	ggg	acg	ggg	ctg	aac	aca	cg	aag	816
Leu	Ala	Leu	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Arg	Lys	
			260					265					270			
gga	ttc	gcc	gag	aag	tgc	gct	gca	aag	atc	gcc	gag	ctg	acc	agc	ctg	864
Gly	Phe	Ala	Glu	Lys	Cys	Ala	Ala	Lys	Ile	Ala	Glu	Leu	Thr	Ser	Leu	
		275					280					285				
ccc	ttc	ggt	acc	gcg	ccc	aac	aag	ttc	gag	gca	ctg	gct	gcc	cg	gat	912
Pro	Phe	Val	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	Arg	Asp	
	290					295					300					
gcc	atg	gtg	gag	gtg	cat	ggg	gtg	ctc	aac	acg	atc	gcc	ggt	agc	ctg	960
Ala	Met	Val	Glu	Val	His	Gly	Val	Leu	Asn	Thr	Ile	Ala	Val	Ser	Leu	
	305				310					315					320	
atg	aag	att	gcc	aac	gat	att	cgt	ttc	ctt	ggc	tcc	gga	ccg	cgt	tgc	1008
Met	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	
				325				330						335		
ggg	ttg	ggg	gag	ctc	tcg	cta	ccg	gag	aac	gag	cca	ggg	agc	tcc	atc	1056
Gly	Leu	Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	
			340					345					350			
atg	ccc	ggc	aag	gtg	aat	ccc	acg	caa	tgc	gag	tcg	ctg	aca	atg	ctc	1104
Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ser	Leu	Thr	Met	Leu	
		355					360					365				
tcc	gcc	cag	gtg	atg	ggc	aat	cag	gtg	gcg	gtg	acc	atc	ggg	gga	tcc	1152
Ser	Ala	Gln	Val	Met	Gly	Asn	Gln	Val	Ala	Val	Thr	Ile	Gly	Gly	Ser	
	370					375					380					
aat	ggg	cac	ttc	gag	ctg	aat	gta	ttc	aag	ccc	ctg	atc	gtg	tcc	aat	1200
Asn	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Leu	Ile	Val	Ser	Asn	
	385				390					395					400	
gtg	ctg	cg	tcc	att	cgg	cta	ttg	tct	gat	ggc	agc	agg	acc	ttc	act	1248
Val	Leu	Arg	Ser	Ile	Arg	Leu	Leu	Ser	Asp	Gly	Ser	Arg	Thr	Phe	Thr	
			405					410						415		
gcc	aac	tgt	gtg	aat	ggc	atc	cag	gcg	aac	cg	gag	aat	att	gcc	aag	1296
Ala	Asn	Cys	Val	Asn	Gly	Ile	Gln	Ala	Asn	Arg	Glu	Asn	Ile	Ala	Lys	
			420				425						430			
atc	atg	aac	gag	tcg	ctc	atg	ctg	gtg	acc	gct	ctg	aat	ccg	cac	att	1344
Ile	Met	Asn	Glu	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	
		435					440					445				
ggg	tac	gac	aag	gct	gcg	aaa	att	gca	aag	acg	gcg	cac	aag	aat	ggc	1392
Gly	Tyr	Asp	Lys	Ala	Ala	Lys	Ile	Ala	Lys	Thr	Ala	His	Lys	Asn	Gly	
	450					455					460					
acc	aca	ctc	aag	gag	gag	gcc	atc	aat	ttg	ggg	tac	ctg	acg	gag	cag	1440
Thr	Thr	Leu	Lys	Glu	Glu	Ala	Ile	Asn	Leu	Gly	Tyr	Leu	Thr	Glu	Gln	
	465				470					475					480	
cag	ttc	aac	gac	tgg	gtg	cga	ccc	gaa	cag	atg	ctg	gga	ccc	aag		1485
Gln	Phe	Asn	Asp	Trp	Val	Arg	Pro	Glu	Gln	Met	Leu	Gly	Pro	Lys		
			485					490						495		
tga																1488

<210> 9564

<211> 495

<212> PRT

<213> Drosophila melanogaster

<400> 9564

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

PF59083SeqList PF59083.txt

```

      85      90      95
Asp Ser Lys Val Ser Glu Ala Ile Ser Lys Ala Ala Asp Asp Val Ile
      100      105      110
Ser Gly Lys Leu Tyr Asp Asp His Phe Pro Leu Val Ile Trp Gln Thr
      115      120      125
Gly Ser Gly Thr Gln Ser Asn Met Asn Val Asn Glu Val Ile Ser Asn
      130      135      140
Arg Ala Ile Glu Leu Leu Gly Gly Lys Leu Gly Ser Lys Thr Pro Val
      145      150      155
His Pro Asn Asp His Val Asn Lys Ser Gln Ser Ser Asn Asp Thr Phe
      160      165      170
Pro Thr Ala Ile His Ile Ser Val Ala Leu Glu Leu Asn Asn Asn Leu
      175      180      185
Lys Pro Ala Ile Lys Thr Leu His Asp Ala Leu Arg Ala Lys Ser Glu
      190      195      200
Glu Phe Lys Asp Ile Ile Lys Ile Gly Arg Thr His Thr Met Asp Ala
      205      210      215
Val Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Ala Gln Gln Leu
      220      225      230
Ala Tyr Ala Gln Glu Arg Ile Asp Ala Cys Leu Pro Arg Val Tyr Glu
      235      240      245
Leu Ala Leu Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Arg Lys
      250      255      260
Gly Phe Ala Glu Lys Cys Ala Ala Lys Ile Ala Glu Leu Thr Ser Leu
      265      270      275
Pro Phe Val Thr Ala Pro Asn Lys Phe Glu Ala Leu Ala Ala Arg Asp
      280      285      290
Ala Met Val Glu Val His Gly Val Leu Asn Thr Ile Ala Val Ser Leu
      295      300      305
Met Lys Ile Ala Asn Asp Ile Arg Phe Leu Gly Ser Gly Pro Arg Cys
      310      315      320
Gly Leu Gly Glu Leu Ser Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile
      325      330      335
Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ser Leu Thr Met Leu
      340      345      350
Ser Ala Gln Val Met Gly Asn Gln Val Ala Val Thr Ile Gly Gly Ser
      355      360      365
Asn Gly His Phe Glu Leu Asn Val Phe Lys Pro Leu Ile Val Ser Asn
      370      375      380
Val Leu Arg Ser Ile Arg Leu Leu Ser Asp Gly Ser Arg Thr Phe Thr
      385      390      395
Ala Asn Cys Val Asn Gly Ile Gln Ala Asn Arg Glu Asn Ile Ala Lys
      400      405      410
Ile Met Asn Glu Ser Leu Met Leu Val Thr Ala Leu Asn Pro His Ile
      415      420      425
Gly Tyr Asp Lys Ala Ala Lys Ile Ala Lys Thr Ala His Lys Asn Gly
      430      435      440
Thr Thr Leu Lys Glu Glu Ala Ile Asn Leu Gly Tyr Leu Thr Glu Gln
      445      450      455
Gln Phe Asn Asp Trp Val Arg Pro Glu Gln Met Leu Gly Pro Lys
      460      465      470
      475      480      485
      490      495

```

<210> 9565

<211> 1410

<212> DNA

<213> Corynebacterium glutamicum ATCC 13032

<220>

<221> CDS

<222> (1)..(1410)

<223> transl_table=11

<400> 9565

```

atg acc gag cag gaa ttc cgt att gag cac gac acc atg ggt gaa gtg
Met Thr Glu Gln Glu Phe Arg Ile Glu His Asp Thr Met Gly Glu Val
1      5      10      15
aag gtt cca gca aag gct ctg tgg cag gca cag acc cag cgc gct gtt
Lys Val Pro Ala Lys Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val
20      25      30

```

48

96

PF59083SeqList PF59083.txt																
gag	aac	ttc	cct	atc	tct	ggt	cgt	ggt	ctg	gaa	tcc	gca	cag	atc	cgc	144
Glu	Asn	Phe	Pro	Ile	Ser	Gly	Arg	Gly	Leu	Glu	Ser	Ala	Gln	Ile	Arg	
		35					40				45					
gca	atg	ggt	ctg	ctg	aag	gca	gct	tgt	gcg	cag	gta	aac	aag	gac	tcc	192
Ala	Met	Gly	Leu	Leu	Lys	Ala	Ala	Cys	Ala	Gln	Val	Asn	Lys	Asp	Ser	
	50					55					60					
ggt	gcg	ctg	gat	gca	gag	aag	gca	gat	gcc	atc	att	gca	gct	ggt	aag	240
Gly	Ala	Leu	Asp	Ala	Glu	Lys	Ala	Asp	Ala	Ile	Ile	Ala	Ala	Gly	Lys	
65					70					75					80	
gag	atc	gcg	tcc	ggt	aag	cat	gac	gct	gag	ttc	cca	att	gat	gtg	ttc	288
Glu	Ile	Ala	Ser	Gly	Lys	His	Asp	Ala	Glu	Phe	Pro	Ile	Asp	Val	Phe	
				85				90						95		
cag	act	ggt	tcc	ggt	act	tcc	tcc	aac	atg	aac	acc	aat	gag	gtt	atc	336
Gln	Thr	Gly	Ser	Gly	Thr	Ser	Ser	Asn	Met	Asn	Thr	Asn	Glu	Val	Ile	
		100						105					110			
gct	tcc	atc	gcg	aag	gct	aac	ggc	ggt	gag	gtt	cac	cca	aat	gac	cac	384
Ala	Ser	Ile	Ala	Lys	Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His	
		115					120					125				
gtc	aac	atg	ggt	cag	tcc	tcc	aat	gac	acc	ttc	cct	act	gca	act	cac	432
Val	Asn	Met	Gly	Gln	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Thr	His		
	130					135					140					
gtt	gct	gca	acc	gaa	gct	gct	gtc	aat	gac	ctc	atc	cca	ggc	ctg	aag	480
Val	Ala	Ala	Thr	Glu	Ala	Ala	Val	Asn	Asp	Leu	Ile	Pro	Gly	Leu	Lys	
145					150					155					160	
gtt	ctg	cac	gag	tct	ttg	gcg	aag	aag	gct	aac	gag	tggt	tct	gag	gtt	528
Val	Leu	His	Glu	Ser	Leu	Ala	Lys	Lys	Ala	Asn	Glu	Trp	Ser	Glu	Val	
				165					170					175		
gtt	aag	tcc	ggc	cgc	acc	cac	ctg	atg	gac	gct	gtt	cca	gta	acc	ctg	576
Val	Lys	Ser	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu	
			180					185					190			
ggc	cag	gag	ttc	ggt	ggc	tac	gct	cgc	cag	atc	cag	ctc	ggc	atc	gag	624
Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Arg	Gln	Ile	Gln	Leu	Gly	Ile	Glu	
		195					200					205				
cgc	gtt	gag	gct	act	ctt	cct	cgc	ctt	ggt	gag	ctg	gct	att	ggt	ggc	672
Arg	Val	Glu	Ala	Thr	Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly	
	210					215					220					
acc	gct	gct	ggt	acc	ggt	atc	aac	acc	tcc	gct	gat	ttc	ggc	ggc	aag	720
Thr	Ala	Ala	Gly	Thr	Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys	
225					230					235					240	
gtt	gtt	gct	gaa	ctg	atc	aac	ttg	acc	gac	gtc	aag	gag	ctc	aag	gaa	768
Val	Val	Ala	Glu	Leu	Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu	
				245					250					255		
gct	gag	aac	cac	ttc	gag	gct	cag	gct	gca	cgc	gac	gct	ctt	gtt	gag	816
Ala	Glu	Asn	His	Phe	Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu	
			260					265					270			
ttc	tcc	ggc	gca	atg	cgc	gtt	atc	gct	gtc	tcc	ttg	tac	aag	atc	gct	864
Phe	Ser	Gly	Ala	Met	Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala	
		275					280					285				
aac	gat	atc	cgc	ctc	atg	ggc	tcc	ggc	cca	ctg	acc	ggt	ctt	ggc	gag	912
Asn	Asp	Ile	Arg	Leu	Met	Gly	Ser	Gly	Pro	Leu	Thr	Gly	Leu	Gly	Glu	
	290					295					300					
atc	cgt	ctc	cca	gac	ctg	cag	cca	ggt	tcc	tcc	atc	atg	cca	ggc	aag	960
Ile	Arg	Leu	Pro	Asp	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	
305					310					315					320	
gtc	aac	cca	gtt	ctc	tgt	gag	acc	gct	acc	cag	gtt	tcc	gct	cag	gtt	1008
Val	Asn	Pro	Val	Leu	Cys	Glu	Thr	Ala	Thr	Gln	Val	Ser	Ala	Gln	Val	
				325					330					335		
atc	ggc	aat	gac	gca	gct	gtt	gcg	ttc	tcc	ggc	acc	cag	ggc	cag	ttc	1056
Ile	Gly	Asn	Asp	Ala	Ala	Val	Ala	Phe	Ser	Gly	Thr	Gln	Gly	Gln	Phe	
			340					345					350			
gag	ctc	aac	gtg	ttc	atc	cca	gtg	atg	gct	cgc	aac	gtg	ctt	gag	tcc	1104
Glu	Leu	Asn	Val	Phe	Ile	Pro	Val	Met	Ala	Arg	Asn	Val	Leu	Glu	Ser	
		355					360					365				
gct	cgc	ctg	ctg	gct	aac	act	tcc	cgc	gtg	ttc	gca	acc	cgt	ctc	gtt	1152
Ala	Arg	Leu	Leu	Ala	Asn	Thr	Ser	Arg	Val	Phe	Ala	Thr	Arg	Leu	Val	
	370					375					380					
gat	ggc	att	gag	cca	aac	gag	gca	cac	atg	aag	gag	ctc	gct	gag	tct	1200
Asp	Gly	Ile	Glu	Pro	Asn	Glu	Ala	His	Met	Lys	Glu	Leu	Ala	Glu	Ser	
385					390					395					400	

PF59083SeqList PF59083.txt

tca	cct	tcc	atc	gtt	acc	cca	ctg	aac	tct	gca	atc	ggc	tac	gaa	gct	1248
Ser	Pro	Ser	Ile	Val	Thr	Pro	Leu	Asn	Ser	Ala	Ile	Gly	Tyr	Glu	Ala	
			405						410					415		
gct	gca	aag	gtg	gct	aag	act	gct	ttg	gct	gag	ggc	aag	acc	atc	cgc	1296
Ala	Ala	Lys	Val	Ala	Lys	Thr	Ala	Leu	Ala	Glu	Gly	Lys	Thr	Ile	Arg	
			420						425					430		
cag	act	gtc	atc	gat	ttg	ggc	ttg	gtt	gat	ggc	gag	aag	ctc	acc	gag	1344
Gln	Thr	Val	Ile	Asp	Leu	Gly	Leu	Val	Asp	Gly	Glu	Lys	Leu	Thr	Glu	
			435						440					445		
gaa	gag	ctg	gac	aag	cgc	ctc	gac	gtt	ctt	gct	atg	gct	cac	acc	gag	1392
Glu	Glu	Leu	Asp	Lys	Arg	Leu	Asp	Val	Leu	Ala	Met	Ala	His	Thr	Glu	
			450								460					
cgc	gag	aac	aag	ttc	taa											1410
Arg	Glu	Asn	Lys	Phe												
465																

<210> 9566

<211> 469

<212> PRT

<213> Corynebacterium glutamicum ATCC 13032

<400> 9566

Met	Thr	Glu	Gln	Glu	Phe	Arg	Ile	Glu	His	Asp	Thr	Met	Gly	Glu	Val	
1				5					10					15		
Lys	Val	Pro	Ala	Lys	Ala	Leu	Trp	Gln	Ala	Gln	Thr	Gln	Arg	Ala	Val	
			20					25					30			
Glu	Asn	Phe	Pro	Ile	Ser	Gly	Arg	Gly	Leu	Glu	Ser	Ala	Gln	Ile	Arg	
			35					40					45			
Ala	Met	Gly	Leu	Leu	Lys	Ala	Ala	Cys	Ala	Gln	Val	Asn	Lys	Asp	Ser	
			50					55				60				
Gly	Ala	Leu	Asp	Ala	Glu	Lys	Ala	Asp	Ala	Ile	Ile	Ala	Ala	Gly	Lys	
65				70					75						80	
Glu	Ile	Ala	Ser	Gly	Lys	His	Asp	Ala	Glu	Phe	Pro	Ile	Asp	Val	Phe	
				85					90					95		
Gln	Thr	Gly	Ser	Gly	Thr	Ser	Ser	Asn	Met	Asn	Thr	Asn	Glu	Val	Ile	
			100					105					110			
Ala	Ser	Ile	Ala	Lys	Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His	
			115					120					125			
Val	Asn	Met	Gly	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Thr	His	
			130					135				140				
Val	Ala	Ala	Thr	Glu	Ala	Ala	Val	Asn	Asp	Leu	Ile	Pro	Gly	Leu	Lys	
145				150						155					160	
Val	Leu	His	Glu	Ser	Leu	Ala	Lys	Lys	Ala	Asn	Glu	Trp	Ser	Glu	Val	
				165					170					175		
Val	Lys	Ser	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu	
			180					185						190		
Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Arg	Gln	Ile	Gln	Leu	Gly	Ile	Glu	
			195					200					205			
Arg	Val	Glu	Ala	Thr	Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly	
			210					215				220				
Thr	Ala	Ala	Gly	Thr	Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys	
225				230						235					240	
Val	Val	Ala	Glu	Leu	Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu	
				245					250					255		
Ala	Glu	Asn	His	Phe	Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu	
			260					265						270		
Phe	Ser	Gly	Ala	Met	Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala	
			275					280					285			
Asn	Asp	Ile	Arg	Leu	Met	Gly	Ser	Gly	Pro	Leu	Thr	Gly	Leu	Gly	Glu	
			290					295				300				
Ile	Arg	Leu	Pro	Asp	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	
305				310						315					320	
Val	Asn	Pro	Val	Leu	Cys	Glu	Thr	Ala	Thr	Gln	Val	Ser	Ala	Gln	Val	
				325					330					335		
Ile	Gly	Asn	Asp	Ala	Val	Ala	Phe	Ser	Gly	Thr	Gln	Gly	Gln	Phe		
			340					345					350			
Glu	Leu	Asn	Val	Phe	Ile	Pro	Val	Met	Ala	Arg	Asn	Val	Leu	Glu	Ser	
			355					360					365			
Ala	Arg	Leu	Leu	Ala	Asn	Thr	Ser	Arg	Val	Phe	Ala	Thr	Arg	Leu	Val	

PF59083SeqList PF59083.txt

370 375 380
 Asp Gly Ile Glu Pro Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser
 385 390 395 400
 Ser Pro Ser Ile Val Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala
 405 410 415
 Ala Ala Lys Val Ala Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg
 420 425 430
 Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu
 435 440 445
 Glu Glu Leu Asp Lys Arg Leu Asp Val Leu Ala Met Ala His Thr Glu
 450 455 460
 Arg Glu Asn Lys Phe
 465

<210> 9567

<211> 1386

<212> DNA

<213> Thermoanaerobacter tengcongensis MB4

<220>

<221> CDS

<222> (1)..(1386)

<223> transl_table=11

<400> 9567

atg ccg cgt att gaa aaa gat ttc ttg ggt gaa tta aca ctt gaa gat	48
Met Pro Arg Ile Glu Lys Asp Phe Leu Gly Glu Leu Thr Leu Glu Asp	
1 5 10 15	
aat gaa ctt tat gga att cat aca aaa cga gct ttg aaa aac ttc tct	96
Asn Glu Leu Tyr Gly Ile His Thr Lys Arg Ala Leu Lys Asn Phe Ser	
20 25 30	
gta tct tca caa aag att gat ata gat ctt gta cga gca att gtg atg	144
Val Ser Ser Gln Lys Ile Asp Ile Asp Leu Val Arg Ala Ile Val Met	
35 40 45	
gtc aaa aaa gca tgc gca att gca aat ttt gag gtt gga aac ctc gat	192
Val Lys Lys Ala Cys Ala Ile Ala Asn Phe Glu Val Gly Asn Leu Asp	
50 55 60	
gaa aaa ata aaa gat gca att gtc ttt gca tgt gat gag att tta gcc	240
Glu Lys Ile Lys Asp Ala Ile Val Phe Ala Cys Asp Glu Ile Leu Ala	
65 70 75 80	
ggc aaa tac acc gag caa ttt gtg gta gac aaa ttc caa ggc ggt gct	288
Gly Lys Tyr Thr Glu Gln Phe Val Val Asp Lys Phe Gln Gly Gly Ala	
85 90 95	
gga aca tct aca aat atg aac gta aat gaa gta att gcc aac ata gca	336
Gly Thr Ser Thr Asn Met Asn Val Asn Glu Val Ile Ala Asn Ile Ala	
100 105 110	
ctc att tat ctt ggc aaa aaa cca gga gag tat caa tac atc cat cct	384
Leu Ile Tyr Leu Gly Lys Lys Pro Gly Glu Tyr Gln Tyr Ile His Pro	
115 120 125	
ata gac cat gtt aat atg tca caa tcg aca aat gat gtc tac cca acc	432
Ile Asp His Val Asn Met Ser Gln Ser Thr Asn Asp Val Tyr Pro Thr	
130 135 140	
gct ttg agg att gca aca ata tgg aat gtg aga gaa ctt tct gaa gag	480
Ala Leu Arg Ile Ala Thr Ile Trp Asn Val Arg Glu Leu Ser Glu Glu	
145 150 155 160	
tgt gca gaa ctc caa aaa agc ttg caa aaa aaa gag cat gag ttt gaa	528
Cys Ala Glu Leu Gln Lys Ser Leu Gln Lys Lys Glu His Glu Phe Glu	
165 170 175	
ggg gta att aag gct ggg cgc act caa ctt caa gat gcc ctt ccc atc	576
Gly Val Ile Lys Ala Gly Arg Thr Gln Leu Gln Asp Ala Leu Pro Ile	
180 185 190	
acc tta ggg caa gag ttt ggg gcg tat gca cag gcg ata tca cgc gat	624
Thr Leu Gly Gln Glu Phe Gly Ala Tyr Ala Gln Ala Ile Ser Arg Asp	
195 200 205	
aga tgg cga ata tat aaa att gaa aga tta aga gtg gta aac ttg	672
Arg Trp Arg Ile Tyr Lys Ile Glu Glu Arg Leu Arg Val Val Asn Leu	
210 215 220	
ggc gca aca gct gtt gga aca gga gtg aat gca agc tta aaa tat atg	720
Gly Ala Thr Ala Val Gly Thr Gly Val Asn Ala Ser Leu Lys Tyr Met	

PF59083SeqList PF59083.txt

225	230	235	240	
ttt aaa gtg ata gaa ctt ttg cgc gat ttt act aaa ata ggc ttg gct				768
Phe Lys Val Ile Glu Leu Leu Arg Asp Phe Thr Lys Ile Gly Leu Ala				
	245	250	255	
cgg tct gat tac ctc atg gat gca aca caa aat gca gat gta ttt gtg				816
Arg Ser Asp Tyr Leu Met Asp Ala Thr Gln Asn Ala Asp Val Phe Val				
	260	265	270	
gaa tgc tcg ggt ctt tta aaa gcc ttg gcg gtg aat cta tca aaa att				864
Glu Cys Ser Gly Leu Leu Lys Ala Leu Ala Val Asn Leu Ser Lys Ile				
	275	280	285	
gca aat gac tta agg ctc tta tca tct ggt cca aac acg ggt tta aac				912
Ala Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Asn Thr Gly Leu Asn				
	290	295	300	
gag ata aac tta cct gct gca caa gca ggt tca agc att atg cct ggt				960
Glu Ile Asn Leu Pro Ala Ala Gln Ala Gly Ser Ile Met Pro Gly				
	305	310	315	
aaa gta aat cct gtc ata cct gaa ctt ata aac acc ata tca ttc cag				1008
Lys Val Asn Pro Val Ile Pro Glu Leu Ile Asn Thr Ile Ser Phe Gln				
	325	330	335	
gtt atg tca aat gat gtt gca ata acc tta gca gcc caa gca ggt cag				1056
Val Met Ser Asn Asp Val Ala Ile Thr Leu Ala Ala Gln Ala Gly Gln				
	340	345	350	
ctt gag cta aat gca ttc ttg cct tta att gca aac aat ttg ctt gaa				1104
Leu Glu Leu Asn Ala Phe Leu Pro Leu Ile Ala Asn Asn Leu Leu Glu				
	355	360	365	
agc ctc aaa att ctc aaa aac gga atc agg ata ttc aga aaa cag tgc				1152
Ser Leu Lys Ile Leu Lys Asn Gly Ile Arg Ile Phe Arg Lys Gln Cys				
	370	375	380	
att gat gga ata aca gca aac aaa gaa aga tgt ctt gag ttt gcc aaa				1200
Ile Asp Gly Ile Thr Ala Asn Lys Glu Arg Cys Leu Glu Phe Ala Lys				
	385	390	400	
aag act cct tct att gcc gct gca ttg att gat aaa ata ggg tat gac				1248
Lys Thr Pro Ser Ile Ala Ala Ala Leu Ile Asp Lys Ile Gly Tyr Asp				
	405	410	415	
aag gca agt gaa att gct aaa aaa gcc att gcc gag aat aag gaa ata				1296
Lys Ala Ser Glu Ile Ala Lys Lys Ala Ile Ala Glu Asn Lys Glu Ile				
	420	425	430	
att gag gtg gta aag gaa ttg aag atc tta aat gag aat gag gct gaa				1344
Ile Glu Val Val Lys Glu Leu Lys Ile Leu Asn Glu Asn Glu Ala Glu				
	435	440	445	
gca cta cta aat cct ttt gaa ttt gta aag ttt aaa gag taa				1386
Ala Leu Leu Asn Pro Phe Glu Phe Val Lys Phe Lys Glu				
	450	455	460	

<210> 9568

<211> 461

<212> PRT

<213> Thermoanaerobacter tengcongensis MB4

<400> 9568

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

PF59083SeqList PF59083.txt

```

145          150          155          160
Cys Ala Glu Leu Gln Lys Ser Leu Gln Lys Lys Glu His Glu Phe Glu
Gly Val Ile Lys Ala Gly Arg Thr Gln Leu Gln Asp Ala Leu Pro Ile
Thr Leu Gly Gln Glu Phe Gly Ala Tyr Ala Gln Ala Ile Ser Arg Asp
Arg Trp Arg Ile Tyr Lys Ile Glu Glu Arg Leu Arg Val Val Asn Leu
Gly Ala Thr Ala Val Gly Thr Gly Val Asn Ala Ser Leu Lys Tyr Met
Phe Lys Val Ile Glu Leu Leu Arg Asp Phe Thr Lys Ile Gly Leu Ala
Arg Ser Asp Tyr Leu Met Asp Ala Thr Gln Asn Ala Asp Val Phe Val
Glu Cys Ser Gly Leu Leu Lys Ala Leu Ala Val Asn Leu Ser Lys Ile
Ala Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Asn Thr Gly Leu Asn
Glu Ile Asn Leu Pro Ala Ala Gln Ala Gly Ser Ser Ile Met Pro Gly
Lys Val Asn Pro Val Ile Pro Glu Leu Ile Asn Thr Ile Ser Phe Gln
Val Met Ser Asn Asp Val Ala Ile Thr Leu Ala Ala Gln Ala Gly Gln
Leu Glu Leu Asn Ala Phe Leu Pro Leu Ile Ala Asn Asn Leu Leu Glu
Ser Leu Lys Ile Leu Lys Asn Gly Ile Arg Ile Phe Arg Lys Gln Cys
Ile Asp Gly Ile Thr Ala Asn Lys Glu Arg Cys Leu Glu Phe Ala Lys
Lys Thr Pro Ser Ile Ala Ala Ala Leu Ile Asp Lys Ile Gly Tyr Asp
Lys Ala Ser Glu Ile Ala Lys Lys Ala Ile Ala Glu Asn Lys Glu Ile
Ile Glu Val Val Lys Glu Leu Lys Ile Leu Asn Glu Asn Glu Ala Glu
Ala Leu Leu Asn Pro Phe Glu Phe Val Lys Phe Lys Glu
450          455          460

```

<210> 9569

<211> 1413

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1413)

<400> 9569

```

atg agc tcc acc aag aag gtt gag acc cgc caa gag agc gac acc ctg      48
Met Ser Ser Thr Lys Lys Val Glu Thr Arg Gln Glu Ser Asp Thr Leu
1      5      10      15
gga ccc atg gag gtg ccc atg gat cgc tat tac ggc gcc cag acg atg      96
Gly Pro Met Glu Val Pro Met Asp Arg Tyr Tyr Gly Ala Gln Thr Met
20      25      30
cgc tgc ctc ata aac ttt cgc att ggc ggc gag gag gag cga atg ccg      144
Arg Cys Leu Ile Asn Phe Arg Ile Gly Gly Glu Glu Glu Arg Met Pro
35      40      45
cgc cag ata atc cag gcc atg ggc ata ctg aag aag gcg gca gcc gaa      192
Arg Gln Ile Ile Gln Ala Met Gly Ile Leu Lys Lys Ala Ala Ala Glu
50      55      60
aca aac caa gaa ttc gga ttg gat ccc aag ttg agc acg gcc atc tcg      240
Thr Asn Gln Glu Phe Gly Leu Asp Pro Lys Ser Thr Ala Ile Ser
65      70      75      80
aat gcg gcc gac gat gtg atc tcc gga aag ctt tac gat gag ggt cac      288
Asn Ala Ala Asp Asp Val Ile Ser Gly Lys Leu Tyr Asp Glu Gly His
85      90      95
ttc ccg ctg ccc att tgg cag acg ggt tcg ggc acc cag agc aac atg      336

```

PF59083SeqList PF59083.txt

Phe	Pro	Leu	Pro	Ile	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	
100								105						110		
aac	agc	aac	gag	gtt	atc	ggg	aat	cgt	gcc	atc	gag	ctg	ctg	ggc	gga	384
Asn	Ser	Asn	Glu	Val	Ile	Gly	Asn	Arg	Ala	Ile	Glu	Leu	Leu	Gly	Gly	
115							120					125				
cgt	att	ggg	acc	aag	gac	cca	gtg	cat	ccc	aac	gac	cat	gtg	aac	aag	432
Arg	Ile	Gly	Thr	Lys	Asp	Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	Lys	
130						135					140					
tcg	cag	agc	tcc	aac	gac	acc	ttt	ccg	tcg	gcc	att	cac	att	gcg	gtg	480
Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Ser	Ala	Ile	His	Ile	Ala	Val	
145					150					155					160	
gcc	act	gcg	ctg	acc	aag	gat	ctc	cga	ccg	gcg	gtc	acc	gct	ctg	cgg	528
Ala	Thr	Ala	Leu	Thr	Lys	Asp	Leu	Arg	Pro	Ala	Val	Thr	Ala	Leu	Arg	
			165					170						175		
gat	tca	ctg	cag	gcc	aag	tcg	aat	gaa	tgg	aag	gat	atc	att	aag	att	576
Asp	Ser	Leu	Gln	Ala	Lys	Ser	Asn	Glu	Trp	Lys	Asp	Ile	Ile	Lys	Ile	
			180					185						190		
gga	cg	act	cac	acc	cag	gat	gca	gtg	ccg	cta	acg	ctg	ggc	cag	gag	624
Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Val	Pro	Leu	Thr	Leu	Gly	Gln	Glu	
		195				200						205				
ttc	agt	ggc	tat	gcc	caa	cag	ctg	acc	aac	ggg	ctg	cag	agg	atc	gat	672
Phe	Ser	Gly	Tyr	Ala	Gln	Gln	Leu	Thr	Asn	Gly	Leu	Gln	Arg	Ile	Asp	
210					215						220					
gcg	gtc	ctg	ccg	cga	gtt	tat	cag	ctc	gca	ctg	ggt	gga	acc	gct	gtg	720
Ala	Val	Leu	Pro	Arg	Val	Tyr	Gln	Leu	Ala	Leu	Gly	Gly	Thr	Ala	Val	
225					230					235					240	
gga	act	gga	ttg	aat	acc	cg	cg	gga	ttc	gcc	gag	aag	tgt	gtc	aag	768
Gly	Thr	Gly	Leu	Asn	Thr	Arg	Arg	Gly	Phe	Ala	Glu	Lys	Cys	Val	Lys	
			245					250						255		
cg	atc	gcc	cag	ctc	agt	gga	ttg	ccc	ttc	gtg	gtg	gcg	ccc	aat	ttt	816
Arg	Ile	Ala	Gln	Leu	Ser	Gly	Leu	Pro	Phe	Val	Val	Ala	Pro	Asn	Phe	
			260					265						270		
ttc	gag	gcc	ctc	gcc	tgt	cga	gat	gcc	atg	gtg	gag	gtg	cat	gga	gcg	864
Phe	Glu	Ala	Leu	Ala	Cys	Arg	Asp	Ala	Met	Val	Glu	Val	His	Gly	Ala	
		275					280					285				
ctc	aat	gtc	ctg	gct	gtt	agc	ctg	atg	aag	gtc	acc	aat	gat	ata	cgt	912
Leu	Asn	Val	Leu	Ala	Val	Ser	Leu	Met	Lys	Val	Thr	Asn	Asp	Ile	Arg	
		290				295					300					
ttc	ctg	gga	tcg	gga	cca	cgt	tgc	ggg	ctg	ggc	gag	ctg	ttt	ctg	ccg	960
Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Phe	Leu	Pro	
305					310					315					320	
gag	aat	gag	ccg	ggc	agt	tct	att	atg	ccc	ggc	aag	gtg	aat	ccc	acg	1008
Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	
			325					330						335		
cag	tgc	gag	gcc	atg	acc	atg	atc	tgc	gcc	cag	gtg	atg	ggc	aac	cac	1056
Gln	Cys	Glu	Ala	Met	Thr	Met	Ile	Cys	Ala	Gln	Val	Met	Gly	Asn	His	
			340					345					350			
gtg	gcc	gtc	tcc	gtc	ggc	ggt	gcc	aat	gga	cac	ttt	gag	ctc	aac	gtt	1104
Val	Ala	Val	Ser	Val	Gly	Gly	Ala	Asn	Gly	His	Phe	Glu	Leu	Asn	Val	
		355					360					365				
ttc	aag	cca	ctg	atc	gca	tcc	aat	gtg	ctc	cg	tcc	atc	aag	ctg	ctg	1152
Phe	Lys	Pro	Leu	Ile	Ala	Ser	Asn	Val	Leu	Arg	Ser	Ile	Lys	Leu	Leu	
		370				375					380					
gct	gat	ggg	tgc	atc	agc	ttc	aac	tgc	aac	tgc	gtc	aag	ggc	att	aag	1200
Ala	Asp	Gly	Cys	Ile	Ser	Phe	Asn	Cys	Asn	Cys	Val	Lys	Gly	Ile	Lys	
			385		390					395					400	
ccc	aac	aag	gag	aag	ctg	gca	aag	atc	gtg	aat	gag	tcg	cta	atg	ctg	1248
Pro	Asn	Lys	Glu	Lys	Leu	Ala	Lys	Ile	Val	Asn	Glu	Ser	Leu	Met	Leu	
			405					410						415		
gtg	aca	gcc	ctc	aat	ccg	cac	att	ggc	tat	gac	aag	tcc	gcc	cag	att	1296
Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	Asp	Lys	Ser	Ala	Gln	Ile	
			420					425					430			
gcc	aag	gcg	gcc	cac	aag	aat	gga	act	act	cta	aag	gtg	gag	gca	ttg	1344
Ala	Lys	Ala	Ala	His	Lys	Asn	Gly	Thr	Thr	Leu	Lys	Val	Glu	Ala	Leu	
		435					440					445				
aac	gcc	ggc	ata	tcg	gag	aag	gat	ttc	aac	gag	tgg	gtg	cg	ccc	gag	1392
Asn	Ala	Gly	Ile	Ser	Glu	Lys	Asp	Phe	Asn	Glu	Trp	Val	Arg	Pro	Glu	
		450				455					460					
aag	atg	ctg	ggt	cct	tct	tag										1413

PF59083SeqList PF59083.txt

Lys Met Leu Gly Pro Ser
465 470

<210> 9570

<211> 470

<212> PRT

<213> Drosophila melanogaster

<400> 9570

Met	Ser	Ser	Thr	Lys	Lys	Val	Glu	Thr	Arg	Gln	Glu	Ser	Asp	Thr	Leu
1				5					10					15	
Gly	Pro	Met	Glu	Val	Pro	Met	Asp	Arg	Tyr	Tyr	Gly	Ala	Gln	Thr	Met
			20					25					30		
Arg	Cys	Leu	Ile	Asn	Phe	Arg	Ile	Gly	Gly	Glu	Glu	Glu	Arg	Met	Pro
		35					40					45			
Arg	Gln	Ile	Ile	Gln	Ala	Met	Gly	Ile	Leu	Lys	Lys	Ala	Ala	Ala	Glu
	50					55					60				
Thr	Asn	Gln	Glu	Phe	Gly	Leu	Asp	Pro	Lys	Leu	Ser	Thr	Ala	Ile	Ser
65					70					75					80
Asn	Ala	Ala	Asp	Asp	Val	Ile	Ser	Gly	Lys	Leu	Tyr	Asp	Glu	Gly	His
				85					90					95	
Phe	Pro	Leu	Pro	Ile	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met
			100					105					110		
Asn	Ser	Asn	Glu	Val	Ile	Gly	Asn	Arg	Ala	Ile	Glu	Leu	Leu	Gly	Gly
		115					120					125			
Arg	Ile	Gly	Thr	Lys	Asp	Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	Lys
	130					135					140				
Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Ser	Ala	Ile	His	Ile	Ala	Val
145					150					155					160
Ala	Thr	Ala	Leu	Thr	Lys	Asp	Leu	Arg	Pro	Ala	Val	Thr	Ala	Leu	Arg
			165					170						175	
Asp	Ser	Leu	Gln	Ala	Lys	Ser	Asn	Glu	Trp	Lys	Asp	Ile	Ile	Lys	Ile
		180						185					190		
Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Val	Pro	Leu	Thr	Leu	Gly	Gln	Glu
		195					200					205			
Phe	Ser	Gly	Tyr	Ala	Gln	Gln	Leu	Thr	Asn	Gly	Leu	Gln	Arg	Ile	Asp
	210					215					220				
Ala	Val	Leu	Pro	Arg	Val	Tyr	Gln	Leu	Ala	Leu	Gly	Gly	Thr	Ala	Val
225					230					235					240
Gly	Thr	Gly	Leu	Asn	Thr	Arg	Arg	Gly	Phe	Ala	Glu	Lys	Cys	Val	Lys
				245					250					255	
Arg	Ile	Ala	Gln	Leu	Ser	Gly	Leu	Pro	Phe	Val	Val	Ala	Pro	Asn	Phe
		260						265					270		
Phe	Glu	Ala	Leu	Ala	Cys	Arg	Asp	Ala	Met	Val	Glu	Val	His	Gly	Ala
		275					280					285			
Leu	Asn	Val	Leu	Ala	Val	Ser	Leu	Met	Lys	Val	Thr	Asn	Asp	Ile	Arg
	290					295					300				
Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Phe	Leu	Pro
305					310					315					320
Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr
				325					330					335	
Gln	Cys	Glu	Ala	Met	Thr	Met	Ile	Cys	Ala	Gln	Val	Met	Gly	Asn	His
			340					345					350		
Val	Ala	Val	Ser	Val	Gly	Gly	Ala	Asn	Gly	His	Phe	Glu	Leu	Asn	Val
		355					360					365			
Phe	Lys	Pro	Leu	Ile	Ala	Ser	Asn	Val	Leu	Arg	Ser	Ile	Lys	Leu	Leu
	370					375					380				
Ala	Asp	Gly	Cys	Ile	Ser	Phe	Asn	Cys	Asn	Cys	Val	Lys	Gly	Ile	Lys
385					390					395					400
Pro	Asn	Lys	Glu	Lys	Leu	Ala	Lys	Ile	Val	Asn	Glu	Ser	Leu	Met	Leu
				405					410					415	
Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	Asp	Lys	Ser	Ala	Gln	Ile
		420						425					430		
Ala	Lys	Ala	Ala	His	Lys	Asn	Gly	Thr	Thr	Leu	Lys	Val	Glu	Ala	Leu
		435					440					445			
Asn	Ala	Gly	Ile	Ser	Glu	Lys	Asp	Phe	Asn	Glu	Trp	Val	Arg	Pro	Glu
	450					455					460				
Lys	Met	Leu	Gly	Pro	Ser										
465					470										

PF59083SeqList PF59083.txt

<210> 9571
 <211> 1437
 <212> DNA
 <213> Yersinia pestis KIM

<220>
 <221> CDS
 <222> (1)..(1437)
 <223> transl_table=11

```

<400> 9571
atg tca aat aac att cgt att gaa gaa gac ctg tta ggt aca cga gaa      48
Met Ser Asn Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Thr Arg Glu
 1      5      10
gtc ccc gca gag gct tac tac ggt gtt cat acc ctg cgt gcg att gaa      96
Val Pro Ala Glu Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Ile Glu
 20      25      30
aac ttc tat atc agt aac agt aaa atc agt gac gtg ccg gaa ttt gta      144
Asn Phe Tyr Ile Ser Asn Ser Lys Ile Ser Asp Val Pro Glu Phe Val
 35      40      45
cgt ggc atg gtc atg gta aaa aaa gcg gcg gca atg gct aac aaa gag      192
Arg Gly Met Val Met Val Lys Lys Ala Ala Ala Met Ala Asn Lys Glu
 50      55      60
ttg cat acc atc ccg cgt aaa att gca gac atc att att cag gca tgt      240
Leu His Thr Ile Pro Arg Lys Ile Ala Asp Ile Ile Ile Gln Ala Cys
 65      70      75
gat gaa gtt ctg gat aaa ggg aaa tgt atg gat cag ttc ccc gtt gat      288
Asp Glu Val Leu Asp Lys Gly Lys Cys Met Asp Gln Phe Pro Val Asp
 85      90      95
gtg ttc cag ggc ggc gca ggt acc tct ctc aat atg aac acc aac gag      336
Val Phe Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr Asn Glu
100      105      110
gtc ttg gcc aat att ggc ctg gag ctg atg ggc cac caa aaa ggg gaa      384
Val Leu Ala Asn Ile Gly Leu Leu Met Gly His Gln Lys Gly Glu
115      120      125
tat cag tac ctt aac cct aac gac cat ctg aac aaa tgc cag tcc acc      432
Tyr Gln Tyr Leu Asn Pro Asn Asp His Leu Asn Lys Cys Gln Ser Thr
130      135      140
aac tat gcc tac cca acc ggt ttc cgc att gcg gtc tac gcc tcc atc      480
Asn Tyr Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Ala Ser Ile
145      150      155
ctc aag ttg atc gat gct atc aac caa tta ggc gaa ggt ttc ggt aga      528
Leu Lys Leu Ile Asp Ala Ile Asn Gln Leu Gly Glu Gly Phe Gly Arg
165      170      175
aaa tct aaa gaa ttc gag aaa att ctg aaa atg ggc cgt acc caa tta      576
Lys Ser Lys Glu Phe Glu Lys Ile Leu Lys Met Gly Arg Thr Gln Leu
180      185      190
cag gat gcc gta ccc atg act ctg ggc cag gaa ttc cgc gct ttc cag      624
Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Arg Ala Phe Gln
195      200      205
gtg tta ttg aat gaa gaa acc aag aac ctg caa cgg acc gcc gag ttg      672
Val Leu Leu Asn Glu Glu Thr Lys Asn Leu Gln Arg Thr Ala Glu Leu
210      215      220
cta ttg gaa gtc aac ctg ggt gcc act gcc atc ggc act gcg ctg aat      720
Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Ala Leu Asn
225      230      235
aca cca gaa ggt tat tca caa ctt gcc gtg cag aaa ctg gca gaa atc      768
Thr Pro Glu Gly Tyr Ser Gln Leu Ala Val Gln Lys Leu Ala Glu Ile
245      250      255
agc gga tta gcc tgt gtt cct gcc gaa gat ttg atc gaa gcg acc tct      816
Ser Gly Leu Ala Cys Val Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser
260      265      270
gat tgc ggc gct tac gtg atg gta cac agc gcc ctg aaa cgc ctg gct      864
Asp Cys Gly Ala Tyr Val Met Val His Ser Ala Leu Lys Arg Leu Ala
275      280      285
gtt aag atg tca aaa atc tgt aac gac cta cgt ttg ctc tca tct ggc      912
Val Lys Met Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly
290      295      300
    
```

PF59083SeqList PF59083.txt

cca	cgt	act	ggg	ttg	aat	gaa	atc	aac	ctg	cca	gaa	ttg	cag	gcg	ggc	960
Pro	Arg	Thr	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	Ala	Gly	
305					310					315					320	
tct	tct	atc	atg	cct	gca	aaa	gtg	aac	ccg	gtg	atc	cct	gaa	gtt	gta	1008
Ser	Ser	Ile	Met		Ala	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	
				325					330					335		
aat	cag	gtt	tgt	ttt	aag	gtg	atc	ggc	aac	gat	act	tgc	att	act	atg	1056
Asn	Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Cys	Ile	Thr	Met	
			340					345					350			
gcg	gct	gaa	gcg	ggg	cag	ctt	cag	tta	aac	ttg	atg	gaa	ccg	gta	att	1104
Ala	Ala		Ala	Gly	Gln	Leu	Gln	Leu	Asn	Leu	Met	Glu	Pro	Val	Ile	
		355					360						365			
ggg	cag	gcc	atg	ttt	gag	tct	atc	cat	atc	ctg	act	aat	gcg	tgt	tac	1152
Gly	Gln	Ala	Met	Phe	Glu	Ser	Ile	His	Ile	Leu	Thr	Asn	Ala	Cys	Tyr	
		370				375					380					
aac	ctg	tta	gag	aag	tgc	aat	ggc	att	acc	gct	aac	aaa	gag	gtc		1200
Asn	Leu	Leu	Glu	Lys	Cys	Ile	Asn	Gly	Ile	Thr	Ala	Asn	Lys	Glu	Val	
385					390				395					400		
tgc	gag	cg	tac	gtc	ttt	aac	tcc	ata	ggc	atc	gtc	act	tat	ctt	aac	1248
Cys	Glu	Arg	Tyr	Val	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	
			405					410						415		
ccg	ttc	att	ggc	cac	cat	aat	ggg	gac	att	gtg	ggg	aaa	atc	tgt	gcg	1296
Pro	Phe	Ile	Gly	His	His	Asn	Gly	Asp	Ile	Val	Gly	Lys	Ile	Cys	Ala	
			420					425					430			
gaa	acc	ggg	aaa	aat	gtg	cgg	gaa	gtg	gtt	ctg	gag	cg	ggg	ttg	tta	1344
Glu	Thr		Lys	Asn	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gly	Leu	Leu	
		435				440						445				
act	gaa	gcc	gaa	ctg	gac	gac	att	ttc	tct	gtt	gaa	aac	ctg	atg	cac	1392
Thr	Glu	Ala	Glu	Leu	Asp	Asp	Ile	Phe	Ser	Val	Glu	Asn	Leu	Met	His	
		450				455					460					
cca	gcc	tat	aaa	gcg	aaa	cgt	tat	acc	gat	gaa	aat	gaa	caa	taa		1437
Pro	Ala	Tyr	Lys	Ala	Lys	Arg	Tyr	Thr	Asp	Glu	Asn	Glu	Gln			
465					470					475						

<210> 9572

<211> 478

<212> PRT

<213> Yersinia pestis KIM

<400> 9572

Met	Ser	Asn	Asn	Ile	Arg	Ile	Glu	Glu	Asp	Leu	Leu	Gly	Thr	Arg	Glu	
1				5					10					15		
Val	Pro	Ala	Glu	Ala	Tyr	Tyr	Gly	Val	His	Thr	Leu	Arg	Ala	Ile	Glu	
			20					25					30			
Asn	Phe	Tyr	Ile	Ser	Asn	Ser	Lys	Ile	Ser	Asp	Val	Pro	Glu	Phe	Val	
		35					40					45				
Arg	Gly	Met	Val	Met	Val	Lys	Lys	Ala	Ala	Ala	Met	Ala	Asn	Lys	Glu	
		50				55					60					
Leu	His	Thr	Ile	Pro	Arg	Lys	Ile	Ala	Asp	Ile	Ile	Ile	Gln	Ala	Cys	
65					70				75						80	
Asp	Glu	Val	Leu	Asp	Lys	Gly	Lys	Cys	Met	Asp	Gln	Phe	Pro	Val	Asp	
				85					90					95		
Val	Phe	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Leu	Asn	Met	Asn	Thr	Asn	Glu	
			100					105					110			
Val	Leu	Ala	Asn	Ile	Gly	Leu	Glu	Leu	Met	Gly	His	Gln	Lys	Gly	Glu	
		115					120					125				
Tyr	Gln	Tyr	Leu	Asn	Pro	Asn	Asp	His	Leu	Asn	Lys	Cys	Gln	Ser	Thr	
		130				135					140					
Asn	Tyr	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Ile	Ala	Val	Tyr	Ala	Ser	Ile	
145					150					155					160	
Leu	Lys	Leu	Ile	Asp	Ala	Ile	Asn	Gln	Leu	Gly	Glu	Gly	Phe	Gly	Arg	
				165					170					175		
Lys	Ser	Lys	Glu	Phe	Glu	Lys	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	
			180					185					190			
Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Arg	Ala	Phe	Gln	
		195					200					205				
Val	Leu	Leu	Asn	Glu	Glu	Thr	Lys	Asn	Leu	Gln	Arg	Thr	Ala	Glu	Leu	
		210				215					220					
Leu	Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Ala	Leu	Asn	

PF59083SeqList PF59083.txt

```

225      230      235      240
Thr Pro Glu Gly Tyr Ser Gln Leu Ala Val Gln Lys Leu Ala Glu Ile
      245      250      255
Ser Gly Leu Ala Cys Val Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser
      260      265      270
Asp Cys Gly Ala Tyr Val Met Val His Ser Ala Leu Lys Arg Leu Ala
      275      280      285
Val Lys Met Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly
      290      295      300
Pro Arg Thr Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly
305      310      315
Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val
      320      325      330
Asn Gln Val Cys Phe Lys Val Ile Gly Asn Asp Thr Cys Ile Thr Met
      335      340      345
Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Leu Met Glu Pro Val Ile
      350      355      360
Gly Gln Ala Met Phe Glu Ser Ile His Ile Leu Thr Asn Ala Cys Tyr
      365      370      375
Asn Leu Leu Glu Lys Cys Ile Asn Gly Ile Thr Ala Asn Lys Glu Val
385      390      395
Cys Glu Arg Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn
      400      405      410
Pro Phe Ile Gly His His Asn Gly Asp Ile Val Gly Lys Ile Cys Ala
      415      420      425
Glu Thr Gly Lys Asn Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu
      430      435      440
Thr Glu Ala Glu Leu Asp Asp Ile Phe Ser Val Glu Asn Leu Met His
      445      450      455
Pro Ala Tyr Lys Ala Lys Arg Tyr Thr Asp Glu Asn Glu Gln
465      470      475

```

<210> 9573

<211> 1452

<212> DNA

<213> Brucella suis 1330

<220>

<221> CDS

<222> (1)..(1452)

<223> transl_table=11

<400> 9573

```

atg aca acc ctg gaa aat att cat ccc ctg aca cgg cgc gag cag gat      48
Met Thr Thr Leu Glu Asn Ile His Pro Leu Thr Arg Arg Glu Gln Asp
1      5      10      15
tcc ctt ggg gag cgc gat att ccc acg gat gcc tat ttc ggc atc cag      96
Ser Leu Gly Glu Arg Asp Ile Pro Thr Asp Ala Tyr Phe Gly Ile Gln
      20      25      30
acc cta cgg gca gtt gaa aac ttc tcg ctt tcc gat gtt gcg ctg aac      144
Thr Leu Arg Ala Val Glu Asn Phe Ser Leu Ser Asp Val Ala Leu Asn
      35      40      45
cat att cct gcc ctg gtt cgc gcc ctt gca atg gtc aag aaa gcg gct      192
His Ile Pro Ala Leu Val Arg Ala Leu Ala Met Val Lys Lys Ala Ala
      50      55      60
gcc acc gcc aat tac aag ctg cgg cag ctg ccg gag ccc aaa tat gcg      240
Ala Thr Ala Asn Tyr Lys Leu Arg Gln Leu Pro Glu Pro Lys Tyr Ala
      65      70      75
gcc atc gtc gcc gcc tgc gac gac atc att gac ggg ctt ttg atg gag      288
Ala Ile Val Ala Ala Cys Asp Asp Ile Ile Asp Gly Leu Leu Met Glu
      80      85      90
caa ttc gtc gtg gat gtg ttt cag ggc ggc gcg ggc acc tca agc aat      336
Gln Phe Val Val Asp Val Phe Gln Gly Gly Ala Gly Thr Ser Ser Asn
      100      105      110
atg aac gca aat gag gtt atc gca aac cgc gcc ctt gaa cat ctg ggg      384
Met Asn Ala Asn Glu Val Ile Ala Asn Arg Ala Leu Glu His Leu Gly
      115      120      125
cgg ccg cga ggc gac tac cag acg atc cat ccc aat gat gac gtc aac      432
Arg Pro Arg Gly Asp Tyr Gln Thr Ile His Pro Asn Asp Asp Val Asn

```

PF59083SeqList PF59083.txt																	
130	atg	tcg	cag	tcc	acc	aat	gat	gtg	tat	cca	acc	gcg	gta	agg	ctg	gcg	480
	Met	Ser	Gln	Ser	Thr	Asn	Asp	Val	Tyr	Pro	Thr	Ala	Val	Arg	Leu	Ala	
145	ctt	ctt	ctc	agc	cag	aac	cag	gtt	cag	acg	gcg	ctg	cac	cgg	ctg	att	528
	Leu	Leu	Leu	Ser	Gln	Asn	Gln	Val	Gln	Thr	Ala	Leu	His	Arg	Leu	Ile	
					165				170								
	gcc	gcc	ttt	gaa	gca	aag	ggg	cgg	gaa	ttc	gcg	acg	gtc	atc	aag	atc	576
	Ala	Ala	Phe	Glu	Ala	Lys	Gly	Arg	Glu	Phe	Ala	Thr	Val	Ile	Lys	Ile	
				180					185								
	ggg	cgc	aca	cag	ttg	cag	gat	gcg	gtt	ccg	atc	act	ctt	gga	cag	gag	624
	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	Ile	Thr	Leu	Gly	Gln	Glu	
			195					200					205				
	ttc	gag	gca	ttt	gcc	gca	acg	ttg	cgg	gag	gac	aca	gcc	cgg	ctg	gag	672
	Phe	Glu	Ala	Phe	Ala	Ala	Thr	Leu	Arg	Glu	Asp	Thr	Ala	Arg	Leu	Glu	
							215					220					
	gag	gtt	gcc	gcg	ctt	ttc	cgc	gaa	gta	aac	ctc	ggt	gga	acc	gct	atc	720
	Glu	Val	Ala	Ala	Leu	Phe	Arg	Glu	Val	Asn	Leu	Gly	Gly	Thr	Ala	Ile	
	225					230					235					240	
	ggc	acg	cgc	atc	aac	gcc	tcg	cac	gcc	tat	gcc	gaa	cag	gcc	atc	gcg	768
	Gly	Thr	Arg	Ile	Asn	Ala	Ser	His	Ala	Tyr	Ala	Glu	Gln	Ala	Ile	Ala	
					245					250					255		
	gaa	ctt	tcg	cag	att	tcc	ggt	atc	gaa	ctg	aaa	gcc	gcc	ggc	aat	ctc	816
	Glu	Leu	Ser	Gln	Ile	Ser	Gly	Ile	Glu	Leu	Lys	Ala	Ala	Gly	Asn	Leu	
			260					265						270			
	gtg	gaa	gcg	agc	tggt	gat	acc	ggt	gcg	ttc	gtc	acc	ttt	tcc	ggg	ata	864
	Val	Glu	Ala	Ser	Trp	Asp	Thr	Gly	Ala	Phe	Val	Thr	Phe	Ser	Gly	Ile	
			275					280					285				
	ttg	cgc	cgg	atc	gca	gtc	aag	ctt	tcc	aag	atc	gcc	aac	gat	ctg	cgg	912
	Leu	Arg	Arg	Ile	Ala	Val	Lys	Leu	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	
			290				295					300					
	cta	ctc	tca	agc	ggg	ccg	cga	agc	ggc	ctt	ggt	gaa	atc	cgc	ctg	cct	960
	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Ser	Gly	Leu	Gly	Glu	Ile	Arg	Leu	Pro	
	305					310					315					320	
	gcg	gtt	cag	ccg	gga	tcg	tcg	atc	atg	ccg	gga	aag	gtc	aat	ccg	gtc	1008
	Ala	Val	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	
					325					330					335		
	ata	ccg	gaa	tcg	gtc	aat	cag	gtc	tcg	tat	cag	gtg	atc	ggc	aat	gac	1056
	Ile	Pro	Glu	Ser	Val	Asn	Gln	Val	Cys	Tyr	Gln	Val	Ile	Gly	Asn	Asp	
				340				345						350			
	ctg	act	gta	acc	atg	gca	gcc	gaa	agc	ggg	caa	ttg	cag	ctc	aac	gcg	1104
	Leu	Thr	Val	Thr	Met	Ala	Ala	Glu	Ser	Gly	Gln	Leu	Gln	Leu	Asn	Ala	
							360					365					
	ttc	gag	ccg	ctg	atc	gtc	tac	aat	atc	ctc	agt	tcc	atg	cga	ctg	ctc	1152
	Phe	Glu	Pro	Leu	Ile	Val	Tyr	Asn	Ile	Leu	Ser	Ser	Met	Arg	Leu	Leu	
							375					380					
	ggc	cgc	gcc	atg	acc	aat	ctg	gcc	gaa	cgt	tcg	gtc	gac	gga	att	gaa	1200
	Gly	Arg	Ala	Met	Thr	Asn	Leu	Ala	Glu	Arg	Cys	Val	Asp	Gly	Ile	Glu	
	385					390					395					400	
	gcc	aat	gtg	gaa	cgc	tgt	cgc	gca	ggc	gcg	gag	gaa	agc	att	tcg	ctt	1248
	Ala	Asn	Val	Glu	Arg	Cys	Arg	Ala	Gly	Ala	Glu	Glu	Ser	Ile	Ser	Leu	
					405				410						415		
	gca	acc	gcc	ctc	gtc	ccg	gtc	gtg	ggc	tat	gcc	agg	gcg	gca	gag	atc	1296
	Ala	Thr	Ala	Leu	Val	Pro	Val	Val	Gly	Tyr	Ala	Arg	Ala	Ala	Glu	Ile	
					420			425						430			
	gcc	aag	cag	gcg	ctt	gcc	tca	ggg	cag	acc	gtc	atg	gaa	gtg	gcg	att	1344
	Ala	Lys	Gln	Ala	Leu	Ala	Ser	Gly	Gln	Thr	Val	Met	Glu	Val	Ala	Ile	
								440					445				
	tcc	aag	ggg	ctg	gac	gca	tct	gcg	ctc	acg	ata	atg	ctt	gac	ccc	ttg	1392
	Ser	Lys	Gly	Leu	Asp	Ala	Ser	Ala	Leu	Thr	Ile	Met	Leu	Asp	Pro	Leu	
							455					460					
	aga	atg	gca	ttc	ccg	ccg	gaa	acg	cac	gac	aag	gag	gca	cat	cat	gca	1440
	Arg	Met	Ala	Phe	Pro	Pro	Glu	Thr	His	Asp	Lys	Glu	Ala	His	His	Ala	
	465					470					475					480	
	tct	gtc	ggc	taa													1452
	Ser	Val	Gly														

PF59083SeqList PF59083.txt

<211> 483

<212> PRT

<213> Brucella suis 1330

<400> 9574

```

Met Thr Thr Leu Glu Asn Ile His Pro Leu Thr Arg Arg Glu Gln Asp
1      5      10      15
Ser Leu Gly Glu Arg Asp Ile Pro Thr Asp Ala Tyr Phe Gly Ile Gln
      20      25      30
Thr Leu Arg Ala Val Glu Asn Phe Ser Leu Ser Asp Val Ala Leu Asn
      35      40      45
His Ile Pro Ala Leu Val Arg Ala Leu Ala Met Val Lys Lys Ala Ala
      50      55      60
Ala Thr Ala Asn Tyr Lys Leu Arg Gln Leu Pro Glu Pro Lys Tyr Ala
65      70      75      80
Ala Ile Val Ala Ala Cys Asp Asp Ile Ile Asp Gly Leu Leu Met Glu
      85      90      95
Gln Phe Val Val Asp Val Phe Gln Gly Gly Ala Gly Thr Ser Ser Asn
      100      105      110
Met Asn Ala Asn Glu Val Ile Ala Asn Arg Ala Leu Glu His Leu Gly
      115      120      125
Arg Pro Arg Gly Asp Tyr Gln Thr Ile His Pro Asn Asp Asp Val Asn
      130      135      140
Met Ser Gln Ser Thr Asn Asp Val Tyr Pro Thr Ala Val Arg Leu Ala
145      150      155      160
Leu Leu Leu Ser Gln Asn Gln Val Gln Thr Ala Leu His Arg Leu Ile
      165      170      175
Ala Ala Phe Glu Ala Lys Gly Arg Glu Phe Ala Thr Val Ile Lys Ile
      180      185      190
Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Ile Thr Leu Gly Gln Glu
      195      200      205
Phe Glu Ala Phe Ala Ala Thr Leu Arg Glu Asp Thr Ala Arg Leu Glu
      210      215      220
Glu Val Ala Ala Leu Phe Arg Glu Val Asn Leu Gly Gly Thr Ala Ile
225      230      235      240
Gly Thr Arg Ile Asn Ala Ser His Ala Tyr Ala Glu Gln Ala Ile Ala
      245      250      255
Glu Leu Ser Gln Ile Ser Gly Ile Glu Leu Lys Ala Ala Gly Asn Leu
      260      265      270
Val Glu Ala Ser Trp Asp Thr Gly Ala Phe Val Thr Phe Ser Gly Ile
      275      280      285
Leu Arg Arg Ile Ala Val Lys Leu Ser Lys Ile Ala Asn Asp Leu Arg
      290      295      300
Leu Leu Ser Ser Gly Pro Arg Ser Gly Leu Gly Glu Ile Arg Leu Pro
305      310      315      320
Ala Val Gln Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val
      325      330      335
Ile Pro Glu Ser Val Asn Gln Val Cys Tyr Gln Val Ile Gly Asn Asp
      340      345      350
Leu Thr Val Thr Met Ala Ala Glu Ser Gly Gln Leu Gln Leu Asn Ala
      355      360      365
Phe Glu Pro Leu Ile Val Tyr Asn Ile Leu Ser Ser Met Arg Leu Leu
      370      375      380
Gly Arg Ala Met Thr Asn Leu Ala Glu Arg Cys Val Asp Gly Ile Glu
385      390      395      400
Ala Asn Val Glu Arg Cys Arg Ala Gly Ala Glu Glu Ser Ile Ser Leu
      405      410      415
Ala Thr Ala Leu Val Pro Val Val Gly Tyr Ala Arg Ala Ala Glu Ile
      420      425      430
Ala Lys Gln Ala Leu Ala Ser Gly Gln Thr Val Met Glu Val Ala Ile
      435      440      445
Ser Lys Gly Leu Asp Ala Ser Ala Leu Thr Ile Met Leu Asp Pro Leu
      450      455      460
Arg Met Ala Phe Pro Pro Glu Thr His Asp Lys Glu Ala His His Ala
465      470      475      480
Ser Val Gly

```

<210> 9575

PF59083SeqList PF59083.txt

<211> 1455
<212> DNA
<213> Drosophila melanogaster

<220>
<221> CDS
<222> (1)..(1455)

```

<400> 9575
atg tct ttc gat cag aag gag att ttc agt ttg atg tac aaa ctg gct      48
Met Ser Phe Asp Gln Lys Glu Ile Phe Ser Leu Met Tyr Lys Leu Ala
1      5      10      15
cgg cta ata gtg ccg gat act cga gtt gaa tat gat tcg atg ggt gcc      96
Arg Leu Ile Val Pro Asp Thr Arg Val Glu Tyr Asp Ser Met Gly Ala
20      25      30
gtg cac att cct ctc gat cga atg ttc ggt ccg caa acc atg aga tcc      144
Val His Ile Pro Leu Asp Arg Met Phe Gly Pro Gln Thr Met Arg Ser
35      40      45
ctg atg aaa ttt cca att ggc gga gtt gag gaa cga atg cca cga ccc      192
Leu Met Lys Phe Pro Ile Gly Gly Val Glu Glu Arg Met Pro Arg Pro
50      55      60
cta ata aaa gcc ctg ggc ata gtg aag aaa tca gct gcg gag acg aac      240
Leu Ile Lys Ala Leu Gly Ile Val Lys Lys Ser Ala Ala Glu Thr Asn
65      70      75      80
aaa atc cat tgt ctg gag gag cat cta tgc gat gcc att tcc aag gcc      288
Lys Ile His Cys Leu Glu Glu His Leu Cys Asp Ala Ile Ser Lys Ala
85      90      95
tgc gat gat gtt ata tcg ggc aaa ctc tat gac gag gaa cac ttt ccg      336
Cys Asp Asp Val Ile Ser Gly Lys Leu Tyr Asp Glu Glu His Phe Pro
100      105      110
ttg gtt ata tgg cag gat gga agc ggc gag cac aca aac atg aac gta      384
Leu Val Ile Trp Gln Asp Gly Ser Gly Glu His Thr Asn Met Asn Val
115      120      125
aac gag gtt ata tgc aat cga gcc atc gaa att ctg ggc ggt cag atg      432
Asn Glu Val Ile Cys Asn Arg Ala Ile Glu Ile Leu Gly Gly Gln Met
130      135      140
ggc tcc aag gag ccg gtg gat ccc aat gaa cat gtc aac atg gcg caa      480
Gly Ser Lys Glu Pro Val Asp Pro Asn Glu His Val Asn Met Ala Gln
145      150      155      160
agt tcc cat gac acc ttc tcg aca gcc gtg gcg atc gcc gtg gcc atg      528
Ser Ser His Asp Thr Phe Ser Thr Ala Val Arg Ile Ala Val Ala Met
165      170      175
cag ttg cag gag acg ctg tat ccc agc tta agg acc ttt att gat ttg      576
Gln Leu Gln Glu Thr Leu Tyr Pro Ser Leu Arg Thr Phe Ile Asp Leu
180      185      190
ctg ggc aag aag tcg aac gat tgg atg gat ttg atc aag att ggt aga      624
Leu Gly Lys Lys Ser Asn Asp Trp Met Asp Leu Ile Lys Ile Gly Arg
195      200      205
acg cat ctg atg gac gca gtt cct ctg tcc ctc ggc cag gag ttc agt      672
Thr His Leu Met Asp Ala Val Pro Leu Ser Leu Gly Gln Glu Phe Ser
210      215      220
ggc tat cag cag caa ctt gtg aac gga agg acg cga ttg gac tgt gcc      720
Gly Tyr Gln Gln Gln Leu Val Asn Gly Arg Thr Arg Leu Asp Cys Ala
225      230      235      240
atg tgc cga ttg tat cag ttg ccc atg ggc ggc acc agt gtg gcc acc      768
Met Cys Arg Leu Tyr Gln Leu Pro Met Gly Gly Thr Ser Val Gly Thr
245      250      255
aaa gtg gac acc aag gcg gaa tat tct gcg cag tgc atc aag cgt ata      816
Lys Val Asp Thr Lys Ala Glu Tyr Ser Ala Gln Cys Ile Lys Arg Ile
260      265      270
gcc gag cta aca ttc cta ccc ttt gtc gag tcc ccg aac ttt ttt gaa      864
Ala Glu Leu Thr Phe Leu Pro Phe Val Glu Ser Pro Asn Phe Phe Glu
275      280      285
tcc atc tcc gcc tgc gat tgc ctg gtg gaa ctg cac ggt gaa ctc aac      912
Ser Ile Ser Ala Cys Asp Cys Leu Val Glu Leu His Gly Glu Leu Asn
290      295      300
acg att gca gcg agt gtg atg aag ata gcg aat gat ata cga ttc ctt      960
Thr Ile Ala Ala Ser Val Met Lys Ile Ala Asn Asp Ile Arg Phe Leu
305      310      315      320

```

PF59083SeqList PF59083.txt

gga	tcg	gga	cca	cgt	tgc	gga	ttt	ggg	gaa	cta	cat	ctg	ccg	gag	aac	1008
Gly	Ser	Gly	Pro	Arg	Cys	Gly	Phe	Gly	Glu	Leu	His	Leu	Pro	Glu	Asn	
				325					330					335		
gaa	cca	ggg	agt	tcc	ata	atg	ccc	ggc	aaa	gtg	aat	ccc	acg	caa	tgc	1056
Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	
			340					345					350			
gag	gcc	atg	tcc	atg	atc	tgt	gcc	cag	gtg	atg	ggc	aac	cat	gtg	gcc	1104
Glu	Ala	Met	Ser	Met	Ile	Cys	Ala	Gln	Val	Met	Gly	Asn	His	Val	Ala	
		355					360					365				
gtc	tcc	atg	ggg	ggg	tcc	tct	ggc	cac	ttt	cag	ctg	aac	acc	ttt	atg	1152
Val	Ser	Met	Gly	Gly	Ser	Ser	Gly	His	Phe	Gln	Leu	Asn	Thr	Phe	Met	
	370					375					380					
ccc	atg	att	gcc	tcc	aat	gtt	ttg	cgc	tcg	att	aca	ctt	ttg	ggc	gat	1200
Pro	Met	Ile	Ala	Ser	Asn	Val	Leu	Arg	Ser	Ile	Thr	Leu	Leu	Gly	Asp	
385					390					395					400	
ggc	atg	aag	tcc	ttt	tgc	acc	aat	tgc	ctc	gag	ggc	atc	gag	ccc	aat	1248
Gly	Met	Lys	Ser	Phe	Cys	Thr	Asn	Cys	Leu	Glu	Gly	Ile	Glu	Pro	Asn	
			405					410						415		
agg	agc	aag	att	ggg	agc	atc	gtc	aag	gag	tcc	ctg	atg	ctg	gtc	act	1296
Arg	Ser	Lys	Ile	Gly	Ser	Ile	Val	Lys	Glu	Ser	Leu	Met	Leu	Val	Thr	
			420					425					430			
gcc	ctc	agt	cca	cac	att	ggc	tac	gaa	cga	tcc	gct	gcg	atc	gcc	aag	1344
Ala	Leu	Ser	Pro	His	Ile	Gly	Tyr	Glu	Arg	Ser	Ala	Ala	Ile	Ala	Lys	
		435				440					445					
gca	gcg	cat	cac	aat	gga	acc	act	ttg	gaa	cag	gag	gcc	ata	ctt	gat	1392
Ala	Ala	His	His	Asn	Gly	Thr	Thr	Leu	Glu	Gln	Glu	Ala	Ile	Leu	Asp	
	450				455						460					
ggc	att	caa	cgg	gag	gac	ttc	agg	gag	tgg	gtg	cag	ccc	agc	aag	atg	1440
Gly	Ile	Gln	Arg	Glu	Asp	Phe	Arg	Glu	Trp	Val	Gln	Pro	Ser	Lys	Met	
465				470					475					480		
ctg	ggg	ccc	gaa	tag												1455
Leu	Gly	Pro	Glu													

<210> 9576

<211> 484

<212> PRT

<213> Drosophila melanogaster

<400> 9576

Met	Ser	Phe	Asp	Gln	Lys	Glu	Ile	Phe	Ser	Leu	Met	Tyr	Lys	Leu	Ala	
1				5					10					15		
Arg	Leu	Ile	Val	Pro	Asp	Thr	Arg	Val	Glu	Tyr	Asp	Ser	Met	Gly	Ala	
			20					25					30			
Val	His	Ile	Pro	Leu	Asp	Arg	Met	Phe	Gly	Pro	Gln	Thr	Met	Arg	Ser	
		35					40					45				
Leu	Met	Lys	Phe	Pro	Ile	Gly	Gly	Val	Glu	Glu	Arg	Met	Pro	Arg	Pro	
	50					55					60					
Leu	Ile	Lys	Ala	Leu	Gly	Ile	Val	Lys	Lys	Ser	Ala	Ala	Glu	Thr	Asn	
65					70					75					80	
Lys	Ile	His	Cys	Leu	Glu	Glu	His	Leu	Cys	Asp	Ala	Ile	Ser	Lys	Ala	
			85						90					95		
Cys	Asp	Asp	Val	Ile	Ser	Gly	Lys	Leu	Tyr	Asp	Glu	Glu	His	Phe	Pro	
			100					105					110			
Leu	Val	Ile	Trp	Gln	Asp	Gly	Ser	Gly	Glu	His	Thr	Asn	Met	Asn	Val	
		115					120					125				
Asn	Glu	Val	Ile	Cys	Asn	Arg	Ala	Ile	Glu	Ile	Leu	Gly	Gly	Gln	Met	
	130					135					140					
Gly	Ser	Lys	Glu	Pro	Val	Asp	Pro	Asn	Glu	His	Val	Asn	Met	Ala	Gln	
145					150					155					160	
Ser	Ser	His	Asp	Thr	Phe	Ser	Thr	Ala	Val	Arg	Ile	Ala	Val	Ala	Met	
			165					170						175		
Gln	Leu	Gln	Glu	Thr	Leu	Tyr	Pro	Ser	Leu	Arg	Thr	Phe	Ile	Asp	Leu	
		180						185					190			
Leu	Gly	Lys	Lys	Ser	Asn	Asp	Trp	Met	Asp	Leu	Ile	Lys	Ile	Gly	Arg	
		195					200					205				
Thr	His	Leu	Met	Asp	Ala	Val	Pro	Leu	Ser	Leu	Gly	Gln	Glu	Phe	Ser	
	210					215					220					
Gly	Tyr	Gln	Gln	Gln	Leu	Val	Asn	Gly	Arg	Thr	Arg	Leu	Asp	Cys	Ala	

PF59083SeqList PF59083.txt

225	Met	Cys	Arg	Leu	Tyr	230	Gln	Leu	Pro	Met	Gly	235	Gly	Thr	Ser	Val	Gly	240	Thr
	Lys	Val	Asp	Thr	Lys	245	Ala	Glu	Tyr	Ser	250	Ala	Gln	Cys	Ile	Lys	255	Arg	Ile
	Ala	Glu	Leu	Thr	Phe	260	Leu	Pro	Phe	265	Val	Glu	Ser	Pro	Asn	270	Phe	Phe	Glu
	Ser	Ile	Ser	Ala	Cys	275	Asp	Cys	Leu	Val	Glu	Leu	His	Gly	Glu	285	Leu	Asn	
	Thr	Ile	Ala	Ala	Ser	290	Val	Met	Lys	Ile	Ala	Asn	300	Ile	Arg	Phe	Leu		
305	Gly	Ser	Gly	Pro	Arg	310	Cys	Gly	Phe	Gly	Glu	Leu	His	Leu	Pro	Glu	Asn		
	Glu	Pro	Gly	Ser	Ser	325	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys		
	Glu	Ala	Met	Ser	Met	340	Ile	Cys	Ala	Gln	Val	Met	Gly	Asn	His	Val	Ala		
	Val	Ser	Met	Gly	Gly	355	Ser	Ser	Gly	His	Phe	Gln	Leu	Asn	Thr	Phe	Met		
	Pro	Met	Ile	Ala	Ser	370	Val	Leu	Arg	Ser	Ile	Thr	Leu	Leu	Gly	Asp			
385	Gly	Met	Lys	Ser	Phe	390	Cys	Thr	Asn	Cys	Leu	Glu	Gly	Ile	Glu	Pro	Asn		
	Arg	Ser	Lys	Ile	Gly	405	Ser	Ile	Val	Lys	Glu	Ser	Leu	Met	Val	Thr			
	Ala	Leu	Ser	Pro	His	420	Ile	Gly	Tyr	Glu	Arg	Ser	Ala	Ala	Ile	Ala	Lys		
	Ala	Ala	His	His	Asn	435	Gly	Thr	Thr	Leu	Glu	Gln	Glu	Ala	Ile	Leu	Asp		
	Gly	Ile	Gln	Arg	Glu	450	Phe	Arg	Glu	Trp	Val	Gln	Pro	Ser	Lys	Met			
465	Leu	Gly	Pro	Glu		470													

<210> 9577

<211> 1404

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1404)

<400> 9577

atg gcc tcc cag gag ttt cgc gtg gag agc gac acc ttt ggc gaa ctg	48
Met Ala Ser Gln Glu Phe Arg Val Glu Ser Asp Thr Phe Gly Glu Leu	
1 5 10 15	
aag gtg ccc gcg gat aag tac tat ggc gcc caa acg atg cga tcc cag	96
Lys Val Pro Ala Asp Lys Tyr Tyr Gly Ala Gln Thr Met Arg Ser Gln	
20 25 30	
atc aat ttc ccc atc ggc gga gcc acc gaa cgg atg ccc aaa ccc gtg	144
Ile Asn Phe Pro Ile Gly Gly Ala Thr Glu Arg Met Pro Lys Pro Val	
35 40 45	
gtc cag gcc atg ggc atc ctg aag aag gcc gcc gcc gag gtg aac aag	192
Val Gln Ala Met Gly Ile Leu Lys Lys Ala Ala Ala Glu Val Asn Lys	
50 55 60	
gag ttc gga ctg gac agc aag gtt agc gag gcg atc tcg aag gcg gcc	240
Glu Phe Gly Leu Asp Ser Lys Val Ser Glu Ala Ile Ser Lys Ala Ala	
65 70 75 80	
gac gat gtg atc tct ggc aag cta tac gac gac cac ttc ccg ctg gtc	288
Asp Asp Val Ile Ser Gly Lys Leu Tyr Asp Asp His Phe Pro Leu Val	
85 90 95	
atc tgg cag acg ggc tgc ggc acg cag agc aac atg aat gtg aat gag	336
Ile Trp Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Val Asn Glu	
100 105 110	
gtg atc agc aat cgt gcc att gag ctg ctg ggc ggc aaa ctg ggc tcc	384
Val Ile Ser Asn Arg Ala Ile Glu Leu Leu Gly Gly Lys Leu Gly Ser	
115 120 125	
aag acg ccc gtg cat ccc aac gat cat gtg aac aaa tcg cag agc tcc	432

PF59083SeqList PF59083.txt

Lys	Thr	Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	Lys	Ser	Gln	Ser	Ser	
130	130					135					140					
aac	gat	acc	ttc	ccc	acc	gcc	att	cac	atc	tcg	gtg	gcg	ctg	gag	ctg	480
Asn	Asp	Thr	Phe	Pro	Thr	Ala	Ile	His	Ile	Ser	Val	Ala	Leu	Glu	Leu	
145					150					155					160	
aac	aac	aac	ctt	aag	ccg	gcg	att	aag	acg	ctg	cac	gat	gcg	ctg	cgt	528
Asn	Asn	Asn	Leu	Lys	Pro	Ala	Ile	Lys	Thr	Leu	His	Asp	Ala	Leu	Arg	
			165				170							175		
gcc	aag	tcg	gag	gag	ttc	aag	gac	att	atc	aag	atc	gga	cgc	acg	cat	576
Ala	Lys	Ser	Glu	Glu	Phe	Lys	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	
			180				185						190			
acg	atg	gat	gcg	gtg	cca	ttg	acg	ctg	ggc	caa	gag	ttc	agc	ggc	tat	624
Thr	Met	Asp	Ala	Val	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	
			195				200					205				
gcc	cag	caa	ttg	gcc	tac	gcc	cag	gag	cgc	atc	gat	gcc	tgt	ctg	ccg	672
Ala	Gln	Leu	Ala	Tyr	Ala	Gln	Glu	Arg	Ile	Asp	Ala	Cys	Leu	Pro		
	210				215						220					
cgc	gtc	tat	gag	ctg	gct	ctg	ggc	ggc	act	gct	gtg	ggg	acg	ggg	ctg	720
Arg	Val	Tyr	Glu	Leu	Ala	Leu	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	
225					230					235					240	
aac	aca	cgc	aag	gga	ttc	gcc	gag	aag	tgc	gct	gca	aag	atc	gcc	gag	768
Asn	Thr	Arg	Lys	Gly	Phe	Ala	Glu	Lys	Cys	Ala	Ala	Lys	Ile	Ala	Glu	
			245						250					255		
ctg	acc	agc	ctg	ccc	ttc	gtt	acc	gcg	ccc	aac	aag	ttc	gag	gca	ctg	816
Leu	Thr	Ser	Leu	Pro	Phe	Val	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	
			260				265						270			
gct	gcc	cgc	gat	gcc	atg	gtg	gag	gtg	cat	ggg	gtg	ctc	aac	acg	atc	864
Ala	Ala	Arg	Asp	Ala	Met	Val	Glu	Val	His	Gly	Val	Leu	Asn	Thr	Ile	
			275				280					285				
gcc	gtt	agc	ctg	atg	aag	att	gcc	aac	gat	att	cgt	ttc	ctt	ggc	tcc	912
Ala	Val	Ser	Leu	Met	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	
	290					295					300					
gga	ccg	cgt	tgc	ggt	ttg	ggt	gag	ctc	tcg	cta	ccg	gag	aac	gag	cca	960
Gly	Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	
305					310					315					320	
ggg	agc	tcc	atc	atg	ccc	ggc	aag	gtg	aat	ccc	acg	caa	tgc	gag	tcg	1008
Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ser	
			325						330					335		
ctg	aca	atg	ctc	tcc	gcc	cag	gtg	atg	ggc	aat	cag	gtg	gcg	gtg	acc	1056
Leu	Thr	Met	Leu	Ser	Ala	Gln	Val	Met	Gly	Asn	Gln	Val	Ala	Val	Thr	
			340				345						350			
atc	ggg	gga	tcc	aat	ggg	cac	ttc	gag	ctg	aat	gta	ttc	aag	ccc	ctg	1104
Ile	Gly	Gly	Ser	Asn	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Leu	
			355				360					365				
atc	gtg	tcc	aat	gtg	ctg	cgc	tcc	att	cgg	cta	ttg	tct	gat	ggc	agc	1152
Ile	Val	Ser	Asn	Val	Leu	Arg	Ser	Ile	Arg	Leu	Leu	Ser	Asp	Gly	Ser	
	370					375					380					
agg	acc	ttc	act	gcc	aac	tgt	gtg	aat	ggc	atc	cag	gcg	aac	cgc	gag	1200
Arg	Thr	Phe	Thr	Ala	Asn	Cys	Val	Asn	Gly	Ile	Gln	Ala	Asn	Arg	Glu	
					390					395					400	
aat	att	gcc	aag	atc	atg	aac	gag	tcg	ctc	atg	ctg	gtg	acc	gct	ctg	1248
Asn	Ile	Ala	Lys	Ile	Met	Asn	Glu	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	
			405						410					415		
aat	ccg	cac	att	ggg	tac	gac	aag	gct	gcg	aaa	att	gca	aag	acg	gcg	1296
Asn	Pro	His	Ile	Gly	Tyr	Asp	Lys	Ala	Ala	Lys	Ile	Ala	Lys	Thr	Ala	
			420				425						430			
cac	aag	aat	ggc	acc	aca	ctc	aag	gag	gag	gcc	atc	aat	ttg	ggg	tac	1344
His	Lys	Asn	Gly	Thr	Thr	Leu	Lys	Glu	Glu	Ala	Ile	Asn	Leu	Gly	Tyr	
			435				440					445				
ctg	acg	gag	cag	cag	ttc	aac	gac	tgg	gtg	cga	ccc	gaa	cag	atg	ctg	1392
Leu	Thr	Glu	Gln	Gln	Phe	Asn	Asp	Trp	Val	Arg	Pro	Glu	Gln	Met	Leu	
	450					455					460					
gga	ccc	aag	tga													1404
Gly	Pro	Lys														
465																

<210> 9578

<211> 467

<212> PRT

<213> Drosophila melanogaster

<400> 9578

Met Ala Ser Gln Glu Phe Arg Val Glu Ser Asp Thr Phe Gly Glu Leu
 1 5 10 15
 Lys Val Pro Ala Asp Lys Tyr Tyr Gly Ala Gln Thr Met Arg Ser Gln
 20 25 30
 Ile Asn Phe Pro Ile Gly Gly Ala Thr Glu Arg Met Pro Lys Pro Val
 35 40 45
 Val Gln Ala Met Gly Ile Leu Lys Lys Ala Ala Glu Val Asn Lys
 50 55 60
 Glu Phe Gly Leu Asp Ser Lys Val Ser Glu Ala Ile Ser Lys Ala Ala
 65 70 75 80
 Asp Asp Val Ile Ser Gly Lys Leu Tyr Asp Asp His Phe Pro Leu Val
 85 90 95
 Ile Trp Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Val Asn Glu
 100 105 110
 Val Ile Ser Asn Arg Ala Ile Glu Leu Leu Gly Gly Lys Leu Gly Ser
 115 120 125
 Lys Thr Pro Val His Pro Asn Asp His Val Asn Lys Ser Gln Ser Ser
 130 135 140
 Asn Asp Thr Phe Pro Thr Ala Ile His Ile Ser Val Ala Leu Glu Leu
 145 150 155 160
 Asn Asn Asn Leu Lys Pro Ala Ile Lys Thr Leu His Asp Ala Leu Arg
 165 170 175
 Ala Lys Ser Glu Glu Phe Lys Asp Ile Ile Lys Ile Gly Arg Thr His
 180 185 190
 Thr Met Asp Ala Val Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr
 195 200 205
 Ala Gln Gln Leu Ala Tyr Ala Gln Glu Arg Ile Asp Ala Cys Leu Pro
 210 215 220
 Arg Val Tyr Glu Leu Ala Leu Gly Gly Thr Ala Val Gly Thr Gly Leu
 225 230 235 240
 Asn Thr Arg Lys Gly Phe Ala Glu Lys Cys Ala Ala Lys Ile Ala Glu
 245 250 255
 Leu Thr Ser Leu Pro Phe Val Thr Ala Pro Asn Lys Phe Glu Ala Leu
 260 265 270
 Ala Ala Arg Asp Ala Met Val Glu Val His Gly Val Leu Asn Thr Ile
 275 280 285
 Ala Val Ser Leu Met Lys Ile Ala Asn Asp Ile Arg Phe Leu Gly Ser
 290 295 300
 Gly Pro Arg Cys Gly Leu Gly Glu Leu Ser Leu Pro Glu Asn Glu Pro
 305 310 315 320
 Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ser
 325 330 335
 Leu Thr Met Leu Ser Ala Gln Val Met Gly Asn Gln Val Ala Val Thr
 340 345 350
 Ile Gly Gly Ser Asn Gly His Phe Glu Leu Asn Val Phe Lys Pro Leu
 355 360 365
 Ile Val Ser Asn Val Leu Arg Ser Ile Arg Leu Leu Ser Asp Gly Ser
 370 375 380
 Arg Thr Phe Thr Ala Asn Cys Val Asn Gly Ile Gln Ala Asn Arg Glu
 385 390 395 400
 Asn Ile Ala Lys Ile Met Asn Glu Ser Leu Met Leu Val Thr Ala Leu
 405 410 415
 Asn Pro His Ile Gly Tyr Asp Lys Ala Ala Lys Ile Ala Lys Thr Ala
 420 425 430
 His Lys Asn Gly Thr Thr Leu Lys Glu Glu Ala Ile Asn Leu Gly Tyr
 435 440 445
 Leu Thr Glu Gln Gln Phe Asn Asp Trp Val Arg Pro Glu Gln Met Leu
 450 455 460
 Gly Pro Lys
 465

<210> 9579

<211> 1512

<212> DNA

<213> Drosophila melanogaster

PF59083SeqList PF59083.txt

<220>

<221> CDS

<222> (1)..(1512)

<400> 9579

atg	ctg	aag	caa	aac	aat	ggt	ctg	cat	ctg	gct	agg	cgc	aat	ctc	tgg	48
Met	Leu	Lys	Gln	Asn	Asn	Gly	Leu	His	Leu	Ala	Arg	Arg	Asn	Leu	Trp	
1				5				10						15		
gtg	gtt	tgc	agt	ggc	ctc	cgt	gcc	aag	gat	tgc	gac	agt	ggc	ggt	aag	96
Val	Val	Cys	Ser	Gly	Leu	Arg	Ala	Lys	Asp	Cys	Asp	Ser	Gly	Gly	Lys	
			20					25					30			
ggc	ggc	aag	ggc	aag	gag	aat	ggc	aag	ttt	cgt	acg	gag	aag	gac	acc	144
Gly	Gly	Lys	Gly	Lys	Glu	Asn	Gly	Lys	Phe	Arg	Thr	Glu	Lys	Asp	Thr	
		35					40					45				
ttc	ggg	gag	cta	aag	gtg	ccg	gcg	gac	aag	ctg	tac	ggc	gca	cag	acg	192
Phe	Gly	Glu	Leu	Lys	Val	Pro	Ala	Asp	Lys	Leu	Tyr	Gly	Ala	Gln	Thr	
	50					55					60					
atg	cgc	tcc	aaa	ttg	aat	ttt	ccc	att	ggc	gac	ata	ggc	gaa	cgt	atg	240
Met	Arg	Ser	Lys	Leu	Asn	Phe	Pro	Ile	Gly	Asp	Ile	Gly	Glu	Arg	Met	
65					70					75					80	
ccg	atg	ccg	gtg	atc	cag	gcc	atg	ggc	ata	ctg	aag	aag	gca	tgt	gcc	288
Pro	Met	Pro	Val	Ile	Gln	Ala	Met	Gly	Ile	Leu	Lys	Lys	Ala	Cys	Ala	
				85				90						95		
gag	gtc	aac	aag	gat	tac	gga	cta	gat	ggc	aag	gtg	tcg	gat	gcc	gta	336
Glu	Val	Asn	Lys	Asp	Tyr	Gly	Leu	Asp	Gly	Lys	Val	Ser	Asp	Ala	Val	
			100					105					110			
tcc	tgc	gcc	tgc	gac	gat	gtc	att	tcc	ggc	aag	cta	tac	aaa	cag	ggt	384
Ser	Cys	Ala	Cys	Asp	Asp	Val	Ile	Ser	Gly	Lys	Leu	Tyr	Lys	Gln	Gly	
		115					120					125				
cac	ttc	cca	ttg	gtc	atc	tgg	caa	acc	ggt	tcg	ggc	acc	cag	acc	aat	432
His	Phe	Pro	Leu	Val	Ile	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Thr	Asn	
	130					135					140					
atg	aac	acc	aac	gag	gtg	atc	agc	aat	gcg	gcc	att	aag	atg	atg	ggc	480
Met	Asn	Thr	Asn	Glu	Val	Ile	Ser	Asn	Ala	Ala	Ile	Lys	Met	Met	Gly	
145				150						155					160	
ggc	gaa	ctg	ggc	agc	aag	aag	ccg	gtg	cat	ccc	aac	gat	cat	gtg	aac	528
Gly	Glu	Leu	Gly	Ser	Lys	Lys	Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	
			165					170						175		
aag	tcg	cag	agc	tcc	aac	gac	acc	ttc	ccc	acg	gcc	att	cac	att	tcg	576
Lys	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Ile	His	Ile	Ser	
			180					185					190			
gtg	ggc	atg	gag	ctg	aac	gag	cgg	ctt	gtt	ccg	gcg	gtt	aca	cac	ttg	624
Val	Gly	Met	Glu	Leu	Asn	Glu	Arg	Leu	Val	Pro	Ala	Val	Thr	His	Leu	
		195					200					205				
agg	gat	gcc	ctc	aag	tcc	aag	tcg	gat	gag	ttc	aag	gac	atc	atc	aag	672
Arg	Asp	Ala	Leu	Lys	Ser	Lys	Ser	Asp	Glu	Phe	Lys	Asp	Ile	Ile	Lys	
	210					215					220					
atc	gga	cgc	acc	cac	ttg	atg	gac	gca	gtt	ccg	ctg	act	ttg	ggc	cag	720
Ile	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Val	Pro	Leu	Thr	Leu	Gly	Gln	
	225				230					235				240		
gaa	ttc	agc	ggt	tat	aca	cag	cag	ttg	acc	aac	ggt	ctg	gaa	agg	atc	768
Glu	Phe	Ser	Gly	Tyr	Thr	Gln	Gln	Leu	Thr	Asn	Gly	Leu	Glu	Arg	Ile	
			245					250						255		
aag	ggc	tgt	ctg	ccg	cgc	gtc	tat	gag	ctg	gct	ctg	ggc	ggc	act	gct	816
Lys	Gly	Cys	Leu	Pro	Arg	Val	Tyr	Glu	Leu	Ala	Leu	Gly	Gly	Thr	Ala	
			260				265						270			
gtg	ggt	acg	ggt	ctg	aac	aca	cgc	aag	gga	ttc	gcc	gag	aag	gtg	gcc	864
Val	Gly	Thr	Gly	Leu	Asn	Thr	Arg	Lys	Gly	Phe	Ala	Glu	Lys	Val	Ala	
		275					280					285				
aag	cgc	att	tcg	gag	cta	acc	tgc	ttg	ccc	ttc	gtg	tcg	gcg	ccc	aac	912
Lys	Arg	Ile	Ser	Glu	Leu	Thr	Cys	Leu	Pro	Phe	Val	Ser	Ala	Pro	Asn	
	290					295					300					
aag	ttc	gag	gca	ctg	gct	gcc	cgc	gat	gcc	atg	gtg	gag	gtg	cat	ggt	960
Lys	Phe	Glu	Ala	Leu	Ala	Ala	Arg	Asp	Ala	Met	Val	Glu	Val	His	Gly	
	305				310					315					320	
gtg	ctc	aac	acg	atc	gcc	gtc	agc	ctg	atg	aag	atc	gcc	aac	gat	atc	1008
Val	Leu	Asn	Thr	Ile	Ala	Val	Ser	Leu	Met	Lys	Ile	Ala	Asn	Asp	Ile	
			325					330						335		
cga	ttg	ctg	gga	tcg	ggt	ccg	cgt	tgc	ggt	ctg	ggc	gaa	cta	atg	ctg	1056

PF59083SeqList PF59083.txt

Arg	Leu	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Met	Leu	
			340					345					350			
ccg	gag	aac	gag	ccc	ggt	agc	tcc	atc	atg	ccc	ggc	aag	gtg	aat	ccc	1104
Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	
		355					360					365				
acg	caa	tgc	gaa	tca	atg	acc	atg	ctg	tgt	gcc	cag	gtg	atg	ggc	aat	1152
Thr	Gln	Cys	Glu	Ser	Met	Thr	Met	Leu	Cys	Ala	Gln	Val	Met	Gly	Asn	
	370					375					380					
cag	gtg	gcg	gtg	acc	atc	ggc	ggc	tcc	aac	ggg	cac	ttc	gag	cta	aat	1200
Gln	Val	Ala	Val	Thr	Ile	Gly	Gly	Ser	Asn	Gly	His	Phe	Glu	Leu	Asn	
	385				390					395					400	
gta	ttc	aaa	ccc	ctg	gtc	gtg	tcc	aat	gtg	ctg	cgc	tcc	att	cgc	ttg	1248
Val	Phe	Lys	Pro	Leu	Val	Val	Ser	Asn	Val	Leu	Arg	Ser	Ile	Arg	Leu	
			405					410						415		
ttg	gct	gat	ggc	agc	atg	acc	ttc	agc	aag	aac	tgc	gtg	gag	gga	ctg	1296
Leu	Ala	Asp	Gly	Ser	Met	Thr	Phe	Ser	Lys	Asn	Cys	Val	Glu	Gly	Leu	
			420				425						430			
cag	gcc	aac	aag	gag	agg	atc	gac	aag	atc	atg	aac	gag	tcc	ttg	atg	1344
Gln	Ala	Asn	Lys	Glu	Arg	Ile	Asp	Lys	Ile	Met	Asn	Glu	Ser	Leu	Met	
		435					440					445				
ctg	gtg	acc	gcg	ctg	aat	ccg	cac	att	ggc	tat	gac	aag	gcc	gcc	ctg	1392
Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	Asp	Lys	Ala	Ala	Leu	
	450					455					460					
atc	gcc	aag	acg	gcg	cac	aag	aat	aag	acg	acc	ttg	aag	gag	gag	gca	1440
Ile	Ala	Lys	Thr	Ala	His	Lys	Asn	Lys	Thr	Leu	Lys	Glu	Glu	Glu	Ala	
	465				470				475						480	
ctg	aag	acc	gga	att	acc	gaa	gag	cag	ttc	aag	gag	tgg	gtc	aat	ccc	1488
Leu	Lys	Thr	Gly	Ile	Thr	Glu	Glu	Gln	Phe	Lys	Glu	Trp	Val	Asn	Pro	
			485					490						495		
aag	gag	atg	ctg	gga	ccg	aag	tga									1512
Lys	Glu	Met	Leu	Gly	Pro	Lys										
			500													

<210> 9580

<211> 503

<212> PRT

<213> Drosophila melanogaster

<400> 9580

Met	Leu	Lys	Gln	Asn	Asn	Gly	Leu	His	Leu	Ala	Arg	Arg	Asn	Leu	Trp	
1				5					10					15		
Val	Val	Cys	Ser	Gly	Leu	Arg	Ala	Lys	Asp	Cys	Asp	Ser	Gly	Gly	Lys	
			20					25					30			
Gly	Gly	Lys	Gly	Lys	Glu	Asn	Gly	Lys	Phe	Arg	Thr	Glu	Lys	Asp	Thr	
		35					40					45				
Phe	Gly	Glu	Leu	Lys	Val	Pro	Ala	Asp	Lys	Leu	Tyr	Gly	Ala	Gln	Thr	
	50					55				60						
Met	Arg	Ser	Lys	Leu	Asn	Phe	Pro	Ile	Gly	Asp	Ile	Gly	Glu	Arg	Met	
65					70				75					80		
Pro	Met	Pro	Val	Ile	Gln	Ala	Met	Gly	Ile	Leu	Lys	Lys	Ala	Cys	Ala	
			85					90						95		
Glu	Val	Asn	Lys	Asp	Tyr	Gly	Leu	Asp	Gly	Lys	Val	Ser	Asp	Ala	Val	
		100						105				110				
Ser	Cys	Ala	Cys	Asp	Asp	Val	Ile	Ser	Gly	Lys	Leu	Tyr	Lys	Gln	Gly	
		115				120						125				
His	Phe	Pro	Leu	Val	Ile	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Thr	Asn	
	130				135						140					
Met	Asn	Thr	Asn	Glu	Val	Ile	Ser	Asn	Ala	Ala	Ile	Lys	Met	Met	Gly	
145					150				155					160		
Gly	Glu	Leu	Gly	Ser	Lys	Lys	Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	
			165					170						175		
Lys	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Ile	His	Ile	Ser	
		180						185					190			
Val	Gly	Met	Glu	Leu	Asn	Glu	Arg	Leu	Val	Pro	Ala	Val	Thr	His	Leu	
		195					200					205				
Arg	Asp	Ala	Leu	Lys	Ser	Lys	Ser	Asp	Glu	Phe	Lys	Asp	Ile	Ile	Lys	
	210					215					220					
Ile	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Val	Pro	Leu	Thr	Leu	Gly	Gln	
225					230					235					240	

PF59083SeqList PF59083.txt

Glu Phe Ser Gly Tyr Thr Gln Gln Leu Thr Asn Gly Leu Glu Arg Ile
 245 250 255
 Lys Gly Cys Leu Pro Arg Val Tyr Glu Leu Ala Leu Gly Gly Thr Ala
 260 265 270
 Val Gly Thr Gly Leu Asn Thr Arg Lys Gly Phe Ala Glu Lys Val Ala
 275 280 285
 Lys Arg Ile Ser Glu Leu Thr Cys Leu Pro Phe Val Ser Ala Pro Asn
 290 295 300
 Lys Phe Glu Ala Leu Ala Ala Arg Asp Ala Met Val Glu Val His Gly
 305 310 315 320
 Val Leu Asn Thr Ile Ala Val Ser Leu Met Lys Ile Ala Asn Asp Ile
 325 330 335
 Arg Leu Leu Gly Ser Gly Pro Arg Cys Gly Leu Gly Glu Leu Met Leu
 340 345 350
 Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro
 355 360 365
 Thr Gln Cys Glu Ser Met Thr Met Leu Cys Ala Gln Val Met Gly Asn
 370 375 380
 Gln Val Ala Val Thr Ile Gly Gly Ser Asn Gly His Phe Glu Leu Asn
 385 390 395 400
 Val Phe Lys Pro Leu Val Val Ser Asn Val Leu Arg Ser Ile Arg Leu
 405 410 415
 Leu Ala Asp Gly Ser Met Thr Phe Ser Lys Asn Cys Val Glu Gly Leu
 420 425 430
 Gln Ala Asn Lys Glu Arg Ile Asp Lys Ile Met Asn Glu Ser Leu Met
 435 440 445
 Leu Val Thr Ala Leu Asn Pro His Ile Gly Tyr Asp Lys Ala Ala Leu
 450 455 460
 Ile Ala Lys Thr Ala His Lys Asn Lys Thr Thr Leu Lys Glu Glu Ala
 465 470 475 480
 Leu Lys Thr Gly Ile Thr Glu Glu Gln Phe Lys Glu Trp Val Asn Pro
 485 490 495
 Lys Glu Met Leu Gly Pro Lys
 500

<210> 9581

<211> 1617

<212> DNA

<213> Corynebacterium efficiens YS-314

<220>

<221> CDS

<222> (1)..(1617)

<223> transl_table=11

<400> 9581

atg	tcg	aac	gag	gat	aag	aag	gtg	tcc	gag	gac	acg	tcc	agc	gag	cag	48
Met	Ser	Asn	Glu	Asp	Lys	Lys	Val	Ser	Glu	Asp	Thr	Ser	Ser	Glu	Gln	
1				5				10						15		
gcg	gag	cag	gtg	gac	cag	acg	gac	cag	acc	gga	aac	ccg	gag	gat	tcc	96
Ala	Glu	Gln	Val	Asp	Gln	Thr	Asp	Gln	Thr	Gly	Asn	Pro	Glu	Asp	Ser	
			20					25					30			
gcg	gtg	gac	ggg	gag	gcc	ctg	gtg	acc	acc	acg	gag	acc	acc	tcc	acc	144
Ala	Val	Asp	Gly	Glu	Ala	Leu	Val	Thr	Thr	Thr	Glu	Thr	Thr	Ser	Thr	
			35				40					45				
ggg	gag	aag	acc	gag	gag	gag	aag	gcc	gag	gaa	aac	cgc	agg	aag	atc	192
Gly	Glu	Lys	Thr	Ala	Ala	Ala	Lys	Ala	Ala	Glu	Asn	Arg	Arg	Lys	Ile	
			50				55				60					
aag	agg	aat	ttc	cgt	gtg	gaa	tcc	gac	ctg	ctg	ggg	gag	atg	gag	atc	240
Lys	Arg	Asn	Phe	Arg	Val	Glu	Ser	Asp	Leu	Leu	Gly	Glu	Met	Glu	Ile	
			65			70				75					80	
ccg	gcc	gat	gcc	tac	tac	ggg	gtc	cac	acc	ctg	cgt	gcc	gtg	gag	aac	288
Pro	Ala	Asp	Ala	Tyr	Tyr	Gly	Val	His	Thr	Leu	Arg	Ala	Val	Glu	Asn	
				85					90					95		
ttc	cag	atc	tca	cgc	acc	acc	atc	aac	cac	gtc	ccg	gag	ttc	atc	cgc	336
Phe	Gln	Ile	Ser	Arg	Thr	Thr	Ile	Asn	His	Val	Pro	Glu	Phe	Ile	Arg	
			100					105					110			
ggc	atg	gtg	cag	gtg	aag	aag	gcc	gcc	gcc	ctg	gcc	aac	cgc	cgc	ctg	384
Gly	Met	Val	Gln	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Arg	Arg	Leu	

PF59083SeqList PF59083.txt

115	120	125		
cac acc ctg ccc gcc gac aag gcc aag gcg atc atc tgg gcc tgt gat	432			
His Thr Leu Pro Ala Asp Lys Ala Lys Ala Ile Ile Trp Ala Cys Asp				
130	135	140		
cag atc ctc gtc gag ggc cgc tgc atg gac cag ttc ccg atc gac gtg	480			
Gln Ile Leu Val Glu Gly Arg Cys Met Asp Gln Phe Pro Ile Asp Val				
145	150	155		
ttc cag ggc ggg gcg ggc acc agc acc aac atg aac acc aat gag gtg	528			
Phe Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Thr Asn Glu Val				
165	170	175		
gtg gcc aac ctg gcg ctg gag tac atg ggg tac gag aag gga cgc tac	576			
Val Ala Asn Leu Ala Leu Glu Tyr Met Gly Tyr Glu Lys Gly Arg Tyr				
180	185	190		
gac atc ctg cac ccc atg gat gac gtg aac atg tcc cag tcc acc aat	624			
Asp Ile Leu His Pro Met Asp Asp Val Asn Met Ser Gln Ser Thr Asn				
195	200	205		
gat gcc tat ccc acg ggt ttc cga ctc ggc atc tat gct gcg atg acc	672			
Asp Ala Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr Ala Ala Met Thr				
210	215	220		
aac ctc atc gcg gag atc gaa cag ctc cag gtc gcc ttc cgg gag aag	720			
Asn Leu Ile Ala Glu Ile Glu Gln Leu Gln Val Ala Phe Arg Glu Lys				
225	230	235		
ggc aat gag ttc atc gac atc atc aag atg ggc cgc acc cag ctc cag	768			
Gly Asn Glu Phe Ile Asp Ile Ile Lys Met Gly Arg Thr Gln Leu Gln				
245	250	255		
gat gcg gtg ccg atg agc ctg ggt gag gag ttc cag gcc ttc gcc gcg	816			
Asp Ala Val Pro Met Ser Leu Gly Glu Glu Phe Gln Ala Phe Ala Ala				
260	265	270		
aac ctg gcc gag gaa cag tcc gtg ctg cgc gcc tcc atg gac cgt ctc	864			
Asn Leu Ala Glu Glu Gln Ser Val Leu Arg Ala Ser Met Asp Arg Leu				
275	280	285		
ctc gag gtc aac ctc ggt gcc acc gcc atc ggt acc ggc gtg aac acc	912			
Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Val Asn Thr				
290	295	300		
ccg gcc gga tac ccg cac cag gtg gtc gcc tcc ctc gag gtc acc	960			
Pro Ala Gly Tyr Arg His Gln Val Val Ala Ser Leu Ser Glu Val Thr				
305	310	315		
ggc ctg gag atc aaa tcc gcc cgt gat ctc atc gag gcc acc tcg gac	1008			
Gly Leu Glu Ile Lys Ser Ala Arg Asp Leu Ile Glu Ala Thr Ser Asp				
325	330	335		
acc ggt gcc tac gtc ctg gcg cat tcc gcg gtc aag cgt gca gcc atg	1056			
Thr Gly Ala Tyr Val Leu Ala His Ser Ala Val Lys Arg Ala Ala Met				
340	345	350		
aaa ctg tcc aag atc tgc aac gat ctg cgc ctg ctg tcc tcc ggc ccg	1104			
Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro				
355	360	365		
cgc gcc gga ctc aac gag atc aac ctc ccg ccg cgt cag gcc gga tcc	1152			
Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg Gln Ala Gly Ser				
370	375	380		
tcc atc atg ccg gcg aag gtc aac ccg gtc atc ccc gag gtg gtc aac	1200			
Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn				
385	390	395		
cag gtc tgc ttc aag gtc ttc ggc aat gac ctc acc gtg gcc atg gcc	1248			
Gln Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr Val Ala Met Ala				
405	410	415		
gcc gag gcc ggt cag ctg cag ctc aat gtg atg gaa ccg gtc atc ggg	1296			
Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly				
420	425	430		
gag tcg ctg ttc cag tcg atc cgt atc ctg ggc aat gcg agc aag acc	1344			
Glu Ser Leu Phe Gln Ser Ile Arg Ile Leu Gly Asn Ala Ser Lys Thr				
435	440	445		
ctg cgg gag aag tgc gtg gtg ggc atc acc gcg aat gcg gat gtc tgc	1392			
Leu Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn Ala Asp Val Cys				
450	455	460		
cgg tcc tat gtg gag aac tcc atc ggc atc atc acc tac ctc aac ccg	1440			
Arg Ser Tyr Val Glu Asn Ser Ile Gly Ile Ile Thr Tyr Leu Asn Pro				
465	470	475		
ttt ttg ggc cat gac atc ggt gat gcc atc ggt aag gag gcc gcg gag	1488			
Phe Leu Gly His Asp Ile Gly Asp Ala Ile Gly Lys Glu Ala Ala Glu				

PF59083SeqList PF59083.txt

				485					490					495				
acg	ggc	cgg	tcc	gtc	cgg	gag	ctg	atc	ctg	gag	aag	aac	ctc	atg	gat			1536
Thr	Gly	Arg	Ser	Val	Arg	Glu	Leu	Ile	Leu	Glu	Lys	Asn	Leu	Met	Asp			
			500				505						510					
gcg	gcg	acc	ctg	gat	acc	gtg	tgt	tcc	aag	gag	aac	ctg	atg	cac	ccg			1584
Ala	Ala	Thr	Leu	Asp	Thr	Val	Leu	Ser	Lys	Glu	Asn	Leu	Met	His	Pro			
		515					520					525						
atc	ttc	cgg	ggc	aag	ctg	tac	ctg	gat	cag	tag								1617
Ile	Phe	Arg	Gly	Lys	Leu	Tyr	Leu	Asp	Gln									
	530					535												

<210> 9582

<211> 538

<212> PRT

<213> Corynebacterium efficiens YS-314

<400> 9582

Met	Ser	Asn	Glu	Asp	Lys	Lys	Val	Ser	Glu	Asp	Thr	Ser	Ser	Glu	Gln			
1				5					10					15				
Ala	Glu	Gln	Val	Asp	Gln	Thr	Asp	Gln	Thr	Gly	Asn	Pro	Glu	Asp	Ser			
			20					25					30					
Ala	Val	Asp	Gly	Glu	Ala	Leu	Val	Thr	Thr	Thr	Glu	Thr	Thr	Ser	Thr			
		35				40						45						
Gly	Glu	Lys	Thr	Ala	Ala	Ala	Lys	Ala	Ala	Glu	Asn	Arg	Arg	Lys	Ile			
	50					55					60							
Lys	Arg	Asn	Phe	Arg	Val	Glu	Ser	Asp	Leu	Leu	Gly	Glu	Met	Glu	Ile			
65					70				75						80			
Pro	Ala	Asp	Ala	Tyr	Tyr	Gly	Val	His	Thr	Leu	Arg	Ala	Val	Glu	Asn			
				85				90						95				
Phe	Gln	Ile	Ser	Arg	Thr	Thr	Ile	Asn	His	Val	Pro	Glu	Phe	Ile	Arg			
			100					105					110					
Gly	Met	Val	Gln	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Arg	Arg	Leu			
		115					120					125						
His	Thr	Leu	Pro	Ala	Asp	Lys	Ala	Lys	Ala	Ile	Ile	Trp	Ala	Cys	Asp			
	130					135					140							
Gln	Ile	Leu	Val	Glu	Gly	Arg	Cys	Met	Asp	Gln	Phe	Pro	Ile	Asp	Val			
145					150				155						160			
Phe	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Thr	Asn	Glu	Val			
				165					170					175				
Val	Ala	Asn	Leu	Ala	Leu	Glu	Tyr	Met	Gly	Tyr	Glu	Lys	Gly	Arg	Tyr			
			180					185					190					
Asp	Ile	Leu	His	Pro	Met	Asp	Asp	Val	Asn	Met	Ser	Gln	Ser	Thr	Asn			
		195				200			205									
Asp	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Leu	Gly	Ile	Tyr	Ala	Ala	Met	Thr			
	210				215					220								
Asn	Leu	Ile	Ala	Glu	Ile	Glu	Gln	Leu	Gln	Val	Ala	Phe	Arg	Glu	Lys			
225				230					235						240			
Gly	Asn	Glu	Phe	Ile	Asp	Ile	Ile	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln			
			245					250						255				
Asp	Ala	Val	Pro	Met	Ser	Leu	Gly	Glu	Glu	Phe	Gln	Ala	Phe	Ala	Ala			
			260				265						270					
Asn	Leu	Ala	Glu	Glu	Gln	Ser	Val	Leu	Arg	Ala	Ser	Met	Asp	Arg	Leu			
		275					280					285						
Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Val	Asn	Thr			
	290				295						300							
Pro	Ala	Gly	Tyr	Arg	His	Gln	Val	Val	Ala	Ser	Leu	Ser	Glu	Val	Thr			
305					310					315					320			
Gly	Leu	Glu	Ile	Lys	Ser	Ala	Arg	Asp	Leu	Ile	Glu	Ala	Thr	Ser	Asp			
			325					330						335				
Thr	Gly	Ala	Tyr	Val	Leu	Ala	His	Ser	Ala	Val	Lys	Arg	Ala	Ala	Met			
			340				345						350					
Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro			
		355					360					365						
Arg	Ala	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Pro	Arg	Gln	Ala	Gly	Ser			
	370				375						380							
Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn			
385					390					395					400			
Gln	Val	Cys	Phe	Lys	Val	Phe	Gly	Asn	Asp	Leu	Thr	Val	Ala	Met	Ala			
				405					410					415				

PF59083SeqList PF59083.txt

Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly
 420 425 430
 Glu Ser Leu Phe Gln Ser Ile Arg Ile Leu Gly Asn Ala Ser Lys Thr
 435 440 445
 Leu Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn Ala Asp Val Cys
 450 455 460
 Arg Ser Tyr Val Glu Asn Ser Ile Gly Ile Ile Thr Tyr Leu Asn Pro
 465 470 475 480
 Phe Leu Gly His Asp Ile Gly Asp Ala Ile Gly Lys Glu Ala Ala Glu
 485 490 495
 Thr Gly Arg Ser Val Arg Glu Leu Ile Leu Glu Lys Asn Leu Met Asp
 500 505 510
 Ala Ala Thr Leu Asp Thr Val Leu Ser Lys Glu Asn Leu Met His Pro
 515 520 525
 Ile Phe Arg Gly Lys Leu Tyr Leu Asp Gln
 530 535

<210> 9583

<211> 1380

<212> DNA

<213> Pseudomonas putida KT2440

<220>

<221> CDS

<222> (1)..(1380)

<223> transl_table=11

<400> 9583

atg atg agt gat acc cgt atc gag cgt gac agc atg ggt gag ctg cag	48
Met Met Ser Asp Thr Arg Ile Glu Arg Asp Ser Met Gly Glu Leu Gln	
1 5 10 15	
gtg ccg gcc cag gcc ctc tac ggc gcc cag acc cag cgc gcg gtc gac	96
Val Pro Ala Gln Ala Leu Tyr Gly Ala Gln Thr Gln Arg Ala Val Asp	
20 25 30	
aac ttc ccg atc agc ggc cag cgt atg ccg gcc cag ttc att cgt gcc	144
Asn Phe Pro Ile Ser Gly Gln Arg Met Pro Ala Gln Phe Ile Arg Ala	
35 40 45	
ttg ttg ctg gcc aag gcc gct gcg gcc aag gcc aac gtc gaa ctg gag	192
Leu Leu Leu Ala Lys Ala Ala Ala Lys Ala Asn Val Glu Leu Glu	
50 55 60	
caa ctg tct gcc ggg cag ggc cag gct atc gtc aag gct gtc gag caa	240
Gln Leu Ser Ala Gly Gln Gly Gln Ala Ile Val Lys Ala Val Glu Gln	
65 70 75 80	
ttg ctg gcc gag gac ttc atc cag cac ttc ccg gtg gat gtg ttc cag	288
Leu Leu Ala Glu Asp Phe Ile Gln His Phe Pro Val Asp Val Phe Gln	
85 90 95	
aca ggc tct ggc acc agt tcg aac atg aac gcc aat gag gtg atc gcc	336
Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Ala Asn Glu Val Ile Ala	
100 105 110	
acc ttg gct acc cat gta ctg ggt gag gcg gtc aat gcc aat gac cac	384
Thr Leu Ala Thr His Val Leu Gly Glu Ala Val Asn Ala Asn Asp His	
115 120 125	
gtc aac tgt ggc cag agc agc aat gac atc att ccg acc acc atc cat	432
Val Asn Cys Gly Gln Ser Ser Asn Asp Ile Ile Pro Thr Thr Ile His	
130 135 140	
gtc agc gcc gcg ttg gcc ctg cac gag cag ttg ctg cca gcc ctg gcg	480
Val Ser Ala Ala Leu Ala Leu His Glu Gln Leu Leu Pro Ala Leu Ala	
145 150 155 160	
cac ctg gta cag gtg atc gag gtc aag tcg gca caa gta cat caa tac	528
His Leu Val Gln Val Ile Glu Val Lys Ser Ala Gln Val His Gln Tyr	
165 170 175	
gtg aag acc ggt cgt act cac ctg atg gac gcg atg ccc gtg cgc atg	576
Val Lys Thr Gly Arg Thr His Leu Met Asp Ala Met Pro Val Arg Met	
180 185 190	
agc cag gtg ctg gat ggc tgg gct gcg cag atc aat gct gcc aag tcg	624
Ser Gln Val Leu Asp Gly Trp Ala Ala Gln Ile Asn Ala Ala Lys Ser	
195 200 205	
cac atc gaa ggt gtg ctg ccg cac ttg cag gcg ctg gcc cag ggc gga	672
His Ile Glu Gly Val Leu Pro His Leu Gln Ala Leu Ala Gln Gly Gly	

PF59083SeqList PF59083.txt

210	215	220	
acc gcc gtg ggt acc ggc atc aac gcc cat ccg cag ttc gct gtc ggt			720
Thr Ala Val Gly Thr Gly Ile Asn Ala His Pro Gln Phe Ala Val Gly			
225	230	235	240
ttc gct cgc cag ctc agt ggc ctg acc aag gtc gag ttc acg ccc ggc			768
Phe Ala Arg Gln Leu Ser Gly Leu Thr Lys Val Glu Phe Thr Pro Gly			
245	250	255	
cag aac ctg ttc gca ctg atc ggc tcg cag gac act gcc gtg gct ttg			816
Gln Asn Leu Phe Ala Leu Ile Gly Ser Gln Asp Thr Ala Val Ala Leu			
260	265	270	
tct ggc cag ctc aag acc acc gct gtg gcg ttg atg aaa atc gcc aac			864
Ser Gly Gln Leu Lys Thr Thr Ala Val Ala Leu Met Lys Ile Ala Asn			
275	280	285	
gat ctg cgc tgg atg aac tcc ggc ccg ctg gcc ggt ctg ggc gaa atc			912
Asp Leu Arg Trp Met Asn Ser Gly Pro Leu Ala Gly Leu Gly Glu Ile			
290	295	300	
gag ctg caa gct ctg cag ccg ggc tct tcg atc atg cca ggc aag gtc			960
Glu Leu Gln Ala Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys Val			
305	310	315	320
aac ccg gtg atc ccg gag gcc act gcc atg gtc gcc gcc caa gtg att			1008
Asn Pro Val Ile Pro Glu Ala Thr Ala Met Val Ala Ala Gln Val Ile			
325	330	335	
ggc aac gac gcg acc atc gcc gtc gca ggt caa gcc ggt aac ttc gag			1056
Gly Asn Asp Ala Thr Ile Ala Val Ala Gly Gln Ala Gly Asn Phe Glu			
340	345	350	
ctg aac gtg atg ctg ccg gtg atc gcc gcg aac ctg ctg gaa agc atc			1104
Leu Asn Val Met Leu Pro Val Ile Ala Arg Asn Leu Leu Glu Ser Ile			
355	360	365	
gag ctg atg gcc aat gtc agc cgc ttg ctg gcc gac aaa gcc atc gcc			1152
Glu Leu Met Ala Asn Val Ser Arg Leu Leu Ala Asp Lys Ala Ile Ala			
370	375	380	
agc ttc aag gtc aac gaa gac aaa ctc aag gaa gcc ctc gcg cgc aac			1200
Ser Phe Lys Val Asn Glu Asp Lys Leu Lys Glu Ala Leu Ala Arg Asn			
385	390	395	400
ccg att ctg gtc acg gcg ttg aat ccg atc atc ggc tac ctc aag gcc			1248
Pro Ile Leu Val Thr Ala Leu Asn Pro Ile Ile Gly Tyr Leu Lys Ala			
405	410	415	
gcc gaa atc gcc aag acc gcc tac aag cag ggt cgt cca atc atc gat			1296
Ala Glu Ile Ala Lys Thr Ala Tyr Lys Gln Gly Arg Pro Ile Ile Asp			
420	425	430	
gtg gcg ctg gag cac acc gac ctg tcc cgc gac cag ctt gaa gcg ctg			1344
Val Ala Leu Glu His Thr Asp Leu Ser Arg Asp Gln Leu Glu Ala Leu			
435	440	445	
ctg gac ccg gaa aaa ctc acc gcc ggc ggt atc tga			1380
Leu Asp Pro Glu Lys Leu Thr Ala Gly Gly Ile			
450	455		

<210> 9584

<211> 459

<212> PRT

<213> Pseudomonas putida KT2440

<400> 9584

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

PF59083SeqList PF59083.txt

Val Asn Cys Gly Gln Ser Ser Asn Asp Ile Ile Pro Thr Thr Ile His
130 135 140
Val Ser Ala Ala Leu Ala Leu His Glu Gln Leu Leu Pro Ala Leu Ala
145 150 155 160
His Leu Val Gln Val Ile Glu Val Lys Ser Ala Gln Val His Gln Tyr
165 170 175
Val Lys Thr Gly Arg Thr His Leu Met Asp Ala Met Pro Val Arg Met
180 185 190
Ser Gln Val Leu Asp Gly Trp Ala Ala Gln Ile Asn Ala Ala Lys Ser
195 200 205
His Ile Glu Gly Val Leu Pro His Leu Gln Ala Leu Ala Gln Gly Gly
210 215 220
Thr Ala Val Gly Thr Gly Ile Asn Ala His Pro Gln Phe Ala Val Gly
225 230 235 240
Phe Ala Arg Gln Leu Ser Gly Leu Thr Lys Val Glu Phe Thr Pro Gly
245 250 255
Gln Asn Leu Phe Ala Leu Ile Gly Ser Gln Asp Thr Ala Val Ala Leu
260 265 270
Ser Gly Gln Leu Lys Thr Thr Ala Val Ala Leu Met Lys Ile Ala Asn
275 280 285
Asp Leu Arg Trp Met Asn Ser Gly Pro Leu Ala Gly Leu Gly Glu Ile
290 295 300
Glu Leu Gln Ala Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys Val
305 310 315 320
Asn Pro Val Ile Pro Glu Ala Thr Ala Met Val Ala Ala Gln Val Ile
325 330 335
Gly Asn Asp Ala Thr Ile Ala Val Ala Gly Gln Ala Gly Asn Phe Glu
340 345 350
Leu Asn Val Met Leu Pro Val Ile Ala Arg Asn Leu Leu Glu Ser Ile
355 360 365
Glu Leu Met Ala Asn Val Ser Arg Leu Leu Ala Asp Lys Ala Ile Ala
370 375 380
Ser Phe Lys Val Asn Glu Asp Lys Leu Lys Glu Ala Leu Ala Arg Asn
385 390 395 400
Pro Ile Leu Val Thr Ala Leu Asn Pro Ile Ile Gly Tyr Leu Lys Ala
405 410 415
Ala Glu Ile Ala Lys Thr Ala Tyr Lys Gln Gly Arg Pro Ile Ile Asp
420 425 430
Val Ala Leu Glu His Thr Asp Leu Ser Arg Asp Gln Leu Glu Ala Leu
435 440 445
Leu Asp Pro Glu Lys Leu Thr Ala Gly Gly Ile
450 455

<210> 9585

<211> 1437

<212> DNA

<213> Pseudomonas putida KT2440

<220>

<221> CDS

<222> (1)..(1437)

<223> transl_table=11

<400> 9585

atg	ata	tac	atc	atg	tcc	tct	gct	gca	tcg	ttc	cgc	gtc	gaa	aaa	gac	48
Met	Ile	Tyr	Ile	Met	Ser	Ser	Ala	Ala	Ser	Phe	Arg	Val	Glu	Lys	Asp	
1				5					10					15		
ttg	ttg	ggt	acc	ctt	gaa	gtt	cct	gca	gat	gcc	tac	tac	ggc	atc	cag	96
Leu	Leu	Gly	Thr	Leu	Glu	Val	Pro	Ala	Asp	Ala	Tyr	Tyr	Gly	Ile	Gln	
				20				25					30			
acc	ctg	cgc	gct	gcc	aac	aac	ttc	cac	ctc	tcc	ggt	gtt	ccg	ctg	tcg	144
Thr	Leu	Arg	Ala	Ala	Asn	Asn	Phe	His	Leu	Ser	Gly	Val	Pro	Leu	Ser	
				35			40					45				
cac	tac	ccg	aag	ctg	gtc	gtg	gcc	ctg	gcc	atg	gtc	aag	cag	gcc	gct	192
His	Tyr	Pro	Lys	Leu	Val	Val	Ala	Leu	Ala	Met	Val	Lys	Gln	Ala	Ala	
				50		55					60					
gcc	gac	gcc	aac	cgt	gag	ctg	ggg	cac	ctg	agc	gat	gcc	aag	cac	gct	240
Ala	Asp	Ala	Asn	Arg	Glu	Leu	Gly	His	Leu	Ser	Asp	Ala	Lys	His	Ala	
65					70					75					80	

PF59083SeqList PF59083.txt																
gcc	att	tcc	gca	gcc	tgc	gcc	cgc	ctg	atc	aaa	ggc	gat	ttc	cac	gac	288
Ala	Ile	Ser	Ala	Ala	Cys	Ala	Arg	Leu	Ile	Lys	Gly	Asp	Phe	His	Asp	
				85					90					95		
cag	ttc	gtg	gta	gac	atg	atc	cag	ggc	ggc	gct	ggt	act	tct	acc	aac	336
Gln	Phe	Val	Val	Asp	Met	Ile	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Thr	Asn	
			100					105					110			
atg	aac	gcc	aac	gaa	gtc	att	gcc	aac	gtt	gcg	ctg	gag	gcc	atg	ggc	384
Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Val	Ala	Leu	Glu	Ala	Met	Gly	
		115					120					125				
cac	cag	aag	ggt	gag	tac	cag	tac	ctg	cac	cct	aac	aac	gac	gtg	aac	432
His	Gln	Lys	Gly	Glu	Tyr	Gln	Tyr	Leu	His	Pro	Asn	Asn	Asp	Val	Asn	
	130					135					140					
atg	gcg	cag	tcg	acc	aac	gac	gcc	tac	ccg	acc	gca	atc	cgc	ctg	ggc	480
Met	Ala	Gln	Ser	Thr	Asn	Asp	Ala	Tyr	Pro	Thr	Ala	Ile	Arg	Leu	Gly	
	145				150				155						160	
ctg	ctg	ctg	ggc	cac	gac	gcg	ctg	ctg	gcc	agc	ctt	gat	agc	ctg	atc	528
Leu	Leu	Leu	Gly	His	Asp	Ala	Leu	Leu	Ala	Ser	Leu	Asp	Ser	Leu	Ile	
			165					170						175		
cag	gcc	ttc	gct	gcc	aag	ggt	aaa	gaa	ttc	gac	cac	gta	ctg	aag	atg	576
Gln	Ala	Phe	Ala	Ala	Lys	Gly	Lys	Glu	Phe	Asp	His	Val	Leu	Lys	Met	
			180					185					190			
ggc	cgt	acc	cag	ctg	cag	gac	gcc	gta	ccg	atg	acc	ctg	ggc	cag	gaa	624
Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	
	195					200					205					
ttc	cgc	gcc	ttc	gcc	acc	acc	act	gaa	gac	ctg	cag	cgc	ctg	cgc		672
Phe	Arg	Ala	Phe	Ala	Thr	Thr	Met	Thr	Glu	Asp	Leu	Gln	Arg	Leu	Arg	
	210					215					220					
tcg	ctg	gct	ccg	gaa	ctg	ctg	acc	gaa	atc	aac	ctg	ggc	ggt	acc	gcc	720
Ser	Leu	Ala	Pro	Glu	Leu	Leu	Thr	Glu	Ile	Asn	Leu	Gly	Gly	Thr	Ala	
	225				230					235					240	
atc	ggt	act	ggc	atc	aac	gcc	gac	cct	ggc	tac	cag	gcc	ttg	gcc	gta	768
Ile	Gly	Thr	Gly	Ile	Asn	Ala	Asp	Pro	Gly	Tyr	Gln	Ala	Leu	Ala	Val	
			245					250					255			
cag	cgc	ctg	gcc	acc	atc	agc	ggc	cac	ccg	ctg	gta	ccg	gct	gcc	gac	816
Gln	Arg	Leu	Ala	Thr	Ile	Ser	Gly	His	Pro	Leu	Val	Pro	Ala	Ala	Asp	
			260				265					270				
ctg	atc	gaa	gcc	acc	tcc	gac	atg	ggc	gcc	ttc	gtg	ctg	ttc	tcc	ggc	864
Leu	Ile	Glu	Ala	Thr	Ser	Asp	Met	Gly	Ala	Phe	Val	Leu	Phe	Ser	Gly	
		275				280						285				
atg	ctc	aag	cgc	acc	gcg	gtc	aag	ctg	tcg	aag	atc	tgc	aac	gac	ctg	912
Met	Leu	Lys	Arg	Thr	Ala	Val	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	
	290					295					300					
cgc	ctg	ctg	tcc	agc	ggc	cca	cgc	acc	ggc	atc	aac	gag	atc	aac	ctg	960
Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Thr	Gly	Ile	Asn	Glu	Ile	Asn	Leu	
	305				310					315					320	
cca	gcg	cgt	cag	cca	ggc	agc	tcg	atc	atg	cca	ggc	aag	gtc	aac	ccg	1008
Pro	Ala	Arg	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	
			325					330					335			
gtt	att	cca	gaa	gct	gtg	aac	cag	gtg	gcc	ttc	gcc	atc	atg	ggc	aac	1056
Val	Ile	Pro	Glu	Ala	Val	Asn	Gln	Val	Ala	Phe	Ala	Ile	Met	Gly	Asn	
			340					345					350			
gac	ctg	gcc	ctg	acc	gtc	gcc	gcc	gaa	ggt	ggt	cag	ctg	cag	ctg	aac	1104
Asp	Leu	Ala	Leu	Thr	Val	Ala	Ala	Glu	Gly	Gly	Gln	Leu	Gln	Leu	Asn	
		355				360						365				
gtg	atg	gag	ccg	ctg	atc	gcc	tac	aag	atc	ttc	gac	tcg	atc	cgc	ctg	1152
Val	Met	Glu	Pro	Leu	Ile	Ala	Tyr	Lys	Ile	Phe	Asp	Ser	Ile	Arg	Leu	
	370					375					380					
ctg	caa	cgc	gcc	atg	gac	atg	ctg	cgc	gag	cac	tgc	atc	gtc	ggc	atc	1200
Leu	Gln	Arg	Ala	Met	Asp	Met	Leu	Arg	Glu	His	Cys	Ile	Val	Gly	Ile	
					390					395				400		
acc	gcc	aac	gaa	cag	cgc	tgc	cgt	gaa	ctg	gtc	gag	cac	tcg	atc	ggc	1248
Thr	Ala	Asn	Glu	Gln	Arg	Cys	Arg	Glu	Leu	Val	Glu	His	Ser	Ile	Gly	
			405					410						415		
ctg	gtt	acc	gca	ctg	aac	ccg	tac	atc	ggc	tac	gaa	aac	gcc	acc	cgt	1296
Leu	Val	Thr	Ala	Leu	Asn	Pro	Tyr	Ile	Gly	Tyr	Glu	Asn	Ala	Thr	Arg	
			420					425					430			
att	gcc	cgc	gtt	gcc	ctg	gaa	agc	ggc	cgc	ggc	gta	ctg	gaa	ctg	gtg	1344
Ile	Ala	Arg	Val	Ala	Leu	Glu	Ser	Gly	Arg	Gly	Val	Leu	Glu	Leu	Val	
		435					440					445				

PF59083SeqList PF59083.txt

cg	g	g	a	ct	ct	g	g	g	a	ct	g	g	a	ct	cg		1392
Arg	Glu	Glu	Lys	Leu	Leu	Asp	Asp	Ala	Met	Leu	Asp	Asp	Ile	Leu	Arg		
	450					455					460						
cc	g	a	a	at	at	gc	cc	cg	ct	gt	cc	ct	a	gc	ta		1437
Pro	Glu	Asn	Met	Ile	Ala	Pro	Arg	Leu	Val	Pro	Leu	Lys	Ala				
	465				470					475							

<210> 9586
 <211> 478
 <212> PRT
 <213> Pseudomonas putida KT2440

<400> 9586

Met	Ile	Tyr	Ile	Met	Ser	Ser	Ala	Ala	Ser	Phe	Arg	Val	Glu	Lys	Asp	
1				5					10					15		
Leu	Leu	Gly	Thr	Leu	Glu	Val	Pro	Ala	Asp	Ala	Tyr	Tyr	Gly	Ile	Gln	
			20					25					30			
Thr	Leu	Arg	Ala	Ala	Asn	Asn	Phe	His	Leu	Ser	Gly	Val	Pro	Leu	Ser	
		35					40					45				
His	Tyr	Pro	Lys	Leu	Val	Val	Ala	Leu	Ala	Met	Val	Lys	Gln	Ala	Ala	
	50					55					60					
Ala	Asp	Ala	Asn	Arg	Glu	Leu	Gly	His	Leu	Ser	Asp	Ala	Lys	His	Ala	
65				70					75						80	
Ala	Ile	Ser	Ala	Ala	Cys	Ala	Arg	Leu	Ile	Lys	Gly	Asp	Phe	His	Asp	
			85					90						95		
Gln	Phe	Val	Val	Asp	Met	Ile	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Thr	Asn	
			100					105					110			
Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Val	Ala	Leu	Glu	Ala	Met	Gly	
	115						120					125				
His	Gln	Lys	Gly	Glu	Tyr	Gln	Tyr	Leu	His	Pro	Asn	Asn	Asp	Val	Asn	
	130					135					140					
Met	Ala	Gln	Ser	Thr	Asn	Asp	Ala	Tyr	Pro	Thr	Ala	Ile	Arg	Leu	Gly	
145					150				155						160	
Leu	Leu	Leu	Gly	His	Asp	Ala	Leu	Leu	Ala	Ser	Leu	Asp	Ser	Leu	Ile	
				165				170						175		
Gln	Ala	Phe	Ala	Ala	Lys	Gly	Lys	Glu	Phe	Asp	His	Val	Leu	Lys	Met	
			180					185					190			
Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	
	195						200					205				
Phe	Arg	Ala	Phe	Ala	Thr	Thr	Met	Thr	Glu	Asp	Leu	Gln	Arg	Leu	Arg	
	210					215					220					
Ser	Leu	Ala	Pro	Glu	Leu	Leu	Thr	Glu	Ile	Asn	Leu	Gly	Gly	Thr	Ala	
225					230					235					240	
Ile	Gly	Thr	Gly	Ile	Asn	Ala	Asp	Pro	Gly	Tyr	Gln	Ala	Leu	Ala	Val	
			245					250						255		
Gln	Arg	Leu	Ala	Thr	Ile	Ser	Gly	His	Pro	Leu	Val	Pro	Ala	Ala	Asp	
			260					265					270			
Leu	Ile	Glu	Ala	Thr	Ser	Asp	Met	Gly	Ala	Phe	Val	Leu	Phe	Ser	Gly	
		275					280					285				
Met	Leu	Lys	Arg	Thr	Ala	Val	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	
	290					295					300					
Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Thr	Gly	Ile	Asn	Glu	Ile	Asn	Leu	
305					310					315					320	
Pro	Ala	Arg	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	
			325					330						335		
Val	Ile	Pro	Glu	Ala	Val	Asn	Gln	Val	Ala	Phe	Ala	Ile	Met	Gly	Asn	
			340					345					350			
Asp	Leu	Ala	Leu	Thr	Val	Ala	Ala	Glu	Gly	Gly	Gln	Leu	Gln	Leu	Asn	
		355					360					365				
Val	Met	Glu	Pro	Leu	Ile	Ala	Tyr	Lys	Ile	Phe	Asp	Ser	Ile	Arg	Leu	
	370					375					380					
Leu	Gln	Arg	Ala	Met	Asp	Met	Leu	Arg	Glu	His	Cys	Ile	Val	Gly	Ile	
385					390					395					400	
Thr	Ala	Asn	Glu	Gln	Arg	Cys	Arg	Glu	Leu	Val	Glu	His	Ser	Ile	Gly	
			405					410						415		
Leu	Val	Thr	Ala	Leu	Asn	Pro	Tyr	Ile	Gly	Tyr	Glu	Asn	Ala	Thr	Arg	
			420					425					430			
Ile	Ala	Arg	Val	Ala	Leu	Glu	Ser	Gly	Arg	Gly	Val	Leu	Glu	Leu	Val	
		435					440					445				

PF59083SeqList PF59083.txt

Arg Glu Glu Lys Leu Leu Asp Asp Ala Met Leu Asp Asp Ile Leu Arg
 450 455 460
 Pro Glu Asn Met Ile Ala Pro Arg Leu Val Pro Leu Lys Ala
 465 470 475

<210> 9587
 <211> 1452
 <212> DNA
 <213> Vibrio vulnificus CMCP6

<220>
 <221> CDS
 <222> (1)..(1452)
 <223> transl_table=11

<400> 9587
 atg gct acc cta act gaa gct cca aaa gca tca act ccg gcc act cgt 48
 Met Ala Thr Leu Thr Glu Ala Pro Lys Ala Ser Thr Pro Ala Thr Arg
 1 5 10 15
 att gaa gaa gat cta tta ggc caa cgt cac gtt ccg gct gac gct tac 96
 Ile Glu Glu Asp Leu Leu Gly Gln Arg His Val Pro Ala Asp Ala Tyr
 20 25 30
 tac ggt att cac acg ctg cgc gcc atc gaa aac ttc aac atc tca aat 144
 Tyr Gly Ile His Thr Leu Arg Ala Ile Glu Asn Phe Asn Ile Ser Asn
 35 40 45
 gtc act att tct gac gta cca gaa ttc gtt cgt ggc atg gtt atg acc 192
 Val Thr Ile Ser Asp Val Pro Glu Phe Val Arg Gly Met Val Met Thr
 50 55 60
 aaa aaa gcc gct gcg ctt gct aac aaa gaa ttg ggc gca att cct aag 240
 Lys Lys Ala Ala Ala Leu Ala Asn Lys Glu Gly Ala Ile Pro Lys
 65 70 75 80
 aat gtc gcg gat tac atc att caa gcg tgt gac cta atg ttg gaa act 288
 Asn Val Ala Asp Tyr Ile Ile Gln Ala Cys Asp Leu Met Leu Glu Thr
 85 90 95
 ggc aaa tgc atg gat cag ttc cca tca gac gta ttc caa ggc ggt gcg 336
 Gly Lys Cys Met Asp Gln Phe Pro Ser Asp Val Phe Gln Gly Gly Ala
 100 105 110
 ggc act tct gtg aac atg aac acc aac gaa gta ctt gcc aac att gct 384
 Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Leu Ala Asn Ile Ala
 115 120 125
 cta gaa tta atg ggc aaa gag aaa ggc gat tac gac gtg gtg aac cca 432
 Leu Glu Leu Met Gly Lys Glu Lys Gly Asp Tyr Asp Val Val Asn Pro
 130 135 140
 aac gat cac gtg aac aag agc caa tca acc aac tgt gcc tac cca acg 480
 Asn Asp His Val Asn Lys Ser Gln Ser Thr Asn Cys Ala Tyr Pro Thr
 145 150 155 160
 ggc ttc cgt att gcg gtt tac aac agc atc cat aaa ttg atg gaa gcg 528
 Gly Phe Arg Ile Ala Val Tyr Asn Ser Ile His Lys Leu Met Glu Ala
 165 170 175
 att gaa tac cta aaa ggt gcg ttt gag ctg aaa tct caa gag ttt aac 576
 Ile Glu Tyr Leu Lys Gly Ala Phe Glu Leu Lys Ser Gln Glu Phe Asn
 180 185 190
 ggc atc cta aaa atg ggc cgt act cag ttg caa gat gcg gtt cca atg 624
 Gly Ile Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met
 195 200 205
 aca gta ggt caa gag ttt cac gct tgg gca gtg acg cta aac gaa gag 672
 Thr Val Gly Gln Glu Phe His Ala Trp Ala Val Thr Leu Asn Glu Glu
 210 215 220
 atc cgt gcg cta gac tac acc tcg aag cta ctt ctt gaa gtg aac cta 720
 Ile Arg Ala Leu Asp Tyr Thr Ser Lys Leu Leu Glu Val Asn Leu
 225 230 235 240
 ggt gca acg gca atc ggt act ggc ttg aac aca cct cct ggt tac caa 768
 Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr Pro Pro Gly Tyr Gln
 245 250 255
 gca ctt gcc gtg gaa cac cta gcg gaa gtg act ggc cta gca gtg gtt 816
 Ala Leu Ala Val Lys His Leu Ala Glu Val Thr Gly Leu Ala Val Val
 260 265 270
 cca gca gaa gac ctt atc gaa gca act tca gac tgt ggt gct tac gta 864
 Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser Asp Gly Ala Tyr Val

PF59083SeqList PF59083.txt

275	280	285	
atg gca cac ggc gct cta aaa cgc cta gcg gtg aaa ttg tct aag atc	912		
Met Ala His Gly Ala Leu Lys Arg Leu Ala Val Lys Leu Ser Lys Ile			
290	295	300	
tgt aac gac ttg cgt ctg ctt tct tct ggt cct cgc gct ggt ttg aac	960		
Cys Asn Asp Leu Arg Leu Ser Ser Gly Pro Arg Ala Gly Leu Asn			
305	310	315	
gaa ctt aac ttg cca gaa atg caa gcc ggt tct tca atc atg cca gca	1008		
Glu Leu Asn Leu Pro Glu Met Gln Ala Gly Ser Ser Ile Met Pro Ala			
325	330	335	
aaa gtt aac cca gtt atc cca gaa gtg gtt aac caa gtg tgt ttc aaa	1056		
Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Val Cys Phe Lys			
340	345	350	
gta ctg ggt aac gac aac acg att tct ttc gca gcc gaa ggc ggt cag	1104		
Val Leu Gly Asn Asp Asn Thr Ile Ser Phe Ala Ala Glu Gly Gly Gln			
355	360	365	
cta cag ctg aac gta atg gag cct gtg att ggt caa gcg atg ttt gaa	1152		
Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Gln Ala Met Phe Glu			
370	375	380	
tcg att tca cta cta caa aac gcg tgt gtg aac cta cgt gac aag tgt	1200		
Ser Ile Ser Leu Leu Gln Asn Ala Cys Val Asn Leu Arg Asp Lys Cys			
385	390	395	
atc gac ggc atc act gtg aac aaa gag atc tgt gaa aac tac gtt tac	1248		
Ile Asp Gly Ile Thr Val Asn Lys Glu Ile Cys Glu Asn Tyr Val Tyr			
405	410	415	
aac tct atc ggt atc gtt act tac cta aac cca tac atc ggc cac cac	1296		
Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro Tyr Ile Gly His His			
420	425	430	
gaa ggt gac atc gtt ggt aag atc tgt gcg gaa acc ggt aag agc gtc	1344		
Glu Gly Asp Ile Val Gly Lys Ile Cys Ala Glu Thr Gly Lys Ser Val			
435	440	445	
cgt gaa gta gtg ctt gag cgt ggc ttg ctg aca tct gaa gag ttg gat	1392		
Arg Glu Val Val Leu Glu Arg Gly Leu Leu Thr Ser Glu Glu Leu Asp			
450	455	460	
gac atc ctg tct gtg cag aac ttc atg cac cca act tac aaa gca aaa	1440		
Asp Ile Leu Ser Val Gln Asn Phe Met His Pro Thr Tyr Lys Ala Lys			
465	470	475	
cgt tac gaa taa	1452		
Arg Tyr Glu			

<210> 9588

<211> 483

<212> PRT

<213> Vibrio vulnificus CMCP6

<400> 9588

Met Ala Thr Leu Thr Glu Ala Pro Lys Ala Ser Thr Pro Ala Thr Arg	
1 5 10 15	
Ile Glu Glu Asp Leu Leu Gly Gln Arg His Val Pro Ala Asp Ala Tyr	
20 25 30	
Tyr Gly Ile His Thr Leu Arg Ala Ile Glu Asn Phe Asn Ile Ser Asn	
35 40 45	
Val Thr Ile Ser Asp Val Pro Glu Phe Val Arg Gly Met Val Met Thr	
50 55 60	
Lys Lys Ala Ala Ala Leu Ala Asn Lys Glu Leu Gly Ala Ile Pro Lys	
65 70 75 80	
Asn Val Ala Asp Tyr Ile Ile Gln Ala Cys Asp Leu Met Leu Glu Thr	
85 90 95	
Gly Lys Cys Met Asp Gln Phe Pro Ser Asp Val Phe Gln Gly Gly Ala	
100 105 110	
Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Leu Ala Asn Ile Ala	
115 120 125	
Leu Glu Leu Met Gly Lys Glu Lys Gly Asp Tyr Asp Val Val Asn Pro	
130 135 140	
Asn Asp His Val Asn Lys Ser Gln Ser Thr Asn Cys Ala Tyr Pro Thr	
145 150 155 160	
Gly Phe Arg Ile Ala Val Tyr Asn Ser Ile His Lys Leu Met Glu Ala	
165 170 175	

PF59083SeqList PF59083.txt

Ile Glu Tyr Leu Lys Gly Ala Phe Glu Leu Lys Ser Gln Glu Phe Asn
180 185 190
Gly Ile Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met
195 200 205
Thr Val Gly Gln Glu Phe His Ala Trp Ala Val Thr Leu Asn Glu Glu
210 215 220
Ile Arg Ala Leu Asp Tyr Thr Ser Lys Leu Leu Leu Glu Val Asn Leu
225 230 235 240
Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr Pro Pro Gly Tyr Gln
245 250 255
Ala Leu Ala Val Lys His Leu Ala Glu Val Thr Gly Leu Ala Val Val
260 265 270
Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser Asp Cys Gly Ala Tyr Val
275 280 285
Met Ala His Gly Ala Leu Lys Arg Leu Ala Val Lys Leu Ser Lys Ile
290 295 300
Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Ala Gly Leu Asn
305 310 315 320
Glu Leu Asn Leu Pro Glu Met Gln Ala Gly Ser Ser Ile Met Pro Ala
325 330 335
Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Val Cys Phe Lys
340 345 350
Val Leu Gly Asn Asp Asn Thr Ile Ser Phe Ala Ala Glu Gly Gly Gln
355 360 365
Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Gln Ala Met Phe Glu
370 375 380
Ser Ile Ser Leu Leu Gln Asn Ala Cys Val Asn Leu Arg Asp Lys Cys
385 390 395 400
Ile Asp Gly Ile Thr Val Asn Lys Glu Ile Cys Glu Asn Tyr Val Tyr
405 410 415
Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro Tyr Ile Gly His His
420 425 430
Glu Gly Asp Ile Val Gly Lys Ile Cys Ala Glu Thr Gly Lys Ser Val
435 440 445
Arg Glu Val Val Leu Glu Arg Gly Leu Leu Thr Ser Glu Glu Leu Asp
450 455 460
Asp Ile Leu Ser Val Gln Asn Phe Met His Pro Thr Tyr Lys Ala Lys
465 470 475 480
Arg Tyr Glu

<210> 9589
<211> 1401
<212> DNA
<213> Bradyrhizobium japonicum USDA 110

<220>
<221> CDS
<222> (1)..(1401)
<223> transl_table=11

<400> 9589
atg agc cgt acg gag cag gat ttc ctc gga cag cgt gag atc gcc gac 48
Met Ser Arg Thr Glu Gln Asp Phe Leu Gly Gln Arg Glu Ile Ala Asp
1 5 10 15
gat att tac tac ggc gtc cag acc atc cgc ggg aag gag aac ttc cac 96
Asp Ile Tyr Tyr Gly Val Gln Thr Ile Arg Gly Lys Glu Asn Phe His
20 25 30
atc acc ggc att ccg atg aac cag gag cct tac ttc gtg aag gcg ctg 144
Ile Thr Gly Ile Pro Met Asn Gln Glu Pro Tyr Phe Val Lys Ala Leu
35 40 45
ggg tac gtg aag aag gcc gcg gcg atg gcc aat cgc gat ctc ggc gtg 192
Gly Tyr Val Lys Lys Ala Ala Met Ala Asn Arg Asp Leu Gly Val
50 55 60
atc gac gcc agg gtg gcc gat gcg atc atc ctc ggc tgc gac cgc gtg 240
Ile Asp Ala Arg Val Ala Asp Ala Ile Ile Leu Gly Cys Asp Arg Val
65 70 75 80
att gcc ggc gac atg atg gat caa ttc gtc acc gac ttc atc cag ggc 288
Ile Ala Gly Asp Met Met Asp Gln Phe Val Thr Asp Phe Ile Gln Gly
Seite 10039

PF59083SeqList PF59083.txt

															85																90																95	
ggc	gcc	ggc	acc	tcg	acc	aac	atg	aac	gcc	aac	gag	gtg	atc	gcc	aac		336																															
Gly	Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn																																	
															100																105																110	
ctc	gcg	ctg	gaa	tcg	ctg	ggc	ttc	aag	aag	ggc	gac	tac	cag	cac	gtc		384																															
Leu	Ala	Leu	Glu	Ser	Leu	Gly	Phe	Lys	Lys	Gly	Asp	Tyr	Gln	His	Val																																	
															115																120																125	
agc	ccg	aac	gat	cat	gtg	aac	tac	ggc	cag	tcg	acc	aac	gac	acc	tat		432																															
Ser	Pro	Asn	Asp	His	Val	Asn	Tyr	Gly	Gln	Ser	Thr	Asn	Asp	Thr	Tyr																																	
															130																135																140	
ccg	acc	gcc	ttt	cgc	ctc	gcg	ctg	atc	ctg	cgg	ctc	gag	agc	tac	atg		480																															
Pro	Thr	Ala	Phe	Arg	Leu	Ala	Leu	Ile	Leu	Arg	Leu	Glu	Ser	Tyr	Met																																	
															145																150																155	
acg	gcg	ctg	cgc	cag	ctc	cag	gag	gcg	ttc	ttc	gcc	aag	ggc	cgt	gag		528																															
Thr	Ala	Leu	Arg	Gln	Leu	Gln	Glu	Ala	Phe	Phe	Ala	Lys	Gly	Arg	Glu																																	
															165																170																175	
ttc	gat	cgc	gtg	ctg	aag	atg	ggc	cgt	acg	cat	ctt	cag	gac	gcc	gtg		576																															
Phe	Asp	Arg	Val	Leu	Lys	Met	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Val																																	
															180																185																190	
ccg	atg	tcg	ctc	ggc	gcc	gaa	ttc	cgc	ggc	tgg	ggt	acc	acc	atg	ggc		624																															
Pro	Met	Ser	Leu	Gly	Ala	Glu	Phe	Arg	Gly	Trp	Gly	Thr	Thr	Met	Gly																																	
															195																200																205	
gag	gag	gtc	gat	cgt	atc	tcc	gag	gca	cgg	gcg	ctg	ctg	cgc	gag	atc		672																															
Glu	Glu	Val	Asp	Arg	Ile	Ser	Glu	Ala	Arg	Ala	Leu	Leu	Arg	Glu	Ile																																	
															210																215																220	
aat	ctc	ggc	gcg	acc	gcg	atc	ggc	acc	tcc	gtc	acc	gcg	gcg	cac	ggc		720																															
Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Ser	Val	Thr	Ala	Ala	His	Gly																																	
															225																230																235	
tat	ccc	aag	ctc	gcc	gtc	cgg	cat	ctg	agc	gcg	ctg	acc	ggc	atc	gac		768																															
Tyr	Pro	Lys	Leu	Ala	Val	Arg	His	Leu	Ser	Ala	Leu	Thr	Gly	Ile	Asp																																	
															245																250																255	
ttc	att	ctc	gcc	ggc	gac	ctc	gtc	gaa	gcg	acc	tcg	gac	acc	ggc	gcc		816																															
Phe	Ile	Leu	Ala	Gly	Asp	Leu	Val	Glu	Ala	Thr	Ser	Asp	Thr	Gly	Ala																																	
															260																265																270	
tat	gtg	cag	ctc	tcc	ggc	gtg	ctc	aag	cgc	acg	gcg	agc	aag	ctg	aca		864																															
Tyr	Val	Gln	Leu	Ser	Gly	Val	Leu	Lys	Arg	Thr	Ala	Ser	Lys	Leu	Thr																																	
															275																280																285	
aaa	atc	tgc	aac	gac	atc	cgg	ttg	ctg	gct	tcg	ggc	ccg	cgc	gcc	ggc		912																															
Lys	Ile	Cys	Asn	Asp	Ile	Arg	Leu	Leu	Ala	Ser	Gly	Pro	Arg	Ala	Gly																																	
															290																295																300	
ttc	aac	gag	atc	aac	ctg	ccg	cag	ctc	cag	ccg	ggc	tcc	tcg	atc	atg		960																															
Phe	Asn	Glu	Ile	Asn	Leu	Pro	Gln	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met																																	
															305																310																315	
ccg	ggg	aag	gtc	aat	ccc	gtg	atc	ccc	gag	gtc	gtc	aac	cag	acc	agc		1008																															
Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln	Thr	Ser																																	
															325																330																335	
ttc	ctt	gtc	atc	ggc	ctc	gac	acc	acg	gtg	acg	ctt	gcc	gcg	tcc	gcc		1056																															
Phe	Leu	Val	Ile	Gly	Leu	Asp	Thr	Thr	Val	Thr	Leu	Ala	Ala	Ser	Ala																																	
															340																345																350	
ggc	cag	ctc	caa	ctc	aat	gtg	atg	gaa	ccg	gtg	atc	tcg	ttc	gcg	ctg		1104																															
Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile	Ser	Phe	Ala	Leu																																	
															355																360																365	
ttc	ttc	tcg	atc	cgc	acc	atg	gag	cgc	gcg	gtc	aac	agc	ctg	cgc	gag		1152																															
Phe	Phe	Ser	Ile	Arg	Thr	Met	Glu	Arg	Ala	Val	Asn	Ser	Leu	Arg	Glu																																	
															370																375																380	
aac	tgc	gtc	gtc	ggc	atc	acc	gcc	aac	gcg	gag	cac	acc	cgc	aac	atg		1200																															
Asn	Cys	Val	Val	Gly	Ile	Thr	Ala	Asn	Ala	Glu	His	Thr	Arg	Asn	Met																																	
															385																390																395	
gtg	ctg	aac	tcg	ctc	ggc	atc	gtc	acg	gtg	ctg	aag	ccg	ctg	ctc	ggc		1248																															
Val	Leu	Asn	Ser	Gly	Ile	Val	Val	Thr	Val	Leu	Lys	Pro	Leu	Gly																																		
															405																410																415	
tac	aag	caa	tgc	gcc	gag	atc	gcg	cgc	gag	ggc	tac	aag	agc	ggc	aag		1296																															
Tyr	Lys	Gln	Cys	Ala	Glu	Ile	Ala	Arg	Glu	Gly	Tyr	Lys	Ser	Gly	Lys																																	
															420																425																430	
tcg	ctg	cac	cag	atc	gtg	gtg	gtc	gag	cgc	aag	ctg	ctg	acg	cag	gag		1344																															
Ser	Leu	His	Gln	Ile	Val	Val	Val	Glu	Arg	Lys	Leu	Leu	Thr	Gln	Glu																																	
															435																440																445	
aag	tgg	gac	gag	atg	ttc	tcg	ttc	gag	cgc	ctg	atc	aat	ccg	gac	ctg		1392																															
Lys	Trp	Asp	Glu	Met	Phe	Ser	Phe	Glu	Arg	Leu	Ile	Asn	Pro	Asp	Leu																																	

450
att gcg tga
ile Ala
465

<210> 9590
<211> 466
<212> PRT
<213> Bradyrhizobium japonicum USDA 110

<400> 9590
Met Ser Arg Thr Glu Gln Asp Phe Leu Gly Gln Arg Glu Ile Ala Asp
1 5 10 15
Asp Ile Tyr Tyr Gly Val Gln Thr Ile Arg Gly Lys Glu Asn Phe His
20 25 30
Ile Thr Gly Ile Pro Met Asn Gln Glu Pro Tyr Phe Val Lys Ala Leu
35 40 45
Gly Tyr Val Lys Lys Ala Ala Ala Met Ala Asn Arg Asp Leu Gly Val
50 55 60
Ile Asp Ala Arg Val Ala Asp Ala Ile Ile Leu Gly Cys Asp Arg Val
65 70 75 80
Ile Ala Gly Asp Met Met Asp Gln Phe Val Thr Asp Phe Ile Gln Gly
85 90 95
Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu Val Ile Ala Asn
100 105 110
Leu Ala Leu Glu Ser Leu Gly Phe Lys Lys Gly Asp Tyr Gln His Val
115 120 125
Ser Pro Asn Asp His Val Asn Tyr Gly Gln Ser Thr Asn Asp Thr Tyr
130 135 140
Pro Thr Ala Phe Arg Leu Ala Leu Ile Leu Arg Leu Glu Ser Tyr Met
145 150 155 160
Thr Ala Leu Arg Gln Leu Gln Glu Ala Phe Phe Ala Lys Gly Arg Glu
165 170 175
Phe Asp Arg Val Leu Lys Met Gly Arg Thr His Leu Gln Asp Ala Val
180 185 190
Pro Met Ser Leu Gly Ala Glu Phe Arg Gly Trp Gly Thr Thr Met Gly
195 200 205
Glu Glu Val Asp Arg Ile Ser Glu Ala Arg Ala Leu Leu Arg Glu Ile
210 215 220
Asn Leu Gly Ala Thr Ala Ile Gly Thr Ser Val Thr Ala Ala His Gly
225 230 235 240
Tyr Pro Lys Leu Ala Val Arg His Leu Ser Ala Leu Thr Gly Ile Asp
245 250 255
Phe Ile Leu Ala Gly Asp Leu Val Glu Ala Thr Ser Asp Thr Gly Ala
260 265 270
Tyr Val Gln Leu Ser Gly Val Leu Lys Arg Thr Ala Ser Lys Leu Thr
275 280 285
Lys Ile Cys Asn Asp Ile Arg Leu Leu Ala Ser Gly Pro Arg Ala Gly
290 295 300
Phe Asn Glu Ile Asn Leu Pro Gln Leu Gln Pro Gly Ser Ser Ile Met
305 310 315 320
Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Thr Ser
325 330 335
Phe Leu Val Ile Gly Leu Asp Thr Thr Val Thr Leu Ala Ala Ser Ala
340 345 350
Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Ser Phe Ala Leu
355 360 365
Phe Phe Ser Ile Arg Thr Met Glu Arg Ala Val Asn Ser Leu Arg Glu
370 375 380
Asn Cys Val Val Gly Ile Thr Ala Asn Ala Glu His Thr Arg Asn Met
385 390 395 400
Val Leu Asn Ser Leu Gly Ile Val Thr Val Leu Lys Pro Leu Leu Gly
405 410 415
Tyr Lys Gln Cys Ala Glu Ile Ala Arg Glu Gly Tyr Lys Ser Gly Lys
420 425 430
Ser Leu His Gln Ile Val Val Val Glu Arg Lys Leu Leu Thr Gln Glu
435 440 445
Lys Trp Asp Glu Met Phe Ser Phe Glu Arg Leu Ile Asn Pro Asp Leu
450 455 460

PF59083SeqList PF59083.txt

Ile Ala
465

<210> 9591
<211> 1413
<212> DNA
<213> Clostridium tetani E88

<220>
<221> CDS
<222> (1)..(1413)
<223> transl_table=11

```

<400> 9591
atg caa tac aga tta gaa agt gat tca gta ggt gaa aaa aga ata cca      48
Met Gln Tyr Arg Leu Glu Ser Asp Ser Val Gly Glu Lys Arg Ile Pro
1      5      10      15
aag gat gct tat tat ggt gtg caa agt ctt aga gca caa gag aat ttt      96
Lys Asp Ala Tyr Tyr Gly Val Gln Ser Leu Arg Ala Gln Glu Asn Phe
20      25      30
atg ata aca gga aaa aaa gtc cac acg gaa atg ata aaa gca tta gca      144
Met Ile Thr Gly Lys Lys Val His Thr Glu Met Ile Lys Ala Leu Ala
35      40      45
gag gta aaa aaa gca aca gct atg aca aat atg caa gtg gaa ctt tta      192
Glu Val Lys Lys Ala Thr Ala Met Thr Asn Met Gln Val Glu Leu Leu
50      55      60
agt aaa aaa gca ggt aac gcc att gta aaa gct tgt gat gaa ata att      240
Ser Lys Lys Ala Gly Asn Ala Ile Val Lys Ala Cys Asp Glu Ile Ile
65      70      75
gaa gga aat tta caa gaa cag ttt ata act gat cct ata caa ggt ggc      288
Glu Gly Asn Leu Gln Glu Gln Phe Ile Thr Asp Pro Ile Gln Gly Gly
85      90      95
gca gga aca tct atg aac atg aat tta aac gaa gta att gct aat aga      336
Ala Gly Thr Ser Met Asn Met Asn Leu Asn Glu Val Ile Ala Asn Arg
100      105      110
gca gta gaa ata tta ggt ggg gaa aag gga gat tat agt ata gtt cat      384
Ala Val Glu Ile Leu Gly Gly Glu Lys Gly Asp Tyr Ser Ile Val His
115      120      125
cct aat gat cat gta aat atg gga caa tct act aac gat gtt att cct      432
Pro Asn Asp His Val Asn Met Gly Gln Ser Thr Asn Asp Val Ile Pro
130      135      140
aca ggg gga aaa ata gca act ata aga ctt tta gat aga gca tta atg      480
Thr Gly Gly Lys Ile Ala Thr Ile Arg Leu Leu Asp Arg Ala Leu Met
145      150      155
tca tta gaa aat tta gat gca ctt aca aat aaa tct aag gaa ttt      528
Ser Leu Glu Asn Leu Val Asp Ala Leu Thr Asn Lys Ser Lys Glu Phe
165      170      175
gat cat att ata aaa atg ggg aga act caa atg caa gat gct gta cca      576
Asp His Ile Ile Lys Met Gly Arg Thr Gln Met Gln Asp Ala Val Pro
180      185      190
ata aga tta gga caa gaa ttt aag gca tat tca aat gct ata aaa agg      624
Ile Arg Leu Gly Gln Glu Phe Lys Ala Tyr Ser Asn Ala Ile Lys Arg
195      200      205
gac ata gtt aga att aag aga gca aaa gaa gaa tta tat cat gta agt      672
Asp Ile Val Arg Ile Lys Arg Ala Lys Glu Glu Leu Tyr His Val Ser
210      215      220
att ggg gct aca gct ata ggt aca ggt ata aat gct gat gag gag tat      720
Ile Gly Ala Thr Ala Ile Gly Thr Gly Ile Asn Ala Asp Glu Glu Tyr
225      230      235
gta aaa aat ata aca cca aat tta tca aaa gta aca aca ctt agc cta      768
Val Lys Asn Ile Thr Pro Asn Leu Ser Lys Val Thr Thr Leu Ser Leu
245      250      255
att caa tgt gaa gat tta gta gat gga act caa aat cta gat tgt ttt      816
Ile Gln Cys Glu Asp Leu Val Asp Gly Thr Gln Asn Leu Asp Cys Phe
260      265      270
gct tca gta tca tca aat tta aag gtt tgt gct tta agt tta tct aaa      864
Ala Ser Val Ser Ser Asn Leu Lys Val Cys Ala Leu Ser Leu Ser Lys
275      280      285
ata gct aat gat tta aga ctt atg tcc tca gga cct aga acc ggt ttt      912

```

PF59083SeqList PF59083.txt

Ile	Ala	Asn	Asp	Leu	Arg	Leu	Met	Ser	Ser	Gly	Pro	Arg	Thr	Gly	Phe	
290	290					295					300					
gga	gaa	ata	aat	ctt	cca	gca	aaa	caa	aat	ggg	tca	tct	ata	atg	cca	960
Gly	Glu	Ile	Asn	Leu	Pro	Ala	Lys	Gln	Asn	Gly	Ser	Ser	Ile	Met	Pro	
305					310					315					320	
gga	aaa	gta	aat	cca	gta	ata	gct	gaa	gtt	gta	aac	caa	gtt	gca	ttt	1008
Gly	Lys	Val	Asn	Pro	Val	Ile	Ala	Glu	Val	Val	Asn	Gln	Val	Ala	Phe	
				325					330					335		
agt	att	gta	gga	aat	gat	gta	act	att	agc	atg	gct	gtt	gaa	gca	gga	1056
Ser	Ile	Val	Gly	Asn	Asp	Val	Thr	Ile	Ser	Met	Ala	Val	Glu	Ala	Gly	
			340					345					350			
caa	tta	gaa	tta	aac	gca	ttt	gag	ccg	gtg	tta	tat	tat	aag	tta	ttt	1104
Gln	Leu	Glu	Leu	Asn	Ala	Phe	Glu	Pro	Val	Leu	Tyr	Tyr	Lys	Leu	Phe	
		355					360					365				
gaa	tct	att	gaa	ata	ttg	aaa	aat	ggg	gtg	gat	aca	ttt	att	cat	aat	1152
Glu	Ser	Ile	Glu	Ile	Leu	Lys	Asn	Gly	Val	Asp	Thr	Phe	Ile	His	Asn	
		370				375					380					
tgt	ata	aat	ggg	ata	aca	gca	aat	gag	gaa	aga	tgt	aaa	aag	tta	gtg	1200
Cys	Ile	Asn	Gly	Ile	Thr	Ala	Asn	Glu	Glu	Arg	Cys	Lys	Lys	Leu	Val	
385					390					395					400	
gat	aat	agt	gtt	gga	ata	att	act	gca	ata	tgt	cca	cat	gta	gga	tat	1248
Asp	Asn	Ser	Val	Gly	Ile	Ile	Thr	Ala	Ile	Cys	Pro	His	Val	Gly	Tyr	
				405				410						415		
aaa	aaa	gca	gct	aaa	gta	gca	aaa	act	gct	ata	cag	act	gga	gaa	tct	1296
Lys	Lys	Ala	Ala	Lys	Val	Ala	Lys	Thr	Ala	Ile	Gln	Thr	Gly	Glu	Ser	
				420				425					430			
gta	aag	gag	ctt	gta	tta	aaa	gaa	aat	tta	tta	tca	gaa	aaa	gaa	ttg	1344
Val	Lys	Glu	Leu	Val	Leu	Lys	Glu	Asn	Leu	Leu	Ser	Glu	Lys	Glu	Leu	
		435					440					445				
gat	aca	ata	ctt	gac	cca	ttt	gga	atg	act	aaa	cca	gga	ata	tct	ggg	1392
Asp	Thr	Ile	Leu	Asp	Pro	Phe	Gly	Met	Thr	Lys	Pro	Gly	Ile	Ser	Gly	
		450				455					460					
aaa	gag	ctg	tta	aaa	aag	taa										1413
Lys	Glu	Leu	Leu	Lys	Lys											
465					470											

<210> 9592

<211> 470

<212> PRT

<213> Clostridium tetani E88

<400> 9592

Met	Gln	Tyr	Arg	Leu	Glu	Ser	Asp	Ser	Val	Gly	Glu	Lys	Arg	Ile	Pro	
1				5					10					15		
Lys	Asp	Ala	Tyr	Tyr	Gly	Val	Gln	Ser	Leu	Arg	Ala	Gln	Glu	Asn	Phe	
			20					25					30			
Met	Ile	Thr	Gly	Lys	Lys	Val	His	Thr	Glu	Met	Ile	Lys	Ala	Leu	Ala	
		35					40					45				
Glu	Val	Lys	Lys	Ala	Thr	Ala	Met	Thr	Asn	Met	Gln	Val	Glu	Leu	Leu	
	50					55					60					
Ser	Lys	Lys	Ala	Gly	Asn	Ala	Ile	Val	Lys	Ala	Cys	Asp	Glu	Ile	Ile	
65					70					75					80	
Glu	Gly	Asn	Leu	Gln	Glu	Gln	Phe	Ile	Thr	Asp	Pro	Ile	Gln	Gly	Gly	
			85					90						95		
Ala	Gly	Thr	Ser	Met	Asn	Met	Asn	Leu	Asn	Glu	Val	Ile	Ala	Asn	Arg	
			100					105					110			
Ala	Val	Glu	Ile	Leu	Gly	Gly	Glu	Lys	Gly	Asp	Tyr	Ser	Ile	Val	His	
		115					120					125				
Pro	Asn	Asp	His	Val	Asn	Met	Gly	Gln	Ser	Thr	Asn	Asp	Val	Ile	Pro	
		130				135						140				
Thr	Gly	Gly	Lys	Ile	Ala	Thr	Ile	Arg	Leu	Leu	Asp	Arg	Ala	Leu	Met	
145					150					155					160	
Ser	Leu	Glu	Asn	Leu	Val	Asp	Ala	Leu	Thr	Asn	Lys	Ser	Lys	Glu	Phe	
			165					170						175		
Asp	His	Ile	Ile	Lys	Met	Gly	Arg	Thr	Gln	Met	Gln	Asp	Ala	Val	Pro	
			180					185					190			
Ile	Arg	Leu	Gly	Gln	Glu	Phe	Lys	Ala	Tyr	Ser	Asn	Ala	Ile	Lys	Arg	
		195					200					205				
Asp	Ile	Val	Arg	Ile	Lys	Arg	Ala	Lys	Glu	Glu	Leu	Tyr	His	Val	Ser	

PF59083SeqList PF59083.txt

210	Ile Gly Ala Thr Ala	215	Ile Gly Thr Gly Ile	220	Asn Ala Asp Glu Glu Tyr
225	Val Lys Asn Ile Thr	230	Pro Asn Leu Ser Lys	235	Val Thr Thr Leu Ser Leu
		245	Leu Val Asp Gly Thr	250	Gln Asn Leu Asp Cys Phe
		260	Asn Leu Lys Val Cys	270	Ala Leu Ser Leu Ser Lys
		280	Leu Met Ser Ser Gly	285	Pro Arg Thr Gly Phe
		295	Ala Lys Gln Asn Gly	300	Ser Ser Ile Met Pro
		310	Val Ile Ala Glu Val	315	Val Asn Gln Val Ala Phe
		325	Pro Val Thr Ile Ser	330	Met Ala Val Glu Ala Gly
		340	Gly Asn Asp Val Thr	345	Met Ala Val Glu Ala Gly
		355	Gln Leu Glu Leu Asn	360	Phe Glu Pro Val Leu Tyr Tyr Lys Leu Phe
		370	Glu Ser Ile Glu Ile	375	Lys Asn Gly Val Asp Thr Phe Ile His Asn
		385	Cys Ile Asn Gly Ile	390	Thr Ala Asn Glu Glu Arg Cys Lys Lys Leu Val
		405	Asp Asn Ser Val Gly	410	Ile Ile Thr Ala Ile Cys Pro His Val Gly Tyr
		420	Lys Lys Ala Ala Lys	425	Val Ala Lys Thr Ala Ile Gln Thr Gly Glu Ser
		435	Val Lys Glu Leu Val	440	Leu Lys Glu Asn Leu Leu Ser Glu Lys Glu Leu
		450	Asp Thr Ile Leu Asp	455	Pro Phe Gly Met Thr Lys Pro Gly Ile Ser Gly
		465	Lys Glu Leu Leu Lys	470	Lys

<210> 9593
 <211> 1401
 <212> DNA
 <213> Lactobacillus plantarum WCFS1

<220>
 <221> CDS
 <222> (1)..(1401)
 <223> transl_table=11

<400> 9593	
atg cga att gaa gct gat tgt att ggt aag tta gct gtt ccg gat gat	48
Met Arg Ile Glu Ala Asp Cys Ile Gly Lys Leu Ala Val Pro Asp Asp	
1 5 10 15	
gct ttg tat gga att cat acg tta cgt gcc gtt cat aat ttt ccg att	96
Ala Leu Tyr Gly Ile His Thr Leu Arg Ala Val His Asn Phe Pro Ile	
20 25 30	
acg acg gaa ttg atg cat cca ctg atc atg caa agt ctt gtt caa atc	144
Thr Thr Glu Leu Met His Pro Leu Ile Met Gln Ser Leu Val Gln Ile	
35 40 45	
aag aaa gcg gcc agt gtg aat gcg gct gcc gga act ttg tct aat	192
Lys Lys Ala Ala Ala Ser Val Asn Ala Ala Ala Gly Thr Leu Ser Asn	
50 55 60	
gat aag gca cac gcc att att gcg gca tgt aat cag tta cta ctg ggg	240
Asp Lys Ala His Ala Ile Ile Ala Ala Cys Asn Gln Leu Leu Leu Gly	
65 70 75 80	
cgt tac gcg gat aac ttc att gtg cca gcg att cag ggg ggt gct ggg	288
Arg Tyr Ala Asp Asn Phe Ile Val Pro Ala Ile Gln Gly Gly Ala Gly	
85 90 95	
acc tcg gct aac atg aac gtc aat gaa gtg gtg gct aat ttg gct cac	336
Thr Ser Ala Asn Met Asn Val Asn Glu Val Val Ala Asn Leu Ala His	
100 105 110	
cgg ttg atg ccg gca gtc gcc gtt cat ccc aat gat gat gtt aat caa	384
Arg Leu Met Pro Ala Val Ala Val His Pro Asn Asp Asp Val Asn Gln	
115 120 125	

PF59083SeqList PF59083.txt

tca	caa	tca	acc	aat	gat	act	ttt	cca	acg	gcc	ggg	aaa	atg	gcg	ctt	432
Ser	Gln	Ser	Thr	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Gly	Lys	Met	Ala	Leu	
	130					135					140					
tgc	atg	caa	ctc	cca	gga	cta	tta	acg	gca	ctc	agc	cgg	ttg	gta	caa	480
Cys	Met	Gln	Leu	Pro	Gly	Leu	Leu	Thr	Ala	Leu	Ser	Arg	Leu	Val	Gln	
145					150					155					160	
acg	tta	ctg	gtt	aaa	tcg	cag	cgt	tat	caa	gat	gcc	atc	aaa	gtt	ggc	528
Thr	Leu	Leu	Val	Lys	Ser	Gln	Arg	Tyr	Gln	Asp	Ala	Ile	Lys	Val	Gly	
				165					170					175		
cga	act	cag	ctt	gaa	gat	gcg	gta	ccg	acg	acg	tac	ggg	cga	acc	ttt	576
Arg	Thr	Gln	Leu	Glu	Asp	Ala	Val	Pro	Thr	Thr	Tyr	Gly	Arg	Thr	Phe	
			180					185					190			
cat	gct	tat	tac	caa	tta	ttc	aag	cgt	gat	ttg	acc	cgt	gta	cgg	cag	624
His	Ala	Tyr	Tyr	Gln	Leu	Phe	Lys	Arg	Asp	Leu	Thr	Arg	Val	Arg	Gln	
		195					200					205				
gcg	ggc	gaa	cat	ctc	cga	atc	gta	aat	ttg	ggg	ggg	act	gca	atc	ggg	672
Ala	Gly	Glu	His	Leu	Arg	Ile	Val	Asn	Leu	Gly	Gly	Thr	Ala	Ile	Gly	
	210					215					220					
acc	ggc	atc	aac	gcg	act	cac	acg	tat	caa	cag	cag	att	tta	gtg	aaa	720
Thr	Gly	Ile	Asn	Ala	Thr	His	Thr	Tyr	Gln	Gln	Gln	Ile	Leu	Val	Lys	
225					230					235					240	
tta	aat	caa	aat	act	gat	tta	gat	tta	gta	gcc	gca	cca	gac	ttg	atc	768
Leu	Asn	Gln	Asn	Thr	Asp	Leu	Asp	Leu	Val	Ala	Ala	Pro	Asp	Leu	Ile	
				245					250					255		
gat	gca	acg	caa	aac	tcg	gat	ttg	ttc	gtg	gaa	ttc	tct	gcg	gcc	atg	816
Asp	Ala	Thr	Gln	Asn	Cys	Asp	Leu	Phe	Val	Glu	Phe	Ser	Ala	Ala	Met	
			260					265					270			
aag	acg	tta	gcc	gtt	gac	ctt	tcc	aag	ttt	agc	aat	gac	tta	aga	ttg	864
Lys	Thr	Leu	Ala	Val	Asp	Leu	Ser	Lys	Phe	Ser	Asn	Asp	Leu	Arg	Leu	
		275					280					285				
ctg	gcg	agc	ggc	cca	caa	gct	ggc	ttt	ggg	gaa	ttg	aat	ttg	ccc	gcg	912
Leu	Ala	Ser	Gly	Pro	Gln	Ala	Gly	Phe	Gly	Glu	Leu	Asn	Leu	Pro	Ala	
	290					295					300					
cag	caa	gca	ggc	tct	tct	att	atg	cca	ggg	aaa	atc	aat	ccg	gtt	att	960
Gln	Gln	Ala	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Ile	Asn	Pro	Val	Ile	
305					310					315					320	
ccg	gag	gtt	gtt	aac	caa	gtt	gcg	ttt	gaa	gtg	att	ggg	cac	gac	acg	1008
Pro	Glu	Val	Val	Asn	Gln	Val	Ala	Phe	Glu	Val	Ile	Gly	His	Asp	Thr	
				325					330					335		
acg	gta	aca	atg	gca	gcg	gaa	gcg	ggc	caa	ttg	gaa	tta	aac	gct	ttt	1056
Thr	Val	Thr	Met	Ala	Ala	Glu	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Ala	Phe	
			340					345					350			
gag	cca	att	atg	tta	cgg	gca	ttg	cta	gcc	agt	gag	cag	cat	tta	cag	1104
Glu	Pro	Ile	Met	Leu	Arg	Ala	Leu	Leu	Ala	Ser	Glu	Gln	His	Leu	Gln	
		355					360					365				
cag	gcc	ttg	act	aca	tta	gtc	gat	cac	tgt	gtg	cgg	caa	ttg	acg	gtc	1152
Gln	Ala	Leu	Thr	Thr	Leu	Val	Asp	His	Cys	Val	Arg	Gln	Leu	Thr	Val	
	370					375					380					
aat	cgc	caa	cgc	tgt	gca	gat	caa	gtg	gca	cat	tcg	gcc	att	acg	gca	1200
Asn	Arg	Gln	Arg	Cys	Ala	Asp	Gln	Val	Ala	His	Ser	Ala	Ile	Thr	Ala	
385					390					395					400	
act	gtt	ttg	gcg	cca	tac	ctt	ggg	tac	gag	acg	act	acc	gcg	ctg	att	1248
Thr	Val	Leu	Ala	Pro	Tyr	Leu	Gly	Tyr	Glu	Thr	Thr	Thr	Ala	Leu	Ile	
				405					410					415		
aaa	gaa	gcg	ctc	acc	act	aac	caa	gca	att	cct	gaa	tta	tta	cat	cga	1296
Lys	Glu	Ala	Leu	Thr	Thr	Asn	Gln	Ala	Ile	Pro	Glu	Leu	Leu	His	Arg	
			420					425					430			
cgt	cgc	ttg	ctt	agc	gat	gat	ttg	gtc	gag	cag	ctg	ttt	tca	ccg	gcc	1344
Arg	Arg	Leu	Leu	Ser	Asp	Asp	Leu	Val	Glu	Gln	Leu	Phe	Ser	Pro	Ala	
		435					440					445				
gga	cta	act	cag	cca	cgt	cca	gag	gtt	att	gaa	caa	cta	cga	gcg	gtt	1392
Gly	Leu	Thr	Gln	Pro	Arg	Pro	Glu	Val	Ile	Glu	Gln	Leu	Arg	Ala	Val	
	450					455					460					
gca	aag	tag														1401
Ala	Lys															
465																

<210> 9594

<211> 466

PF59083SeqList PF59083.txt

<212> PRT

<213> Lactobacillus plantarum WCFS1

<400> 9594

```

Met Arg Ile Glu Ala Asp Cys Ile Gly Lys Leu Ala Val Pro Asp Asp
1      5      10      15
Ala Leu Tyr Gly Ile His Thr Leu Arg Ala Val His Asn Phe Pro Ile
      20      25      30
Thr Thr Glu Leu Met His Pro Leu Ile Met Gln Ser Leu Val Gln Ile
      35      40      45
Lys Lys Ala Ala Ser Val Asn Ala Ala Ala Gly Thr Leu Ser Asn
      50      55      60
Asp Lys Ala His Ala Ile Ile Ala Ala Cys Asn Gln Leu Leu Leu Gly
65      70      75      80
Arg Tyr Ala Asp Asn Phe Ile Val Pro Ala Ile Gln Gly Gly Ala Gly
      85      90      95
Thr Ser Ala Asn Met Asn Val Asn Glu Val Val Ala Asn Leu Ala His
      100      105      110
Arg Leu Met Pro Ala Val Ala Val His Pro Asn Asp Asp Val Asn Gln
      115      120      125
Ser Gln Ser Thr Asn Asp Thr Phe Pro Thr Ala Gly Lys Met Ala Leu
      130      135      140
Cys Met Gln Leu Pro Gly Leu Leu Thr Ala Leu Ser Arg Leu Val Gln
145      150      155      160
Thr Leu Leu Val Lys Ser Gln Arg Tyr Gln Asp Ala Ile Lys Val Gly
      165      170      175
Arg Thr Gln Leu Glu Asp Ala Val Pro Thr Thr Tyr Gly Arg Thr Phe
      180      185      190
His Ala Tyr Tyr Gln Leu Phe Lys Arg Asp Leu Thr Arg Val Arg Gln
      195      200      205
Ala Gly Glu His Leu Arg Ile Val Asn Leu Gly Gly Thr Ala Ile Gly
      210      215      220
Thr Gly Ile Asn Ala Thr His Thr Tyr Gln Gln Gln Ile Leu Val Lys
225      230      235      240
Leu Asn Gln Asn Thr Asp Leu Asp Leu Val Ala Ala Pro Asp Leu Ile
      245      250      255
Asp Ala Thr Gln Asn Cys Asp Leu Phe Val Glu Phe Ser Ala Ala Met
      260      265      270
Lys Thr Leu Ala Val Asp Leu Ser Lys Phe Ser Asn Asp Leu Arg Leu
      275      280      285
Leu Ala Ser Gly Pro Gln Ala Gly Phe Gly Glu Leu Asn Leu Pro Ala
      290      295      300
Gln Gln Ala Gly Ser Ser Ile Met Pro Gly Lys Ile Asn Pro Val Ile
305      310      315      320
Pro Glu Val Val Asn Gln Val Ala Phe Glu Val Ile Gly His Asp Thr
      325      330      335
Thr Val Thr Met Ala Ala Glu Ala Gly Gln Leu Glu Leu Asn Ala Phe
      340      345      350
Glu Pro Ile Met Leu Arg Ala Leu Leu Ala Ser Glu Gln His Leu Gln
      355      360      365
Gln Ala Leu Thr Thr Leu Val Asp His Cys Val Arg Gln Leu Thr Val
      370      375      380
Asn Arg Gln Arg Cys Ala Asp Gln Val Ala His Ser Ala Ile Thr Ala
385      390      395      400
Thr Val Leu Ala Pro Tyr Leu Gly Tyr Glu Thr Thr Thr Ala Leu Ile
      405      410      415
Lys Glu Ala Leu Thr Thr Asn Gln Ala Ile Pro Glu Leu Leu His Arg
      420      425      430
Arg Arg Leu Leu Ser Asp Asp Leu Val Glu Gln Leu Phe Ser Pro Ala
      435      440      445
Gly Leu Thr Gln Pro Arg Pro Glu Val Ile Glu Gln Leu Arg Ala Val
      450      455      460
Ala Lys
465

```

<210> 9595

<211> 1452

<212> DNA

<213> Vibrio parahaemolyticus RIMD 2210633

PF59083SeqList PF59083.txt

<220>
 <221> CDS
 <222> (1)..(1452)
 <223> transl_table=11

<400> 9595

atg gct acc cta tct gat gct cca aaa aca gca aac caa gcc act cgt	48
Met Ala Thr Leu Ser Asp Ala Pro Lys Thr Ala Asn Gln Ala Thr Arg	
1 5 10 15	
att gaa gaa gat cta tta ggt caa cgt cat gtc cct gct gat gcg tac	96
Ile Glu Glu Asp Leu Leu Gly Gln Arg His Val Pro Ala Asp Ala Tyr	
20 25 30	
tac ggc att cat acc cta cgt gcg atc gaa aac ttc aac atc tct aac	144
Tyr Gly Ile His Thr Leu Arg Ala Ile Glu Asn Phe Asn Ile Ser Asn	
35 40 45	
gta act att tct gac gta cct gag ttc gta cgc ggc atg gtg atg acg	192
Val Thr Ile Ser Asp Val Pro Glu Phe Val Arg Gly Met Val Met Thr	
50 55 60	
aag aaa gca gcg gcg ttg gcg aac aaa gaa ctt ggc gct att cct aaa	240
Lys Lys Ala Ala Ala Leu Ala Asn Lys Glu Leu Gly Ala Ile Pro Lys	
65 70 75 80	
gaa gtt gct aac tac atc cta gaa gcg tgt gat ttg atc cta gaa aca	288
Glu Val Ala Asn Tyr Ile Leu Glu Ala Cys Asp Leu Ile Leu Glu Thr	
85 90 95	
ggc aag tgt atg gat cag ttc cct tca gac gta ttc caa ggc ggc gcg	336
Gly Lys Cys Met Asp Gln Phe Pro Ser Asp Val Phe Gln Gly Gly Ala	
100 105 110	
ggg act tcc gtt aac atg aac act aac gaa gtt atc gcg aac gtt gca	384
Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Ile Ala Asn Val Ala	
115 120 125	
ctt gaa cta atg ggc aaa gaa aaa ggc caa tac gag ttc atc aac ccg	432
Leu Glu Leu Met Gly Lys Glu Lys Gly Gln Tyr Glu Phe Ile Asn Pro	
130 135 140	
aac gac cac gtt aac aag agc caa tct act aac tgt gcg tac cca act	480
Asn Asp His Val Asn Lys Ser Gln Ser Thr Asn Cys Ala Tyr Pro Thr	
145 150 155 160	
ggg ttc cgt atc gcg gtt tac aac agc gta cac aaa cta atg gaa gcg	528
Gly Phe Arg Ile Ala Val Tyr Asn Ser Val His Lys Leu Met Glu Ala	
165 170 175	
att gaa tac cta aaa ggc gca ttc gat ctt aaa gca act gaa ttc aaa	576
Ile Glu Tyr Leu Lys Gly Ala Phe Asp Leu Lys Ala Thr Glu Phe Lys	
180 185 190	
gac gta ttg aag atg ggt cgt act cag ctt caa gac gcg gta cca atg	624
Asp Val Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met	
195 200 205	
act gtt ggt caa gag ttc cac gct tgg gct gta acg cta aac gaa gag	672
Thr Val Gly Gln Glu Phe His Ala Trp Ala Val Thr Leu Asn Glu Glu	
210 215 220	
att cgt gct cta gat tac act tct aaa ctc cta gaa atc aac cta	720
Ile Arg Ala Leu Asp Tyr Thr Ser Lys Leu Leu Leu Glu Ile Asn Leu	
225 230 235 240	
ggg gca acc gca atc ggt act ggt ctt aac aca cca act ggt tac caa	768
Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr Pro Thr Gly Tyr Gln	
245 250 255	
gct cta gca gta aaa cac cta gcg gaa gta act ggc ctt gac gtt gtg	816
Ala Leu Ala Val Lys His Leu Ala Glu Val Thr Gly Leu Asp Val Val	
260 265 270	
cct gca gaa gac cta atc gaa gcg act tct gac tgt ggt gca tac gta	864
Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser Asp Cys Gly Ala Tyr Val	
275 280 285	
atg act cac ggc gcg cta aaa cgt cta gca gtg aaa cta tcg aag atc	912
Met Thr His Gly Ala Leu Lys Arg Leu Ala Val Lys Leu Ser Lys Ile	
290 295 300	
tgt aac gac ctt cgt cta ctt tct tct ggt cct gcg ggt cta aac	960
Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Ala Gly Leu Asn	
305 310 315 320	
gaa ttg aac cta cct gaa atg caa gca ggt tct tca atc atg cca gcg	1008
Glu Leu Asn Leu Pro Glu Met Gln Ala Gly Ser Ser Ile Met Pro Ala	

PF59083SeqList PF59083.txt

aaa gta aac cca gtt atc cca gaa gta gta aac caa gtt tgc ttc aaa	1056
Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Val Cys Phe Lys	
325 330 335	
gtt cta ggt aac gac aac acg gtt tct ttc gca gca gaa ggc ggt cag	1104
Val Leu Gly Asn Asp Asn Thr Val Ser Phe Ala Ala Glu Gly Gly Gln	
340 345 350	
cta cag cta aac gta atg gaa cca gtt atc gca caa agc atg ttt gag	1152
Leu Gln Leu Asn Val Met Glu Pro Val Ile Ala Gln Ser Met Phe Glu	
360 365 370	
tct atc tct cta cta cac aat gcg tgt gtg aac cta cgt gat aaa tgt	1200
Ser Ile Ser Leu Leu His Asn Ala Cys Val Asn Leu Arg Asp Lys Cys	
385 390 395	
atc gac ggc atc act gta aac aaa gaa atc tgt gag aac tac gtt tac	1248
Ile Asp Gly Ile Thr Val Asn Lys Glu Ile Cys Glu Asn Tyr Val Tyr	
405 410 415	
aac tca atc ggt atc gta act tac cta aac cca tac att ggc cac cac	1296
Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro Tyr Ile Gly His His	
420 425 430	
gaa ggt gac att gtc ggt aag att tgt gca gaa act ggt aag agt gtt	1344
Glu Gly Asp Ile Val Gly Lys Ile Cys Ala Glu Thr Gly Lys Ser Val	
435 440 445	
cgt gaa gtc gtg ctt gag cgc ggc ctg cta act gca gaa gaa ctt gat	1392
Arg Glu Val Val Leu Glu Arg Gly Leu Leu Thr Ala Glu Glu Leu Asp	
450 455 460	
gaa atc tta aca gtt gaa aac ttc atg cat cct act tac aaa gcg aaa	1440
Glu Ile Leu Thr Val Glu Asn Phe Met His Pro Thr Tyr Lys Ala Lys	
465 470 475	
cgc tac gag taa	1452
Arg Tyr Glu	

<210> 9596

<211> 483

<212> PRT

<213> *Vibrio parahaemolyticus* RIMD 2210633

<400> 9596

Met Ala Thr Leu Ser Asp Ala Pro Lys Thr Ala Asn Gln Ala Thr Arg	
1 5 10 15	
Ile Glu Glu Asp Leu Leu Gly Gln Arg His Val Pro Ala Asp Ala Tyr	
20 25 30	
Tyr Gly Ile His Thr Leu Arg Ala Ile Glu Asn Phe Asn Ile Ser Asn	
35 40 45	
Val Thr Ile Ser Asp Val Pro Glu Phe Val Arg Gly Met Val Met Thr	
50 55 60	
Lys Lys Ala Ala Ala Leu Ala Asn Lys Glu Leu Gly Ala Ile Pro Lys	
65 70 75 80	
Glu Val Ala Asn Tyr Ile Leu Glu Ala Cys Asp Leu Ile Leu Glu Thr	
85 90 95	
Gly Lys Cys Met Asp Gln Phe Pro Ser Asp Val Phe Gln Gly Gly Ala	
100 105 110	
Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Ile Ala Asn Val Ala	
115 120 125	
Leu Glu Leu Met Gly Lys Glu Lys Gly Gln Tyr Glu Phe Ile Asn Pro	
130 135 140	
Asn Asp His Val Asn Lys Ser Gln Ser Thr Asn Cys Ala Tyr Pro Thr	
145 150 155 160	
Gly Phe Arg Ile Ala Val Tyr Asn Ser Val His Lys Leu Met Glu Ala	
165 170 175	
Ile Glu Tyr Leu Lys Gly Ala Phe Asp Leu Lys Ala Thr Glu Phe Lys	
180 185 190	
Asp Val Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met	
195 200 205	
Thr Val Gly Gln Glu Phe His Ala Trp Ala Val Thr Leu Asn Glu Glu	
210 215 220	
Ile Arg Ala Leu Asp Tyr Thr Ser Lys Leu Leu Leu Glu Ile Asn Leu	
225 230 235 240	
Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr Pro Thr Gly Tyr Gln	

PF59083SeqList PF59083.txt

```

      245      250      255
Ala Leu Ala Val Lys His Leu Ala Glu Val Thr Gly Leu Asp Val Val
      260      265      270
Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser Asp Cys Gly Ala Tyr Val
      275      280      285
Met Thr His Gly Ala Leu Lys Arg Leu Ala Val Lys Leu Ser Lys Ile
      290      295      300
Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Ala Gly Leu Asn
      305      310      315
Glu Leu Asn Leu Pro Glu Met Gln Ala Gly Ser Ser Ile Met Pro Ala
      320      325      330
Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Val Cys Phe Lys
      335      340      345
Val Leu Gly Asn Asp Asn Thr Val Ser Phe Ala Ala Glu Gly Gly Gln
      350      355      360
Leu Gln Leu Asn Val Met Glu Pro Val Ile Ala Gln Ser Met Phe Glu
      365      370      375
Ser Ile Ser Leu Leu His Asn Ala Cys Val Asn Leu Arg Asp Lys Cys
      380      385      390
Ile Asp Gly Ile Thr Val Asn Lys Glu Ile Cys Glu Asn Tyr Val Tyr
      395      400      405
Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro Tyr Ile Gly His His
      410      415      420
Glu Gly Asp Ile Val Gly Lys Ile Cys Ala Glu Thr Gly Lys Ser Val
      425      430      435
Arg Glu Val Val Leu Glu Arg Gly Leu Leu Thr Ala Glu Glu Leu Asp
      440      445      450
Glu Ile Leu Thr Val Glu Asn Phe Met His Pro Thr Tyr Lys Ala Lys
      455      460      465
Arg Tyr Glu
      470      475      480

```

<210> 9597

<211> 1461

<212> DNA

<213> Bacteroides thetaiotaomicron VPI-5482

<220>

<221> CDS

<222> (1)..(1461)

<223> transl_table=11

<400> 9597

```

atg tgt tat tgt tat aaa aca acc gat atg gaa cag aaa tta tca aaa      48
Met Cys Tyr Cys Tyr Lys Thr Thr Asp Met Glu Gln Lys Leu Ser Lys
1      5      10
aaa act cgt aca gag agc gac ttg ata ggt agt cgt gaa gtg ccg gaa      96
Lys Thr Arg Thr Glu Ser Asp Leu Ile Gly Ser Arg Glu Val Pro Glu
      20      25      30
agt gca ttg tat gga gta cag aca ctc cgt ggt att gaa aac ttt cgc      144
Ser Ala Leu Tyr Gly Val Gln Thr Leu Arg Gly Ile Glu Asn Phe Arg
      35      40      45
atc agc aag ttt cat ttg aat gag tat ccc ctg ttt att cag gca ttg      192
Ile Ser Lys Phe His Leu Asn Glu Tyr Pro Leu Phe Ile Gln Ala Leu
      50      55      60
gcc atc act aaa atg gga gct gcc gtt gcc aac cgt gaa ctg gat tta      240
Ala Ile Thr Lys Met Gly Ala Ala Val Ala Asn Arg Glu Leu Asp Leu
      65      70      75
ttg act gag gaa cag acg gat gcc ata ctg aag gct tgt aaa gaa ata      288
Leu Thr Glu Glu Gln Thr Asp Ala Ile Leu Lys Ala Cys Lys Glu Ile
      80      85      90
ctg gaa gga aaa cat cat gac caa ttc cct gta gat atg ata cag ggt      336
Leu Glu Gly Lys His His Asp Gln Phe Pro Val Asp Met Ile Gln Gly
      95      100      105
gga gcc gga acc acc acc aat atg gcc aat gaa gtg att gcc aac      384
Gly Ala Gly Thr Thr Thr Asn Met Asn Ala Asn Glu Val Ile Ala Asn
      110      115      120
cgt gca ctg gaa ctg atg gga cat gca cgc gga gag tat cac tac tgc      432
Arg Ala Leu Glu Leu Met Gly His Ala Arg Gly Glu Tyr His Tyr Cys

```

PF59083SeqList PF59083.txt

130	tcg cct aac gat cac gtc	135	aat cgt tcg caa tct acc aat gat gcg tat	480
Ser Pro Asn Asp His Val	150	Asn Arg Ser Gln Ser Thr Asn Asp Ala Tyr		
145	cct aca gcc att cac att ggt ctg tat tat acc cat ctt aaa ttg gtg	155	Pro Thr Ala Ile His Ile Gly Leu Tyr Tyr Thr His Leu Lys Leu Val	528
Pro Thr Ala Ile His 165	170	aaa cac ttt gca aca ctg atc gag gct ttc cga aag aaa gga gcg gag	576	
Lys His Phe Ala Thr Leu Ile	185	Lys His Phe Arg Lys Lys Gly Ala Glu		
180	ttt gca cac atc atc aag atg gga cgt acc caa ctg gaa gat gcc gta	190	Phe Ala His Ile Ile Lys Met Gly Arg Thr Gln Leu Glu Asp Ala Val	624
Phe Ala His 195	200	ccg atg aca cta gga caa acc ttt aat gga ttc gca agt att ttg gaa	672	
Pro Met Thr Leu Gly Gln Thr 215	205	Pro Met Thr Leu Gly Gln Thr 220		
220	cat gaa ctg aag aat ctc gat ttt gcc gca cag gat ttt ctg acg gtc	230	His Glu Leu Lys Asn Leu Asp Phe Ala Ala Gln Asp Phe Leu Thr Val	720
His Glu Leu Lys Asn Leu 230	235	aac atg ggt gcg aca gcc atc gga acc gga att acc gcc gaa ccg gaa	768	
Asn Met Gly Ala Thr 245	250	Asn Met Gly Ala Thr 255		
245	tat gcg gaa aag tgc att gct gcc ctg cgc aag att aca gga ctg gat	260	Tyr Ala Glu Lys Cys Ile Ala Ala Leu Arg Lys Ile Thr Gly Leu Asp	816
Tyr Ala Glu Lys Cys Ile 260	265	atc aaa ctg gca gat gac ctg ata ggc gct act tcg gat act tcc tgc	864	
Ile Lys Leu Ala Asp Asp Leu Ile Gly Ala Thr Ser Asp Thr Ser Cys	280	275		
275	atg gta gga tat tct tcg gcc atg cgg cgt gta gct gtc aag atg aac	285	Met Val Gly Tyr Ser Ser Met Arg Arg Val Ala Val Lys Met Asn	912
Met Val Gly Tyr Ser Ser 290	295	300		
290	aag att tgt aat gat ctg agg cta ttg gct tcc ggt cct cgt tgc gga	310	Lys Ile Cys Asn Asp Leu Arg Leu Leu Ala Ser Gly Pro Arg Cys Gly	960
Lys Ile Cys Asn Asp Leu 310	315	320		
310	ctg gga gaa atc aat ctg cct gcc atg cag ccg ggc tct tcc att atg	325	Leu Gly Glu Ile Asn Leu Pro Ala Met Gln Pro Gly Ser Ser Ile Met	1008
Leu Gly Glu Ile Asn Leu 325	330	335		
325	ccg gga aag gtg aat cct gtc att ccg gaa gtc atg aat cag gtc tct	340	Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Met Asn Gln Val Ser	1056
Pro Gly Lys Val Asn Pro 340	345	350		
340	tat aaa gtg ata gga aac gac ctt tgt gtg gct atg agt gga gag gct	355	Tyr Lys Val Ile Gly Asn Asp Leu Cys Val Ala Met Ser Gly Glu Ala	1104
Tyr Lys Val Ile Gly Asn 355	360	365		
355	gcg cag atg gaa ctg aat gcg atg gaa cct gtc atg gca caa tgc tgt	370	Ala Gln Met Glu Leu Asn Ala Met Glu Pro Val Met Ala Gln Cys Cys	1152
Ala Gln Met Glu Leu Asn 370	375	380		
370	ttt gaa tct gcg gat ttg ttg atg aac ggt ttt gat aca ttg cgt acc	385	Phe Glu Ser Ala Asp Leu Leu Met Asn Gly Phe Asp Thr Leu Arg Thr	1200
Phe Glu Ser Ala Asp Leu 385	390	400		
385	tta tgt att gat ggt atc aca gcc aat gaa gaa aaa tgc cgt ccg gat	405	Leu Cys Ile Asp Gly Ile Thr Ala Asn Glu Glu Lys Cys Arg Arg Asp	1248
Leu Cys Ile Asp Gly Ile 405	410	415		
405	gta cac aac agt atc gga gta gtg acc gca ctg aat ccc gta att ggc	420	Val His Asn Ser Ile Gly Val Val Thr Ala Leu Asn Pro Val Ile Gly	1296
Val His Asn Ser Ile Gly 420	425	430		
420	tat aaa cat tct aca aag ata gcg aag gag gct ctg gaa acg ggt aaa	435	Tyr Lys His Ser Thr Lys Ile Ala Lys Glu Ala Leu Glu Thr Gly Lys	1344
Tyr Lys His Ser Thr Lys 435	440	445		
435	gga gtg tat gag ctg gtg ctg gaa cat aac att ctt tcc aaa gaa gac	450	Gly Val Tyr Glu Leu Val Leu Glu His Asn Ile Leu Ser Lys Glu Asp	1392
Gly Val Tyr Glu Leu Val 450	455	460		
450	ctg gat acg atc ttg aaa ccg gaa aat atg att aaa ccg gtg aaa ctg	465	Leu Asp Thr Ile Leu Lys Pro Glu Asn Met Ile Lys Pro Val Lys Leu	1440
Leu Asp Thr Ile Leu Lys 465	470	475		
465	gat att cat ccg aat cat tga	480	Asp Ile His Pro Asn His	1461
Asp Ile His Pro Asn His 485	485			

PF59083SeqList PF59083.txt

<211> 486

<212> PRT

<213> Bacteroides thetaiotaomicron VPI-5482

<400> 9598

```

Met Cys Tyr Cys Tyr Lys Thr Thr Asp Met Glu Gln Lys Leu Ser Lys
1      5      10      15
Lys Thr Arg Thr Glu Ser Asp Leu Ile Gly Ser Arg Glu Val Pro Glu
      20      25      30
Ser Ala Leu Tyr Gly Val Gln Thr Leu Arg Gly Ile Glu Asn Phe Arg
      35      40      45
Ile Ser Lys Phe His Leu Asn Glu Tyr Pro Leu Phe Ile Gln Ala Leu
      50      55      60
Ala Ile Thr Lys Met Gly Ala Ala Val Ala Asn Arg Glu Leu Asp Leu
65      70      75      80
Leu Thr Glu Glu Gln Thr Asp Ala Ile Leu Lys Ala Cys Lys Glu Ile
      85      90      95
Leu Glu Gly Lys His His Asp Gln Phe Pro Val Asp Met Ile Gln Gly
      100      105      110
Gly Ala Gly Thr Thr Thr Asn Met Asn Ala Asn Glu Val Ile Ala Asn
      115      120      125
Arg Ala Leu Glu Leu Met Gly His Ala Arg Gly Glu Tyr His Tyr Cys
      130      135      140
Ser Pro Asn Asp His Val Asn Arg Ser Gln Ser Thr Asn Asp Ala Tyr
145      150      155      160
Pro Thr Ala Ile His Ile Gly Leu Tyr Tyr Thr His Leu Lys Leu Val
      165      170      175
Lys His Phe Ala Thr Leu Ile Glu Ala Phe Arg Lys Lys Gly Ala Glu
      180      185      190
Phe Ala His Ile Ile Lys Met Gly Arg Thr Gln Leu Glu Asp Ala Val
      195      200      205
Pro Met Thr Leu Gly Gln Thr Phe Asn Gly Phe Ala Ser Ile Leu Glu
      210      215      220
His Glu Leu Lys Asn Leu Asp Phe Ala Ala Gln Asp Phe Leu Thr Val
225      230      235      240
Asn Met Gly Ala Thr Ala Ile Gly Thr Gly Ile Thr Ala Glu Pro Glu
      245      250      255
Tyr Ala Glu Lys Cys Ile Ala Ala Leu Arg Lys Ile Thr Gly Leu Asp
      260      265      270
Ile Lys Leu Ala Asp Asp Leu Ile Gly Ala Thr Ser Asp Thr Ser Cys
      275      280      285
Met Val Gly Tyr Ser Ser Ala Met Arg Arg Val Ala Val Lys Met Asn
      290      295      300
Lys Ile Cys Asn Asp Leu Arg Leu Leu Ala Ser Gly Pro Arg Cys Gly
305      310      315      320
Leu Gly Glu Ile Asn Leu Pro Ala Met Gln Pro Gly Ser Ser Ile Met
      325      330      335
Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Met Asn Gln Val Ser
      340      345      350
Tyr Lys Val Ile Gly Asn Asp Leu Cys Val Ala Met Ser Gly Glu Ala
      355      360      365
Ala Gln Met Glu Leu Asn Ala Met Glu Pro Val Met Ala Gln Cys Cys
      370      375      380
Phe Glu Ser Ala Asp Leu Leu Met Asn Gly Phe Asp Thr Leu Arg Thr
385      390      395      400
Leu Cys Ile Asp Gly Ile Thr Ala Asn Glu Glu Lys Cys Arg Arg Asp
      405      410      415
Val His Asn Ser Ile Gly Val Val Thr Ala Leu Asn Pro Val Ile Gly
      420      425      430
Tyr Lys His Ser Thr Lys Ile Ala Lys Glu Ala Leu Glu Thr Gly Lys
      435      440      445
Gly Val Tyr Glu Leu Val Leu Glu His Asn Ile Leu Ser Lys Glu Asp
      450      455      460
Leu Asp Thr Ile Leu Lys Pro Glu Asn Met Ile Lys Pro Val Lys Leu
465      470      475      480
Asp Ile His Pro Asn His
      485

```

<210> 9599

PF59083SeqList PF59083.txt

<211> 1413
<212> DNA
<213> Streptomyces avermitilis MA-4680

<220>
<221> CDS
<222> (1)..(1413)
<223> transl_table=11

<400> 9599

atg acc gcc gca gcc cac cgc agc gaa cac gac ctg ctc gga gac cgc	48
Met Thr Ala Ala Ala His Arg Ser Glu His Asp Leu Leu Gly Asp Arg	
1 5 10 15	
gac gtc ccc gcc gag gcg tac tgg ggc atc cac tcc ctg cgc gcc aag	96
Asp Val Pro Ala Glu Ala Tyr Trp Gly Ile His Ser Leu Arg Ala Lys	
20 25 30	
gag aac ttc ccc atc acg ggg acg ccg atc tcc acg tac ccg cat ctg	144
Glu Asn Phe Pro Ile Thr Gly Thr Pro Ile Ser Thr Tyr Pro His Leu	
35 40 45	
atc gac gcc ctc gcc gcc gtg aag gag gcc gcc gcc ctc gcc aac gag	192
Ile Asp Ala Leu Ala Ala Val Lys Glu Ala Ala Ala Leu Ala Asn Glu	
50 55 60	
gaa ctc ggc ctg ctg gag ccg aag aag gcc gcg gcc atc gtg gcc gcc	240
Glu Leu Gly Leu Leu Glu Pro Lys Lys Ala Ala Ala Ile Val Ala Ala	
65 70 75 80	
tgc cgg gag atc cgg gac ggc aag ctg cac gac cag ttc gtc gtc gac	288
Cys Arg Glu Ile Arg Asp Gly Lys Leu His Asp Gln Phe Val Val Asp	
85 90 95	
gtc atc cag ggc ggc gcg ggc acc tcg acg aac atg aac gcc aac gag	336
Val Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Asn Glu	
100 105 110	
gtc atc gcc aac cgg gcc ctt gaa ctg ctc ggc cac gcc aag ggc gag	384
Val Ile Ala Asn Arg Ala Leu Glu Leu Leu Gly His Ala Lys Gly Glu	
115 120 125	
tac cgg cac ctg cac ccc aac gag gac gtc aac ctc ggc cag tcg acc	432
Tyr Arg His Leu His Pro Asn Glu Asp Val Asn Leu Gly Gln Ser Thr	
130 135 140	
aac gac gtc tac ccg acc gcc gtg aag atc gcg acc gtg ttc gcg gtg	480
Asn Asp Val Tyr Pro Thr Ala Val Lys Ile Ala Thr Val Phe Ala Val	
145 150 155 160	
cgc ggt ctg ctc aag gcc atg gcg gtg ctc cag gac gcc ttc gcc cgc	528
Arg Gly Leu Leu Lys Ala Met Ala Val Leu Gln Asp Ala Phe Ala Arg	
165 170 175	
aag gcc gtc gag ttc cgt gac gtg ctg aag atg ggc cgc acc cag ctc	576
Lys Ala Val Glu Phe Arg Asp Val Leu Lys Met Gly Arg Thr Gln Leu	
180 185 190	
cag gac gcg gtg ccc atg acg ctg ggg cag gag ttc tcc gcg tac gcc	624
Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Ser Ala Tyr Ala	
195 200 205	
gtc atg ctc gac gag gac cgc agc cgg ctg gcc gag gcc gtc gaa ctg	672
Val Met Leu Asp Glu Asp Arg Ser Arg Leu Ala Glu Ala Val Glu Leu	
210 215 220	
atc cac gag atc aac ctg ggc gcc acg gcg atc ggc acc gga ctc aac	720
Ile His Glu Ile Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn	
225 230 235 240	
gcg ccc gcc gga tac gcc gag tcg gcc cgc cgc cag ctc gcc gcc ctc	768
Ala Pro Ala Gly Tyr Ala Glu Ser Ala Arg Arg Gln Leu Ala Ala Leu	
245 250 255	
acc ggg ctg ccg ctg gtc acc gcc gcc aac ctg gtc gag gcc acc cag	816
Thr Gly Leu Pro Leu Val Thr Ala Ala Asn Leu Val Glu Ala Thr Gln	
260 265 270	
gac tgc ggt gcc ttc gtc cag atg tcg ggg gtg ctc aag cgg atc gcc	864
Asp Cys Gly Ala Phe Val Gln Met Ser Gly Val Leu Lys Arg Ile Ala	
275 280 285 290	
gtc aag ctc tcc aag agc tgc aac gac ctg cgg ctg tcg tcc ggg	912
Val Lys Leu Ser Lys Ser Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly	
295 300	
ccg cgc gcg ggg ctc aac gag atc aac ctg ccg ccg gta cag gcc ggt	960
Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Val Gln Ala Gly	

PF59083SeqList PF59083.txt

305	tcg agc atc atg ccc ggc aag gtc aac ccg gtc atc ccc gag gtc gtc	310	315	320	
Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Val					1008
aac cag gtc gcc ttc gag gtc atc ggc aac gac gtc gcg atc acc atg		325	330	335	1056
Asn Gln Val Ala Phe Glu Val Ile Gly Asn Asp Val Ala Ile Thr Met					
gcc gcc gag gcg ggg cag ctc cag ctc aac gcc ttc gag ccg atc atc		340	345	350	1104
Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Ala Phe Glu Pro Ile Ile					
ctg cac tcg ctg tcc gag agc atc acg cat ctg cgg gcc gcc tgc ctg		355	360	365	1152
Leu His Ser Leu Ser Glu Ser Ile Thr His Leu Arg Ala Ala Cys Leu					
acg ctc gcc gag gcg tgc gtc gac ggg atc acg gcc aac acc gag gaa		370	375	380	1200
Thr Leu Ala Glu Arg Cys Val Asp Gly Ile Thr Ala Asn Thr Glu Glu					
ctg cgc gcc gcc gtg gag aac tcc atc ggc ctg gtg acc gcc ctc aac		385	390	395	1248
Leu Arg Ala Ala Val Glu Asn Ser Ile Gly Leu Val Thr Ala Leu Asn					
ccg cac atc ggg tac acg gcg gcc acc gcc atc gcc aag gag gcc ctc		405	410	415	1296
Pro His Ile Gly Tyr Thr Ala Ala Thr Ala Ile Ala Lys Glu Ala Leu					
gcc acc ggg cgc ggg gtc gcc gaa ctc gtc ctg gag aag ggc ctg ttg		420	425	430	1344
Ala Thr Gly Arg Gly Val Ala Glu Leu Val Leu Glu Lys Gly Leu Leu					
ccg gcc gac gcg ctc gcg tcg ctg ctg cgg ccc gag gtg ctc gcg ggc		435	440	445	1392
Pro Ala Asp Arg Leu Ala Ser Leu Leu Arg Pro Glu Val Leu Ala Gly					
agc ggc tcc ccg cag atc tga		450	455	460	1413
Ser Gly Ser Pro Gln Ile					
465		470			

<210> 9600

<211> 470

<212> PRT

<213> Streptomyces avermitilis MA-4680

<400> 9600

Met Thr Ala Ala Ala His Arg Ser Glu His Asp Leu Leu Gly Asp Arg	1	5	10	15
Asp Val Pro Ala Glu Ala Tyr Trp Gly Ile His Ser Leu Arg Ala Lys	20	25	30	
Glu Asn Phe Pro Ile Thr Gly Thr Pro Ile Ser Thr Tyr Pro His Leu	35	40	45	
Ile Asp Ala Leu Ala Ala Val Lys Glu Ala Ala Ala Leu Ala Asn Glu	50	55	60	
Glu Leu Gly Leu Leu Glu Pro Lys Lys Ala Ala Ala Ile Val Ala Ala	65	70	75	80
Cys Arg Glu Ile Arg Asp Gly Lys Leu His Asp Gln Phe Val Val Asp	85	90	95	
Val Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu	100	105	110	
Val Ile Ala Asn Arg Ala Leu Glu Leu Leu Gly His Ala Lys Gly Glu	115	120	125	
Tyr Arg His Leu His Pro Asn Glu Asp Val Asn Leu Gly Gln Ser Thr	130	135	140	
Asn Asp Val Tyr Pro Thr Ala Val Lys Ile Ala Thr Val Phe Ala Val	145	150	155	160
Arg Gly Leu Leu Lys Ala Met Ala Val Leu Gln Asp Ala Phe Ala Arg	165	170	175	
Lys Ala Val Glu Phe Arg Asp Val Leu Lys Met Gly Arg Thr Gln Leu	180	185	190	
Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Ser Ala Tyr Ala	195	200	205	
Val Met Leu Asp Glu Asp Arg Ser Arg Leu Ala Glu Ala Val Glu Leu	210	215	220	
Ile His Glu Ile Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn	225	230	235	240
Ala Pro Ala Gly Tyr Ala Glu Ser Ala Arg Arg Gln Leu Ala Ala Leu				

PF59083SeqList PF59083.txt

```

      245      250      255
Thr Gly Leu Pro Leu Val Thr Ala Ala Asn Leu Val Glu Ala Thr Gln
      260      265      270
Asp Cys Gly Ala Phe Val Gln Met Ser Gly Val Leu Lys Arg Ile Ala
      275      280      285
Val Lys Leu Ser Lys Ser Cys Asn Asp Leu Arg Leu Ser Ser Gly
      290      295      300
Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Val Gln Ala Gly
      305      310      315
Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Val
      320      325      330
Asn Gln Val Ala Phe Glu Val Ile Gly Asn Asp Val Ala Ile Thr Met
      335      340      345
Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Ala Phe Glu Pro Ile Ile
      350      355      360
Leu His Ser Leu Ser Glu Ser Ile Thr His Leu Arg Ala Ala Cys Leu
      365      370      375
Thr Leu Ala Glu Arg Cys Val Asp Gly Ile Thr Ala Asn Thr Glu Glu
      380      385      390
Leu Arg Ala Ala Val Glu Asn Ser Ile Gly Leu Val Thr Ala Leu Asn
      395      400      405
Pro His Ile Gly Tyr Thr Ala Ala Thr Ala Ile Ala Lys Glu Ala Leu
      410      415      420
Ala Thr Gly Arg Gly Val Ala Glu Leu Val Leu Glu Lys Gly Leu Leu
      425      430      435
Pro Ala Asp Arg Leu Ala Ser Leu Leu Arg Pro Glu Val Leu Ala Gly
      440      445      450
Ser Gly Ser Pro Gln Ile
      455      460      465

```

<210> 9601

<211> 1434

<212> DNA

<213> Bacillus anthracis str. Ames

<220>

<221> CDS

<222> (1)..(1434)

<223> transl_table=11

<400> 9601

```

atg ata gca acg aag gat ata cgt ata gaa aaa gac ttt tta ggt gaa      48
Met Ile Ala Thr Lys Asp Ile Arg Ile Glu Lys Asp Phe Leu Gly Glu
1      5      10      15
aag gaa gta cca agt ata gct tat tac ggt gta caa aca tta cgc gct      96
Lys Glu Val Pro Ser Ile Ala Tyr Tyr Gly Val Gln Thr Leu Arg Ala
20      25      30
gta gaa aac ttc ccg att aca gga tat cgc att cat ccg tca ctc att      144
Val Glu Asn Phe Pro Ile Thr Gly Tyr Arg Ile His Pro Ser Leu Ile
35      40      45
acg gca atg gca att gtg aaa aaa gcg gcg gca ctt gca aat atg gat      192
Thr Ala Met Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met Asp
50      55      60
act gga tac tta gcg aaa gat att gga cat gaa att gcg gag gca gcg      240
Thr Gly Tyr Leu Ala Lys Asp Ile Gly His Glu Ile Ala Glu Ala Ala
65      70      75      80
caa gag att gtt gat gga aag ttc cat gat caa ttt att gtg gat cca      288
Gln Glu Ile Val Asp Gly Lys Phe His Asp Gln Phe Ile Val Asp Pro
85      90      95
atc caa ggt ggt gct gga act tct att aat atg aat aca aac gaa gta      336
Ile Gln Gly Gly Ala Gly Thr Ser Ile Asn Met Asn Thr Asn Glu Val
100      105      110
atc gct aat cga gcg tta gaa cgt atg gga tat gaa aaa ggc gag tat      384
Ile Ala Asn Arg Ala Leu Glu Met Gly Tyr Glu Lys Gly Glu Tyr
115      120      125
gca aaa att agc cca aat acg cat gta aac atg gct caa tca acg aat      432
Ala Lys Ile Ser Pro Asn Thr His Val Asn Met Ala Gln Ser Thr Asn
130      135      140
gat gcg ttt cca acg ggg att cat att gca act ctt atg agg tta gaa      480

```

PF59083SeqList PF59083.txt

Asp 145	Ala	Phe	Pro	Thr	Gly 150	Ile	His	Ile	Ala	Thr 155	Leu	Met	Arg	Leu	Glu 160	
gaa	ctt	ctt	att	aca	atg	gaa	gaa	ctt	cat	gct	gct	ttt	cgt	gca	aaa	528
Glu	Leu	Leu	Ile	Thr 165	Met	Glu	Glu	Leu	His 170	Ala	Ala	Phe	Arg	Ala 175	Lys	
gca	aaa	gag	ttc	gat	cac	gtc	att	aaa	atg	gga	cgt	aca	cat	tta	caa	576
Ala	Lys	Glu	Phe	Asp	His	Val	Ile	Lys	Met	Gly	Arg	Thr	His 190	Leu	Gln	
gat	gct	gtg	ccg	att	cgt	ctt	ggg	caa	gaa	ttt	gaa	gcg	tat	agc	cga	624
Asp	Ala	Val 195	Pro	Ile	Arg	Leu	Gly 200	Gln	Glu	Phe	Glu	Tyr	Ser	Arg		
gtg	ctt	gcg	cgt	gat	ata	aaa	aga	att	aaa	cag	tct	cgc	caa	cat	tta	672
Val	Leu	Ala	Arg	Asp	Ile	Lys 215	Arg	Ile	Lys	Gln	Ser	Arg	Gln	His	Leu	
tat	gaa	gtg	aat	atg	ggg	gcg	aca	gct	gtt	ggg	acg	gga	tta	aat	gca	720
Tyr 225	Glu	Val	Asn	Met	Gly 230	Ala	Thr	Ala	Val	Gly 235	Thr	Gly	Leu	Asn	Ala 240	
aac	cct	acg	tac	att	gaa	caa	gtg	gtt	aaa	cac	ttg	cga	aca	ttt	agc	768
Asn	Pro	Thr	Tyr	Ile 245	Glu	Gln	Val	Val	Lys 250	His	Leu	Arg	Thr	Phe 255	Ser	
gga	ttt	cca	ctt	ggt	gca	gag	cat	ttg	gtt	gat	gca	acg	caa	aat		816
Gly	Phe	Pro	Leu	Val 260	Gly	Ala	Glu	His	Leu	Val	Asp	Ala	Thr 270	Gln	Asn	
aca	gat	gca	tac	aca	gaa	gta	tct	gca	gca	tta	aaa	gta	tgt	atg	atg	864
Thr	Asp	Ala	Tyr	Thr	Glu	Val	Ser	Ala	Ala	Leu	Lys	Val	Cys	Met	Met	
aat	atg	tct	aaa	att	gcg	aat	gac	ctt	cgt	att	atg	gca	tct	ggg	cca	912
Asn	Met	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Ile	Met	Ala	Ser	Gly	Pro	
cgt	gtt	gga	ttg	gcg	gaa	att	caa	tta	cca	gct	cgc	caa	cca	ggg	tca	960
Arg	Val	Gly	Leu	Ala	Glu	Ile	Gln	Leu	Pro	Ala	Arg	Gln	Pro	Gly	Ser	
305					310					315					320	
tct	att	atg	ccg	ggg	aaa	gta	aat	cct	gtt	atg	gca	gaa	gta	att	aat	1008
Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Val	Ile	Asn	
				325					330					335		
caa	gtg	gct	ttc	caa	gta	att	ggg	aat	gat	cat	aca	att	tgc	tta	gcg	1056
Gln	Val	Ala	Phe	Gln	Val	Ile	Gly	Asn	Asp	His	Thr	Ile	Cys	Leu	Ala	
				340					345				350			
tca	gaa	gcc	gga	caa	ttg	gag	ctc	aac	gta	atg	gag	ccg	gtg	ctt	gta	1104
Ser	Glu	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Leu	Val	
		355					360					365				
ttt	aat	tta	att	caa	tct	att	agt	att	atg	aat	aac	gga	ttc	cgt	gta	1152
Phe	Asn	Leu	Ile	Gln	Ser	Ile	Ser	Ile	Met	Asn	Asn	Gly	Phe	Arg	Val	
		370				375					380					
ttc	cgt	gaa	tat	tgt	att	aaa	gga	att	aca	gca	aat	gaa	gaa	ttg	ctg	1200
Phe	Arg	Glu	Tyr	Cys	Ile	Lys	Gly	Ile	Thr	Ala	Asn	Glu	Glu	Leu	Leu	
				390						395					400	
aag	caa	tat	gtt	gag	aaa	agt	gtt	gga	att	aca	gca	gtt	aac	cct		1248
Lys	Gln	Tyr	Val	Glu	Lys	Ser	Val	Gly	Ile	Thr	Ala	Val	Asn	Pro		
				405					410				415			
cat	att	ggg	tat	gaa	gca	gca	tct	cgc	att	gca	cgt	gaa	gcg	att	gaa	1296
His	Ile	Gly	Tyr	Glu	Ala	Ala	Ser	Arg	Ile	Ala	Arg	Glu	Ala	Ile	Glu	
			420					425					430			
aca	gga	aaa	tct	gtt	agg	gag	tta	tgt	tta	gaa	cat	ggg	gta	ctg	aca	1344
Thr	Gly	Lys	Ser	Val	Arg	Glu	Leu	Cys	Leu	Glu	His	Gly	Val	Leu	Thr	
				435			440					445				
gaa	gaa	gaa	ttg	gat	att	att	tta	gat	cca	ttc	gaa	atg	acg	cat	cct	1392
Glu	Glu	Glu	Leu	Asp	Ile	Ile	Leu	Asp	Pro	Phe	Glu	Met	Thr	His	Pro	
		450				455					460					
gaa	att	gct	ggg	gct	tct	tta	aag	gat	aag	atg	taa					1434
Glu	Ile	Ala	Gly	Ala	Ser	Leu	Leu	Lys	Asp	Lys	Lys	Met				
				470					475							

<210> 9602

<211> 477

<212> PRT

<213> Bacillus anthracis str. Ames

<400> 9602

PF59083SeqList PF59083.txt

```

Met Ile Ala Thr Lys Asp Ile Arg Ile Glu Lys Asp Phe Leu Gly Glu
1      5      10      15
Lys Glu Val Pro Ser Ile Ala Tyr Tyr Gly Val Gln Thr Leu Arg Ala
      20      25      30
Val Glu Asn Phe Pro Ile Thr Gly Tyr Arg Ile His Pro Ser Leu Ile
      35      40      45
Thr Ala Met Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met Asp
      50      55      60
Thr Gly Tyr Leu Ala Lys Asp Ile Gly His Glu Ile Ala Glu Ala Ala
65      70      75      80
Gln Glu Ile Val Asp Gly Lys Phe His Asp Gln Phe Ile Val Asp Pro
      85      90      95
Ile Gln Gly Gly Ala Gly Thr Ser Ile Asn Met Asn Thr Asn Glu Val
      100      105      110
Ile Ala Asn Arg Ala Leu Glu Arg Met Gly Tyr Glu Lys Gly Glu Tyr
      115      120      125
Ala Lys Ile Ser Pro Asn Thr His Val Asn Met Ala Gln Ser Thr Asn
      130      135      140
Asp Ala Phe Pro Thr Gly Ile His Ile Ala Thr Leu Met Arg Leu Glu
145      150      155      160
Glu Leu Leu Ile Thr Met Glu Glu Leu His Ala Ala Phe Arg Ala Lys
      165      170      175
Ala Lys Glu Phe Asp His Val Ile Lys Met Gly Arg Thr His Leu Gln
      180      185      190
Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser Arg
      195      200      205
Val Leu Ala Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His Leu
      210      215      220
Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn Ala
225      230      235      240
Asn Pro Thr Tyr Ile Glu Gln Val Val Lys His Leu Arg Thr Phe Ser
      245      250      255
Gly Phe Pro Leu Val Gly Ala Glu His Leu Val Asp Ala Thr Gln Asn
      260      265      270
Thr Asp Ala Tyr Thr Glu Val Ser Ala Ala Leu Lys Val Cys Met Met
      275      280      285
Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Ile Met Ala Ser Gly Pro
      290      295      300
Arg Val Gly Leu Ala Glu Ile Gln Leu Pro Ala Arg Gln Pro Gly Ser
305      310      315      320
Ser Ile Met Pro Gly Lys Val Asn Pro Val Met Ala Glu Val Ile Asn
      325      330      335
Gln Val Ala Phe Gln Val Ile Gly Asn Asp His Thr Ile Cys Leu Ala
      340      345      350
Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu Val
      355      360      365
Phe Asn Leu Ile Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg Val
      370      375      380
Phe Arg Glu Tyr Cys Ile Lys Gly Ile Thr Ala Asn Glu Glu Leu Leu
385      390      395      400
Lys Gln Tyr Val Glu Lys Ser Val Gly Ile Ile Thr Ala Val Asn Pro
      405      410      415
His Ile Gly Tyr Glu Ala Ala Ser Arg Ile Ala Arg Glu Ala Ile Glu
      420      425      430
Thr Gly Lys Ser Val Arg Glu Leu Cys Leu Glu His Gly Val Leu Thr
      435      440      445
Glu Glu Glu Leu Asp Ile Ile Leu Asp Pro Phe Glu Met Thr His Pro
      450      455      460
Glu Ile Ala Gly Ala Ser Leu Leu Lys Asp Lys Lys Met
465      470      475

```

<210> 9603

<211> 1533

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1533)

PF59083SeqList PF59083.txt

```

<400> 9603
atg gcc gct ttg aca atg cag ttt gaa gga gag aag aaa aac gta tcc      48
Met Ala Ala Leu Thr Met Gln Phe Glu Gly Glu Lys Lys Asn Val Ser
1      5      10      15
gaa gtt gca gac gta acc ctc aag caa gaa gat gaa caa caa gaa cgt      96
Glu Val Ala Asp Val Thr Leu Lys Gln Glu Asp Glu Gln Gln Glu Arg
20      25      30
aga tct tat tcg acg ccg ttt agg gaa gag aga gac acc ttt ggc ccg      144
Arg Ser Tyr Ser Thr Pro Phe Arg Glu Glu Arg Asp Thr Phe Gly Pro
35      40      45
atc caa gtt cct tcc gat aaa tta tgg gga gca cag acg cag aga tcg      192
Ile Gln Val Pro Ser Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser
50      55      60
ctt cag aac ttc gag att ggt ggt gac cgc gag cga atg ccc gaa cca      240
Leu Gln Asn Phe Glu Ile Gly Gly Asp Arg Glu Arg Met Pro Glu Pro
65      70      75
atc gtc cga gct ttt ggt gtc ttg aag aaa tgt gct gcc aag gtt aac      288
Ile Val Arg Ala Phe Gly Val Leu Lys Lys Cys Ala Ala Lys Val Asn
85      90      95
atg gag tat ggt ctt gat cca atg att ggg gaa gcc ata atg gaa gct      336
Met Glu Tyr Gly Leu Asp Pro Met Ile Gly Glu Ala Ile Met Glu Ala
100      105      110
gca caa gaa gta gca gaa gga aag ctc aat gat cat ttc cct ctt gtt      384
Ala Gln Glu Val Ala Glu Gly Lys Leu Asn Asp His Phe Pro Leu Val
115      120      125
gta tgg caa act ggt agt ggg acg cag agt aat atg aat gct aat gag      432
Val Trp Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu
130      135      140
gtc att gcc aat aga gca gct gag att ctt ggt cac aaa cgt ggt gaa      480
Val Ile Ala Asn Arg Ala Ala Glu Ile Leu Gly His Lys Arg Gly Glu
145      150      155
aaa att gtg cac cca aat gac cat gtg aac aga tca caa tct tct aat      528
Lys Ile Val His Pro Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn
165      170      175
gac act ttt cca act gtc atg cac att gca gct gca acc gag att act      576
Asp Thr Phe Pro Thr Val Met His Ile Ala Ala Ala Thr Glu Ile Thr
180      185      190
tcg agg cta atc cct agt ttg aaa aat ttg cat agc tct ttg gaa tct      624
Ser Arg Leu Ile Pro Ser Leu Lys Asn Leu His Ser Ser Leu Glu Ser
195      200      205
aag tcc ttc gag ttt aaa gat ata gtg aaa atc gga aga act cat act      672
Lys Ser Phe Glu Phe Lys Asp Ile Val Lys Ile Gly Arg Thr His Thr
210      215      220
caa gat gct aca cct ttg aca tta gga caa gaa ttt ggt ggc tat gct      720
Gln Asp Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Gly Gly Tyr Ala
225      230      235
act caa gtt gag tat gga ctt aat aga gtc gca tgt act cta ccc cgc      768
Thr Gln Val Glu Tyr Gly Leu Asn Arg Val Ala Cys Thr Leu Pro Arg
245      250      255
atc tat cag ctt gca caa ggt gga act gct gtt ggg acc gga tta aac      816
Ile Tyr Gln Leu Ala Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn
260      265      270
act aag aaa ggg ttt gat gta aag atc gct gct gca gta gct gaa gaa      864
Thr Lys Lys Gly Phe Asp Val Lys Ile Ala Ala Ala Val Ala Glu Glu
275      280      285
aca aac ttg cca ttc gtc acc gca gaa aac aag ttt gaa gct ctg gct      912
Thr Asn Leu Pro Phe Val Thr Ala Glu Asn Lys Phe Glu Ala Leu Ala
290      295      300
gca cac gat gct tgt gtt gaa aca agt gga tct ctt aac aca atc gcc      960
Ala His Asp Ala Cys Val Glu Thr Ser Gly Ser Leu Asn Thr Ile Ala
305      310      315
aca tca ttg atg aag att gcc aat gat ata cgt ttt ctt gga agt ggt      1008
Thr Ser Leu Met Lys Ile Ala Asn Asp Ile Arg Phe Leu Gly Ser Gly
325      330      335
cca aga tgt ggt ctt ggt gaa ctt tct ctg cct gag aat gaa cca gga      1056
Pro Arg Cys Gly Leu Gly Glu Leu Ser Leu Pro Glu Asn Glu Pro Gly
340      345      350
agc agt att atg cct gga aag gta aat cct aca cag tgt gag gcc ttg      1104
350

```

PF59083SeqList PF59083.txt

Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	
		355					360					365				
act	atg	gtt	tgt	gct	caa	gtt	atg	gga	aac	cat	gta	gcc	gtg	aca	att	1152
Thr	Met	Val	Cys	Ala	Gln	Val	Met	Gly	Asn	His	Val	Ala	Val	Thr	Ile	
		370					375					380				
ggg	ggg	tcg	aat	ggg	cat	ttt	gaa	ttg	aat	gta	ttc	aag	ccg	gtt	atc	1200
Gly	Gly	Ser	Asn	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Ile	
		385			390					395					400	
gca	agc	gct	ctc	tta	cat	tcc	att	aga	cta	ata	gca	gat	gct	tca	gct	1248
Ala	Ser	Ala	Leu	Leu	His	Ser	Ile	Arg	Leu	Ile	Ala	Asp	Ala	Ser	Ala	
				405					410					415		
tca	ttt	gag	aaa	aac	tgt	gtt	aga	ggc	att	gag	gcc	aac	aga	gaa	agg	1296
Ser	Phe	Glu	Lys	Asn	Cys	Val	Arg	Gly	Ile	Glu	Ala	Asn	Arg	Glu	Arg	
			420					425					430			
atc	tca	aag	cta	ttg	cac	gag	tct	ctt	atg	ctt	gtg	aca	tca	ttg	aat	1344
Ile	Ser	Lys	Leu	Leu	His	Glu	Ser	Leu	Met	Leu	Val	Thr	Ser	Leu	Asn	
			435				440					445				
cct	aaa	att	ggc	tat	gac	aat	gct	gca	gca	gta	gcc	aaa	aga	gct	cac	1392
Pro	Lys	Ile	Gly	Tyr	Asp	Asn	Ala	Ala	Ala	Val	Ala	Lys	Arg	Ala	His	
			450			455					460					
aaa	gaa	gga	tgc	aca	tta	aag	gta	aac	aat	aaa	cta	tta	acg	ttt	tca	1440
Lys	Glu	Gly	Cys	Thr	Leu	Lys	Val	Asn	Asn	Lys	Leu	Leu	Thr	Phe	Ser	
					470					475					480	
tca	cta	aat	aaa	tcg	gaa	ttt	aaa	ccc	att	ttt	agc	aag	aga	aaa	cat	1488
Ser	Leu	Asn	Lys	Ser	Glu	Phe	Lys	Pro	Ile	Phe	Ser	Lys	Arg	Lys	His	
				485					490					495		
gtt	cat	gtt	tgt	tac	aat	ata	ttt	gtt	gtt	cta	ttt	tgg	att	taa		1533
Val	His	Val	Cys	Tyr	Asn	Ile	Phe	Val	Val	Leu	Phe	Trp	Ile			
			500					505					510			

<210> 9604

<211> 510

<212> PRT

<213> Arabidopsis thaliana

<400> 9604

Met	Ala	Ala	Leu	Thr	Met	Gln	Phe	Glu	Gly	Glu	Lys	Lys	Asn	Val	Ser	
1				5					10					15		
Glu	Val	Ala	Asp	Val	Thr	Leu	Lys	Gln	Glu	Asp	Glu	Gln	Gln	Glu	Arg	
			20					25					30			
Arg	Ser	Tyr	Ser	Thr	Pro	Phe	Arg	Glu	Glu	Arg	Asp	Thr	Phe	Gly	Pro	
			35				40					45				
Ile	Gln	Val	Pro	Ser	Asp	Lys	Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	
			50			55				60						
Leu	Gln	Asn	Phe	Glu	Ile	Gly	Gly	Asp	Arg	Glu	Arg	Met	Pro	Glu	Pro	
					70					75					80	
Ile	Val	Arg	Ala	Phe	Gly	Val	Leu	Lys	Lys	Cys	Ala	Ala	Lys	Val	Asn	
				85					90					95		
Met	Glu	Tyr	Gly	Leu	Asp	Pro	Met	Ile	Gly	Glu	Ala	Ile	Met	Glu	Ala	
			100					105					110			
Ala	Gln	Glu	Val	Ala	Glu	Gly	Lys	Leu	Asn	Asp	His	Phe	Pro	Leu	Val	
			115				120					125				
Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	
			130			135					140					
Val	Ile	Ala	Asn	Arg	Ala	Glu	Ile	Leu	Gly	His	Lys	Arg	Gly	Glu		
					150				155					160		
Lys	Ile	Val	His	Pro	Asn	Asp	His	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	
				165					170					175		
Asp	Thr	Phe	Pro	Thr	Val	Met	His	Ile	Ala	Ala	Ala	Thr	Glu	Ile	Thr	
			180					185					190			
Ser	Arg	Leu	Ile	Pro	Ser	Leu	Lys	Asn	Leu	His	Ser	Ser	Leu	Glu	Ser	
			195				200					205				
Lys	Ser	Phe	Glu	Phe	Lys	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Thr	
					215						220					
Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	
					230					235					240	
Thr	Gln	Val	Glu	Tyr	Gly	Leu	Asn	Arg	Val	Ala	Cys	Thr	Leu	Pro	Arg	
				245					250					255		
Ile	Tyr	Gln	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	

PF59083SeqList PF59083.txt

```

      260      265      270
Thr Lys Lys Gly Phe Asp Val Lys Ile Ala Ala Ala Val Ala Glu Glu
      275      280      285
Thr Asn Leu Pro Phe Val Thr Ala Glu Asn Lys Phe Glu Ala Leu Ala
      290      295      300
Ala His Asp Ala Cys Val Thr Ser Gly Ser Leu Asn Thr Ile Ala
      305      310      315
Thr Ser Leu Met Lys Ile Ala Asn Asp Ile Arg Phe Leu Gly Ser Gly
      320      325      330
Pro Arg Cys Gly Leu Gly Glu Leu Ser Leu Pro Glu Asn Glu Pro Gly
      335      340      345
Ser Ser Ile Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu
      350      355      360
Thr Met Val Cys Ala Gln Val Met Gly Asn His Val Ala Val Thr Ile
      365      370      375
Gly Gly Ser Asn Gly His Phe Glu Leu Asn Val Phe Lys Pro Val Ile
      380      385      390
Ala Ser Ala Leu Leu His Ser Ile Arg Leu Ile Ala Asp Ala Ser Ala
      395      400      405
Ser Phe Glu Lys Leu Leu His Val Arg Gly Ile Glu Ala Asn Arg Glu Arg
      410      415      420
Ile Ser Lys Leu Leu His Glu Ser Leu Met Leu Val Thr Ser Leu Asn
      425      430      435
Pro Lys Ile Gly Tyr Asp Asn Ala Ala Ala Val Ala Lys Arg Ala His
      440      445      450
Lys Glu Gly Cys Thr Leu Lys Val Asn Asn Lys Leu Leu Thr Phe Ser
      455      460      465
Ser Leu Asn Lys Ser Glu Phe Lys Pro Ile Phe Ser Lys Arg Lys His
      470      475      480
Val His Val Cys Tyr Asn Ile Phe Val Val Leu Phe Trp Ile
      485      490      495
      500      505      510

```

<210> 9605

<211> 1440

<212> DNA

<213> wigglesworthia glossinidia endosymbiont of Glossina brevipalpis

<220>

<221> CDS

<222> (1)..(1440)

<223> transl_table=11

<400> 9605

```

atg tta aat tct att cga atc gaa caa gat atg att gga ata cgt gaa      48
Met Leu Asn Ser Ile Arg Ile Glu Gln Asp Met Ile Gly Ile Arg Glu
1      5      10      15
att tca aat gaa ttt tat tat ggc att cat act ctt aga gct ata gaa      96
Ile Ser Asn Glu Phe Tyr Tyr Gly Ile His Thr Leu Arg Ala Ile Glu
      20      25      30
aat ttc aaa att agt aaa aat act att aac gat tat cct gaa tta atc      144
Asn Phe Lys Ile Ser Lys Asn Thr Ile Asn Asp Tyr Pro Glu Leu Ile
      35      40      45
aag gga atg gtg atg gtg aaa aaa gca tct gct ctt gca aac aaa cat      192
Lys Gly Met Val Met Val Lys Lys Ala Ser Ala Leu Ala Asn Lys His
      50      55      60
tta aaa gtt tta tca gaa aaa aac gca aaa att ata gta aga gct tgt      240
Leu Lys Val Leu Ser Glu Lys Asn Ala Lys Ile Ile Val Arg Ala Cys
      65      70      75
gat tgt att tta aaa aaa caa aat att tat ctt gat caa ttt cca gta      288
Asp Cys Ile Leu Lys Lys Gln Asn Ile Tyr Leu Asp Gln Phe Pro Val
      80      85      90
gac gct ttt caa gga gga gct gga aca tct gta aat atg aat gtt aat      336
Asp Ala Phe Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Val Asn
      100      105      110
gaa gtt ttg act aat att gga tta gaa ata atg ggt aag aaa aaa gga      384
Glu Val Leu Thr Asn Ile Gly Leu Glu Ile Met Gly Lys Lys Lys Gly
      115      120      125
gat tat aag ttt ctt aat cca aat gat cat tta aat tta agt caa tcc      432
Asp Tyr Lys Phe Leu Asn Pro Asn Asp His Leu Asn Leu Ser Gln Ser

```

PF59083SeqList PF59083.txt																	
130	aca	aac	gat	gca	tat	cca	act	gga	ctt	cgt	tta	tca	ata	tat	aaa	tct	480
	Thr	Asn	Asp	Ala	Tyr	Pro	Thr	Gly	Leu	Arg	Leu	Ser	Ile	Tyr	Lys	Ser	
145	ata	tac	aaa	tta	att	aaa	tca	atc	ata	tta	att	gaa	gat	agt	ttt	tat	528
	Ile	Tyr	Lys	Leu	Ile	Lys	Ser	Ile	Ile	Leu	Ile	Glu	Asp	Ser	Phe	Tyr	
					165					170							
	aaa	aaa	tca	aaa	gaa	ttt	tct	aaa	ata	ata	aaa	atg	ggt	aga	acg	caa	576
	Lys	Lys	Ser	Lys	Glu	Phe	Ser	Lys	Ile	Ile	Lys	Met	Gly	Arg	Thr	Gln	
				180					185					190			
	tta	caa	gat	gct	gtc	cca	atg	aca	ttg	ggt	caa	gaa	ttt	tat	gct	ttt	624
	Leu	Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Tyr	Ala	Phe	
			195				200						205				
	aaa	aca	tct	tta	aaa	aaa	gaa	aga	ata	aat	tta	att	aat	aca	tct	aaa	672
	Lys	Thr	Ser	Leu	Lys	Lys	Glu	Arg	Ile	Asn	Leu	Ile	Asn	Thr	Ser	Lys	
			210				215					220					
	tta	tta	tta	gat	att	aat	ctt	gga	gga	aca	gca	ata	gga	act	aaa	tta	720
	Leu	Leu	Leu	Asp	Ile	Asn	Leu	Gly	Gly	Thr	Ala	Ile	Gly	Thr	Lys	Leu	
	225				230					235						240	
	aat	act	cct	aaa	gga	tat	caa	aaa	gta	gtt	gta	aaa	caa	tta	tca	att	768
	Asn	Thr	Pro	Lys	Gly	Tyr	Gln	Lys	Val	Val	Val	Lys	Gln	Leu	Ser	Ile	
				245					250						255		
	gtt	agc	gga	ata	cag	ttc	aat	cca	gta	aaa	gat	ctt	ata	gaa	tct	aca	816
	Val	Ser	Gly	Ile	Gln	Phe	Asn	Pro	Val	Lys	Asp	Leu	Ile	Glu	Ser	Thr	
			260						265					270			
	tat	gat	tgt	gga	ata	tat	act	att	gtg	cat	gga	aat	tta	aaa	aat	tta	864
	Tyr	Asp	Cys	Gly	Ile	Tyr	Thr	Ile	Val	His	Gly	Asn	Leu	Lys	Asn	Leu	
			275				280						285				
	gct	att	aga	tta	tct	aaa	att	tgt	aat	gat	tta	aga	tta	ttg	tca	tct	912
	Ala	Ile	Arg	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	
	290					295						300					
	ggg	cca	aga	gct	ggg	tta	aat	gaa	ata	aat	tta	cct	gaa	ctt	caa	gct	960
	Gly	Pro	Arg	Ala	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	Ala	
	305				310					315						320	
	gga	tct	tcg	ata	atg	cct	gct	aaa	gtt	aac	cca	gtt	tta	cca	gaa	gta	1008
	Gly	Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Leu	Pro	Glu	Val	
				325					330						335		
	gtt	aat	cag	gta	tgt	ttt	aag	gta	tgt	gga	aat	gat	att	tgc	gta	atg	1056
	Val	Asn	Gln	Val	Cys	Phe	Lys	Val	Cys	Gly	Asn	Asp	Ile	Cys	Val	Met	
			340						345					350			
	atg	gca	gca	gag	tca	ggt	caa	tta	caa	tta	aat	gct	atg	gaa	cca	gta	1104
	Met	Ala	Ala	Glu	Ser	Gly	Gln	Leu	Gln	Leu	Asn	Ala	Met	Glu	Pro	Val	
			355				360						365				
	ata	agt	caa	tct	ata	ttt	gaa	tca	ata	aat	att	ctc	aaa	aat	gct	att	1152
	Ile	Ser	Gln	Ser	Ile	Phe	Glu	Ser	Ile	Asn	Ile	Leu	Lys	Asn	Ala	Ile	
			370				375					380					
	tta	tct	tta	aaa	gaa	aaa	tgt	ata	gat	gga	atc	aca	gca	aat	aaa	aaa	1200
	Leu	Ser	Leu	Lys	Glu	Lys	Cys	Ile	Asp	Gly	Ile	Thr	Ala	Asn	Lys	Lys	
	385				390					395						400	
	att	tgt	gaa	tct	tat	gta	tta	aat	tct	ata	gga	ata	gtt	gca	tat	tta	1248
	Ile	Cys	Glu	Ser	Tyr	Val	Leu	Asn	Ser	Ile	Gly	Ile	Val	Ala	Tyr	Leu	
				405					410						415		
	aat	cct	ttt	att	ggt	cat	cat	aac	gga	gat	ata	atc	gga	aaa	att	tgt	1296
	Asn	Pro	Phe	Ile	Gly	His	His	Asn	Gly	Asp	Ile	Ile	Gly	Lys	Ile	Cys	
			420						425					430			
	tct	aaa	agc	ggt	aga	agt	gta	aaa	gaa	gtt	gta	ttg	gaa	aaa	gga	ttt	1344
	Ser	Lys	Ser	Gly	Arg	Ser	Val	Lys	Glu	Val	Val	Leu	Glu	Lys	Gly	Phe	
			435				440						445				
	tta	aca	gaa	aaa	gaa	ctt	aat	gat	att	ttt	tca	ttt	aat	aat	tta	ata	1392
	Leu	Thr	Glu	Lys	Glu	Leu	Asn	Asp	Ile	Phe	Ser	Phe	Asn	Asn	Leu	Ile	
			450				455					460					
	cat	cca	aaa	tat	aaa	aat	aaa	aat	agt	tct	gaa	gat	tta	tca	atc		1437
	His	Pro	Lys	Tyr	Lys	Asn	Lys	Asn	Ser	Ser	Glu	Asp	Leu	Ser	Ile		
	465				470						475						
	taa																1440

PF59083SeqList PF59083.txt

<211> 479

<212> PRT

<213> wigglesworthia glossinidia endosymbiont of Glossina brevipalpis

<400> 9606

```

Met Leu Asn Ser Ile Arg Ile Glu Gln Asp Met Ile Gly Ile Arg Glu
1      5      10      15
Ile Ser Asn Glu Phe Tyr Tyr Gly Ile His Thr Leu Arg Ala Ile Glu
      20      25      30
Asn Phe Lys Ile Ser Lys Asn Thr Ile Asn Asp Tyr Pro Glu Leu Ile
      35      40      45
Lys Gly Met Val Met Val Lys Lys Ala Ser Ala Leu Ala Asn Lys His
      50      55      60
Leu Lys Val Leu Ser Glu Lys Asn Ala Lys Ile Ile Val Arg Ala Cys
65      70      75      80
Asp Cys Ile Leu Lys Lys Gln Asn Ile Tyr Leu Asp Gln Phe Pro Val
      85      90      95
Asp Ala Phe Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Val Asn
      100      105      110
Glu Val Leu Thr Asn Ile Gly Leu Glu Ile Met Gly Lys Lys Gly
      115      120      125
Asp Tyr Lys Phe Leu Asn Pro Asn Asp His Leu Asn Leu Ser Gln Ser
      130      135      140
Thr Asn Asp Ala Tyr Pro Thr Gly Leu Arg Leu Ser Ile Tyr Lys Ser
145      150      155      160
Ile Tyr Lys Leu Ile Lys Ser Ile Ile Leu Ile Glu Asp Ser Phe Tyr
      165      170      175
Lys Lys Ser Lys Glu Phe Ser Lys Ile Ile Lys Met Gly Arg Thr Gln
      180      185      190
Leu Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Tyr Ala Phe
      195      200      205
Lys Thr Ser Leu Lys Lys Glu Arg Ile Asn Leu Ile Asn Thr Ser Lys
      210      215      220
Leu Leu Leu Asp Ile Asn Leu Gly Gly Thr Ala Ile Gly Thr Lys Leu
225      230      235      240
Asn Thr Pro Lys Gly Tyr Gln Lys Val Val Val Lys Gln Leu Ser Ile
      245      250      255
Val Ser Gly Ile Gln Phe Asn Pro Val Lys Asp Leu Ile Glu Ser Thr
      260      265      270
Tyr Asp Cys Gly Ile Tyr Thr Ile Val His Gly Asn Leu Lys Asn Leu
      275      280      285
Ala Ile Arg Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser
      290      295      300
Gly Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala
305      310      315      320
Gly Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Leu Pro Glu Val
      325      330      335
Val Asn Gln Val Cys Phe Lys Val Cys Gly Asn Asp Ile Cys Val Met
      340      345      350
Met Ala Ala Glu Ser Gly Gln Leu Gln Leu Asn Ala Met Glu Pro Val
      355      360      365
Ile Ser Gln Ser Ile Phe Glu Ser Ile Asn Ile Leu Lys Asn Ala Ile
      370      375      380
Leu Ser Leu Lys Glu Lys Cys Ile Asp Gly Ile Thr Ala Asn Lys Lys
385      390      395      400
Ile Cys Glu Ser Tyr Val Leu Asn Ser Ile Gly Ile Val Ala Tyr Leu
      405      410      415
Asn Pro Phe Ile Gly His His Asn Gly Asp Ile Ile Gly Lys Ile Cys
      420      425      430
Ser Lys Ser Gly Arg Ser Val Lys Glu Val Val Leu Glu Lys Gly Phe
      435      440      445
Leu Thr Glu Lys Glu Leu Asn Asp Ile Phe Ser Phe Asn Asn Leu Ile
      450      455      460
His Pro Lys Tyr Lys Asn Lys Asn Ser Ser Glu Asp Leu Ser Ile
465      470      475

```

<210> 9607

<211> 1428

<212> DNA

<213> Haemophilus ducreyi 35000HP

<220>

<221> CDS

<222> (1)..(1428)

<223> transl_table=11

<400> 9607

atg agt aat gtg cgt att gaa gtg gat tta ctc ggc gaa aga gaa gtg	48
Met Ser Asn Val Arg Ile Glu Val Asp Leu Leu Gly Glu Arg Glu Val	
1 5 10 15	
cca aat cag gtc tat tgg gga att cat act tta aga gcg gtt gaa aat	96
Pro Asn Gln Val Tyr Trp Gly Ile His Thr Leu Arg Ala Val Glu Asn	
20 25 30	
ttt aat att tct aac aat act att tca gat ata cct gaa ttt gtc cgt	144
Phe Asn Ile Ser Asn Asn Thr Ile Ser Asp Ile Pro Glu Phe Val Arg	
35 40 45	
ggg atg gtt atg gtg aaa aaa gcc acc gca tta gca aat ggc gaa tta	192
Gly Met Val Met Val Lys Lys Ala Thr Ala Leu Ala Asn Gly Glu Leu	
50 55 60	
ggg gca att ccc aaa aaa gtg gca cag gct att gtg caa gcg tgt gat	240
Gly Ala Ile Pro Lys Lys Val Ala Gln Ala Ile Val Gln Ala Cys Asp	
65 70 75 80	
gaa att tta gtg aat ggt cgt tgt atg gat caa ttt ccg tca gat gtt	288
Glu Ile Leu Val Asn Gly Arg Cys Met Asp Gln Phe Pro Ser Asp Val	
85 90 95	
tat caa ggc ggt gcc ggt acc tcg gtt aat atg aac act aat gag gtt	336
Tyr Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val	
100 105 110	
att gct aac tta gcg ctt gaa atg cta ggg cat aaa aaa ggg gaa tat	384
Ile Ala Asn Leu Ala Leu Glu Met Leu Gly His Lys Lys Gly Glu Tyr	
115 120 125	
cat att att gat cca atg gat cac gtt aat gct agt caa tca acg aat	432
His Ile Ile Asp Pro Met Asp His Val Asn Ala Ser Gln Ser Thr Asn	
130 135 140	
gat gct tat cct aca gga ttc cgc att gct gtg tat aac agc tta atg	480
Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Asn Ser Leu Met	
145 150 155 160	
cat tta att gaa caa gtc ctt tat tta caa cag ggc ttt gaa gag aaa	528
His Leu Ile Glu Gln Val Leu Tyr Leu Gln Gly Phe Glu Glu Lys	
165 170 175	
gcg gtc gaa ttt gcc aat gtt ctt aaa atg ggg cgg aca cag ttg caa	576
Ala Val Glu Phe Ala Asn Val Leu Lys Met Gly Arg Thr Gln Leu Gln	
180 185 190	
gat gca gtg cct atg aca gtt ggt caa gaa ttt aaa gca ttt gcg gtg	624
Asp Ala Val Pro Met Thr Val Gly Gln Glu Phe Lys Ala Phe Ala Val	
195 200 205	
tta tta gca gaa gaa gta cgt aat tta aaa cgt act gct caa tta tta	672
Leu Leu Ala Glu Glu Val Arg Asn Leu Lys Arg Thr Ala Gln Leu Leu	
210 215 220	
ctt gag gtt aac tta ggc gca act gca att ggc acg ggg tta aat aca	720
Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr	
225 230 235 240	
ccg gca ggt tat tca gaa tta gcg gta aaa tat tta tca gaa gta aca	768
Pro Ala Gly Tyr Ser Glu Leu Ala Val Lys Tyr Leu Ser Glu Val Thr	
245 250 255	
ggg tta gct tgt gtt tta tca gaa aat tta att gaa gca act tca gat	816
Gly Leu Ala Cys Val Leu Ser Glu Asn Leu Ile Glu Ala Thr Ser Asp	
260 265 270	
tgt ggt gct tat gta atg gta cac ggt gcg ttg aaa cgt act gcg gtt	864
Cys Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Thr Ala Val	
275 280 285	
aag tta tct aaa gta tgt aat gat tta cgc tta ctt tca tct gga cct	912
Lys Leu Ser Lys Val Cys Asn Asp Leu Arg Leu Ser Ser Gly Pro	
290 295 300	
aga gcg ggt ttg aat gaa att aat ctg ccg gaa ttg caa gcg ggt tct	960
Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly Ser	
305 310 315 320	
tct att atg cca gct aaa gta aat cca gtg gta cct gag gtg gtt aat	1008

PF59083SeqList PF59083.txt

Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Val	Pro	Glu	Val	Val	Asn	
				325					330					335		
caa	gta	tgc	ttt	aaa	gtg	ata	ggg	aat	gat	aca	acc	gtt	act	ttt	gca	1056
Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Thr	Val	Thr	Phe	Ala	
			340					345					350			
gca	gaa	gcg	ggg	cag	tta	caa	ttg	aat	gta	atg	gag	ccg	gtg	att	gga	1104
Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile	Gly	
		355					360					365				
cag	gca	atg	ttt	gaa	tct	att	gcc	att	tta	gca	aat	gcg	tgt	gtc	aat	1152
Gln	Ala	Met	Phe	Glu	Ser	Ile	Ala	Ile	Leu	Ala	Asn	Ala	Cys	Val	Asn	
	370					375					380					
tta	cgt	gat	aaa	tgc	gtc	gat	ggc	atc	agt	gtc	aat	aaa	gaa	atc	tgc	1200
Leu	Arg	Asp	Lys	Cys	Val	Asp	Gly	Ile	Ser	Val	Asn	Lys	Glu	Ile	Cys	
	385				390				395						400	
gaa	aat	ttt	gtg	ttt	aat	tca	att	ggg	att	gtc	act	tat	ctt	aat	cca	1248
Glu	Asn	Phe	Val	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	Pro	
				405				410						415		
ttt	att	ggc	cat	cat	aat	ggc	gat	att	gtg	ggg	aag	att	tgt	gct	gaa	1296
Phe	Ile	Gly	His	His	Asn	Gly	Asp	Ile	Val	Gly	Lys	Ile	Cys	Ala	Glu	
			420				425						430			
acg	ggg	aaa	ggg	gta	cgt	gaa	gtc	att	ctc	gaa	aaa	gga	ttg	ctc	acc	1344
Thr	Gly	Lys	Gly	Val	Arg	Glu	Val	Ile	Leu	Glu	Lys	Gly	Leu	Leu	Thr	
		435					440					445				
gaa	gct	cag	tta	gat	gat	att	ctt	tca	gtg	gaa	aat	tta	atg	cac	cca	1392
Glu	Ala	Gln	Leu	Asp	Asp	Ile	Leu	Ser	Val	Glu	Asn	Leu	Met	His	Pro	
	450				455						460					
att	tat	aaa	gca	aaa	cgg	ttt	acg	gaa	gat	gaa	taa					1428
Ile	Tyr	Lys	Ala	Lys	Arg	Phe	Thr	Glu	Asp	Glu						
	465				470					475						

<210> 9608

<211> 475

<212> PRT

<213> Haemophilus ducreyi 35000HP

<400> 9608

Met	Ser	Asn	Val	Arg	Ile	Glu	Val	Asp	Leu	Leu	Gly	Glu	Arg	Glu	Val	
1				5					10					15		
Pro	Asn	Gln	Val	Tyr	Trp	Gly	Ile	His	Thr	Leu	Arg	Ala	Val	Glu	Asn	
			20					25					30			
Phe	Asn	Ile	Ser	Asn	Asn	Thr	Ile	Ser	Asp	Ile	Pro	Glu	Phe	Val	Arg	
		35					40					45				
Gly	Met	Val	Met	Val	Lys	Lys	Ala	Thr	Ala	Leu	Ala	Asn	Gly	Glu	Leu	
	50					55					60					
Gly	Ala	Ile	Pro	Lys	Lys	Val	Ala	Gln	Ala	Ile	Val	Gln	Ala	Cys	Asp	
	65				70				75						80	
Glu	Ile	Leu	Val	Asn	Gly	Arg	Cys	Met	Asp	Gln	Phe	Pro	Ser	Asp	Val	
				85					90					95		
Tyr	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Val	Asn	Met	Asn	Thr	Asn	Glu	Val	
			100					105					110			
Ile	Ala	Asn	Leu	Ala	Leu	Glu	Met	Leu	Gly	His	Lys	Lys	Gly	Glu	Tyr	
		115				120						125				
His	Ile	Ile	Asp	Pro	Met	Asp	His	Val	Asn	Ala	Ser	Gln	Ser	Thr	Asn	
	130					135					140					
Asp	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Ile	Ala	Val	Tyr	Asn	Ser	Leu	Met	
	145				150				155					160		
His	Leu	Ile	Glu	Gln	Val	Leu	Tyr	Leu	Gln	Gln	Gly	Phe	Glu	Glu	Lys	
			165						170					175		
Ala	Val	Glu	Phe	Ala	Asn	Val	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	
			180					185					190			
Asp	Ala	Val	Pro	Met	Thr	Val	Gly	Gln	Glu	Phe	Lys	Ala	Phe	Ala	Val	
		195					200					205				
Leu	Leu	Ala	Glu	Glu	Val	Arg	Asn	Leu	Lys	Arg	Thr	Ala	Gln	Leu	Leu	
	210					215					220					
Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Leu	Asn	Thr	
	225				230					235					240	
Pro	Ala	Gly	Tyr	Ser	Glu	Leu	Ala	Val	Lys	Tyr	Leu	Ser	Glu	Val	Thr	
			245						250					255		
Gly	Leu	Ala	Cys	Val	Leu	Ser	Glu	Asn	Leu	Ile	Glu	Ala	Thr	Ser	Asp	

PF59083SeqList PF59083.txt

```

      260      265      270
Cys Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Thr Ala Val
      275      280      285
Lys Leu Ser Lys Val Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro
      290      295      300
Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly Ser
      305      310      315
Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val Asn
      320      325      330
Gln Val Cys Phe Lys Val Ile Gly Asn Asp Thr Thr Val Thr Phe Ala
      335      340      345
Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly
      350      355      360
Gln Ala Met Phe Glu Ser Ile Ala Ile Leu Ala Asn Ala Cys Val Asn
      365      370      375
Leu Arg Asp Lys Cys Val Asp Gly Ile Ser Val Asn Lys Glu Ile Cys
      380      385      390
Glu Asn Phe Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro
      395      400      405
Phe Ile Gly His Asn Gly Asp Ile Val Gly Lys Ile Cys Ala Glu
      410      415      420
Thr Gly Lys Gly Val Arg Glu Val Ile Leu Glu Lys Gly Leu Leu Thr
      425      430      435
Glu Ala Gln Leu Asp Asp Ile Leu Ser Val Glu Asn Leu Met His Pro
      440      445      450
Ile Tyr Lys Ala Lys Arg Phe Thr Glu Asp Glu
      455      460      465
      470      475

```

<210> 9609

<211> 1404

<212> DNA

<213> Chromobacterium violaceum ATCC 12472

<220>

<221> CDS

<222> (1)..(1404)

<223> transl_table=11

<400> 9609

```

atg tcc acc cgt atc gaa cac gac ctg ctc ggc aac cgc gac gtg ccg      48
Met Ser Thr Arg Ile Glu His Asp Leu Leu Gly Asn Arg Asp Val Pro
      1      5      10      15
gcc gac gcc tac tgg ggc gtg cac acg ctg cgc gcc atc gaa aac ttc      96
Ala Asp Ala Tyr Trp Gly Val His Thr Leu Arg Ala Ile Glu Asn Phe
      20      25      30
ccg atc acc ggc cag acc atc gcc ggc tac ggc gac ctg atc cgc gcg      144
Pro Ile Thr Gly Gln Thr Ile Ala Gly Tyr Gly Asp Leu Ile Arg Ala
      35      40      45
ctg gcc tgc atc aag caa gcc gcc gcc cag gcc aac cgc gat ctc ggc      192
Leu Ala Cys Ile Lys Gln Ala Ala Ala Gln Ala Asn Arg Asp Leu Gly
      50      55      60
att ctc gac ccc aag ctg gcc cag gcc atc gtc gac gcc tgc gag gag      240
Ile Leu Asp Pro Lys Leu Ala Gln Ala Ile Val Asp Ala Cys Glu Glu
      65      70      75      80
atc cgc gcc ggc aag ctg cac gac cag ttc gtc gac gtg atc cag      288
Ile Arg Ala Gly Lys Leu His Asp Gln Phe Val Val Asp Val Ile Gln
      85      90      95
ggc ggc gcc ggc act tcc acc aat atg aac gcc aac gag gtg atc gcc      336
Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu Val Ile Ala
      100      105      110
aac cgc gcg ctg gag ctg ctg ggc cac gcc aag ggc gag tac cag cat      384
Asn Arg Ala Leu Glu Leu Leu Gly His Ala Lys Gly Glu Tyr Gln His
      115      120      125
ctg cac ccg aac gag cac gtc aac ctg tgc cag agc acc aac gac gtc      432
Leu His Pro Asn Glu His Val Asn Leu Cys Gln Ser Thr Asn Asp Val
      130      135      140
tac ccg acc gcg ctg cgc ctg gcc gcc ttc tgg ggc gtg ctg aag ctg      480
Tyr Pro Thr Ala Leu Arg Leu Ala Ala Phe Trp Gly Val Leu Lys Leu
      145      150      155      160

```


PF59083SeqList PF59083.txt

gtg	tcg	cgg	atg	gaa	acg	ctg	cgc	aag	gcc	ttc	gag	gac	aag	gcc	gag	528
Val	Ser	Arg	Met	Glu	Thr	Leu	Arg	Lys	Ala	Phe	Glu	Asp	Lys	Ala	Glu	
			165						170					175		
gaa	ttc	aag	gac	atc	ctg	aag	atg	ggc	cgc	acc	cag	ctg	cag	gac	gcg	576
Glu	Phe	Lys	Asp	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	
			180					185					190			
gtg	ccg	atg	acg	ctg	ggc	cag	gag	ttc	cag	acc	tat	gct	gtg	atg	ctg	624
Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Gln	Thr	Tyr	Ala	Val	Met	Leu	
			195				200				205					
ggc	gag	gac	gag	cag	cgt	ctg	aag	gaa	gcc	agc	gcc	ctg	atg	ctg	gag	672
Gly	Glu	Asp	Glu	Gln	Arg	Leu	Lys	Glu	Ala	Ser	Ala	Leu	Met	Leu	Glu	
	210					215					220					
atc	aac	ctc	ggc	gcc	acc	gcg	atc	ggc	acc	ggc	atc	acc	gcc	cac	ccg	720
Ile	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Thr	Ala	His	Pro	
225					230					235					240	
gac	tac	gcc	aag	ctg	gtg	tgc	ctg	cat	ctg	tcc	gag	ctg	gtg	ggc	agc	768
Asp	Tyr	Ala	Lys	Leu	Val	Cys	Leu	His	Leu	Ser	Glu	Leu	Val	Gly	Ser	
			245					250						255		
cag	ctg	atc	acc	gcg	ccc	aac	ctg	atc	gag	gcc	acc	cag	gac	tgc	ggc	816
Gln	Leu	Ile	Thr	Ala	Pro	Asn	Leu	Ile	Glu	Ala	Thr	Gln	Asp	Cys	Gly	
			260					265					270			
gcc	ttc	gtc	cag	ctg	tcc	ggc	gtg	atc	aag	cgc	gcg	gcg	gtc	aaa	ctg	864
Ala	Phe	Val	Gln	Leu	Ser	Gly	Val	Ile	Lys	Arg	Ala	Ala	Val	Lys	Leu	
			275				280					285				
tcc	aag	acc	tgc	aac	gac	ctg	cgc	ctg	ctg	tcg	tcc	ggc	ccg	cgc	gca	912
Ser	Lys	Thr	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Ala	
	290					295					300					
ggc	ttc	ggc	gag	atc	aat	ctg	ccg	gcg	cgc	cag	gcc	ggc	tcg	tcc	atc	960
Gly	Phe	Gly	Glu	Ile	Asn	Leu	Pro	Ala	Arg	Gln	Ala	Gly	Ser	Ser	Ile	
305					310					315					320	
atg	ccg	ggc	aag	gtc	aat	ccg	gtg	att	ccg	gaa	gtg	gtg	agc	cag	gtg	1008
Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Ser	Gln	Val	
			325					330						335		
gcg	tat	gaa	gtc	atc	ggc	aac	gac	gtc	acc	atc	acc	atg	gcg	gcc	gag	1056
Ala	Tyr	Glu	Val	Ile	Gly	Asn	Asp	Val	Thr	Ile	Thr	Met	Ala	Ala	Glu	
			340					345					350			
gcc	ggc	cag	ctg	cag	ctg	aac	gcc	ttc	gag	ccg	gtg	atc	gcc	tac	agc	1104
Ala	Gly	Gln	Leu	Gln	Leu	Asn	Ala	Phe	Glu	Pro	Val	Ile	Ala	Tyr	Ser	
		355					360					365				
ctg	ttc	cgc	agc	gcc	ggc	cac	ctg	gcc	aac	gcc	tgc	gac	acg	ctg	acc	1152
Leu	Phe	Arg	Ser	Ala	Gly	His	Leu	Ala	Asn	Ala	Cys	Asp	Thr	Leu	Thr	
	370					375					380					
gag	cac	tgc	gtc	aag	ggc	atc	acc	gcc	aac	cgc	gag	cgg	ctg	cgc	ctg	1200
Glu	His	Cys	Val	Lys	Gly	Ile	Thr	Ala	Asn	Arg	Glu	Arg	Leu	Arg	Leu	
385					390					395					400	
agc	gtg	gaa	agc	tcg	atc	ggc	ctg	gtc	acc	gcg	ctg	aac	ccg	gtg	atc	1248
Ser	Val	Glu	Ser	Ser	Ile	Gly	Leu	Val	Thr	Ala	Leu	Asn	Pro	Val	Ile	
			405					410						415		
ggc	tac	gag	gcc	gcc	acc	cgc	gtc	gcc	gcc	gaa	gcc	cac	gcc	aac	ggc	1296
Gly	Tyr	Glu	Ala	Ala	Thr	Arg	Val	Ala	Ala	Glu	Ala	His	Ala	Asn	Gly	
			420					425					430			
agc	agc	gtc	gcc	gac	gtg	gtg	ctg	gcc	cat	ggc	ctg	ctc	acc	cgc	gag	1344
Ser	Ser	Val	Ala	Asp	Val	Val	Leu	Ala	His	Gly	Leu	Leu	Thr	Arg	Glu	
		435					440					445				
cag	ctg	gac	gac	atc	ctg	cag	ccg	gag	acc	ctg	acc	cgg	ccg	cgc	tgg	1392
Gln	Leu	Asp	Asp	Ile	Leu	Gln	Pro	Glu	Thr	Leu	Thr	Arg	Pro	Arg	Trp	
		450				455					460					
gtg	acg	ctg	taa													1404
Val	Thr	Leu														
465																

<210> 9610

<211> 467

<212> PRT

<213> Chromobacterium violaceum ATCC 12472

<400> 9610

Met Ser Thr Arg Ile Glu His Asp Leu Leu Gly Asn Arg Asp Val Pro
1 5 10 15

PF59083SeqList PF59083.txt

Ala Asp Ala Tyr Trp Gly Val His Thr Leu Arg Ala Ile Glu Asn Phe
 20 25 30
 Pro Ile Thr Gly Gln Thr Ile Ala Gly Tyr Gly Asp Leu Ile Arg Ala
 35 40 45
 Leu Ala Cys Ile Lys Gln Ala Ala Gln Ala Asn Arg Asp Leu Gly
 50 55 60
 Ile Leu Asp Pro Lys Leu Ala Gln Ala Ile Val Asp Ala Cys Glu Glu
 65 70 75 80
 Ile Arg Ala Gly Lys Leu His Asp Gln Phe Val Val Asp Val Ile Gln
 85 90 95
 Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu Val Ile Ala
 100 105 110
 Asn Arg Ala Leu Glu Leu Leu Gly His Ala Lys Gly Glu Tyr Gln His
 115 120 125
 Leu His Pro Asn Glu His Val Asn Leu Cys Gln Ser Thr Asn Asp Val
 130 135 140
 Tyr Pro Thr Ala Leu Arg Leu Ala Ala Phe Trp Gly Val Leu Lys Leu
 145 150 155 160
 Val Ser Arg Met Glu Thr Leu Arg Lys Ala Phe Glu Asp Lys Ala Glu
 165 170 175
 Glu Phe Lys Asp Ile Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala
 180 185 190
 Val Pro Met Thr Leu Gly Gln Glu Phe Gln Thr Tyr Ala Val Met Leu
 195 200 205
 Gly Glu Asp Glu Gln Arg Leu Lys Glu Ala Ser Ala Leu Met Leu Glu
 210 215 220
 Ile Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Ile Thr Ala His Pro
 225 230 235 240
 Asp Tyr Ala Lys Leu Val Cys Leu His Leu Ser Glu Leu Val Gly Ser
 245 250 255
 Gln Leu Ile Thr Ala Pro Asn Leu Ile Glu Ala Thr Gln Asp Cys Gly
 260 265 270
 Ala Phe Val Gln Leu Ser Gly Val Ile Lys Arg Ala Ala Val Lys Leu
 275 280 285
 Ser Lys Thr Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Ala
 290 295 300
 Gly Phe Gly Glu Ile Asn Leu Pro Ala Arg Gln Ala Gly Ser Ser Ile
 305 310 315 320
 Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Val Ser Gln Val
 325 330 335
 Ala Tyr Glu Val Ile Gly Asn Asp Val Thr Ile Thr Met Ala Ala Glu
 340 345 350
 Ala Gly Gln Leu Gln Leu Asn Ala Phe Glu Pro Val Ile Ala Tyr Ser
 355 360 365
 Leu Phe Arg Ser Ala Gly His Leu Ala Asn Ala Cys Asp Thr Leu Thr
 370 375 380
 Glu His Cys Val Lys Gly Ile Thr Ala Asn Arg Glu Arg Leu Arg Leu
 385 390 395 400
 Ser Val Glu Ser Ser Ile Gly Leu Val Thr Ala Leu Asn Pro Val Ile
 405 410 415
 Gly Tyr Glu Ala Ala Thr Arg Val Ala Ala Glu Ala His Ala Asn Gly
 420 425 430
 Ser Ser Val Ala Asp Val Val Leu Ala His Gly Leu Leu Thr Arg Glu
 435 440 445
 Gln Leu Asp Asp Ile Leu Gln Pro Glu Thr Leu Thr Arg Pro Arg Trp
 450 455 460
 Val Thr Leu
 465

<210> 9611

<211> 1428

<212> DNA

<213> Porphyromonas gingivalis w83

<220>

<221> CDS

<222> (1)..(1428)

<223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 9611
atg gaa tta aaa aag act aca cgt atc gaa agc gat ctt atc gga gaa      48
Met Glu Leu Lys Lys Thr Thr Arg Ile Glu Ser Asp Leu Ile Gly Glu
1      5      10      15
cgc gag ata ccc ggc cat att cta tat ggc gta cag acg ctg cgt ggt      96
Arg Glu Ile Pro Gly His Ile Leu Tyr Gly Val Gln Thr Leu Arg Gly
20      25      30
ata gaa aac ttc ccc atc agc aat ttt cat ctg aac gat tac ccc ctg      144
Ile Glu Asn Phe Pro Ile Ser Asn Phe His Leu Asn Asp Tyr Pro Leu
35      40      45
ttt atc aat ggc ttg gcc atg acg aaa tgg gcg gct gca gtg gcc aat      192
Phe Ile Asn Gly Leu Ala Met Thr Lys Trp Ala Ala Ala Val Ala Asn
50      55      60
cat cgg ctc ggt ctc ttg acc gat gcc cag aaa gac ggc atc gtg aaa      240
His Arg Leu Gly Leu Leu Thr Asp Ala Gln Lys Asp Gly Ile Val Lys
65      70      75
gcc tgc aag gaa atc ctc gaa ggc aag cac cac gag cat ttc ccc gtg      288
Ala Cys Lys Glu Ile Leu Glu Gly Lys His His Glu His Phe Pro Val
85      90      95
gat atg atc caa ggc ggt gca gga acg acc acg aat atg aac gcc aac      336
Asp Met Ile Gln Gly Gly Ala Gly Thr Thr Asn Met Asn Ala Asn
100      105      110
gag gtg att tgc aac cgt gcc ttg cag atc atg gga cac gag gca ggc      384
Glu Val Ile Cys Asn Arg Ala Leu Gln Ile Met Gly His Glu Ala Gly
115      120      125
gaa ttt gcc cac ctc tcc ccc aat gat cac gtg aac tgc tcg cag agc      432
Glu Phe Ala His Leu Ser Pro Asn Asp His Val Asn Cys Ser Gln Ser
130      135      140
acc aac gat gct tat ccg aca gct atc cac ctc ggc ctt tac gct aca      480
Thr Asn Asp Ala Tyr Pro Thr Ala Ile His Leu Gly Leu Tyr Ala Thr
145      150      155
tat ctg aag ttc cgc ccc cat ctt ctg gat ctc atc gag tcg ctg cgt      528
Tyr Leu Lys Phe Arg Pro His Leu Leu Asp Leu Ile Glu Ser Leu Arg
165      170      175
gcc aag agc cgc gaa ttt gcc cat gta ctc ctc aag atg gga cgt act cag      576
Ala Lys Ser Arg Glu Phe Ala His Val Leu Lys Met Gly Arg Thr Gln
180      185      190
ctc gaa gat gct gtg cct atg tct ctg gga cag acg ttc ggc gga ttt      624
Leu Glu Asp Ala Val Pro Met Ser Leu Gly Gln Thr Phe Gly Gly Phe
195      200      205
gct tcc atc ttg cag gat gaa atc aaa aat ctg gac ttt gcc gcc gaa      672
Ala Ser Ile Leu Gln Asp Glu Ile Lys Asn Leu Asp Phe Ala Ala Glu
210      215      220
gag ttc ctg acc gtg aat atg ggt gct acg gct atc ggc acg ggt atc      720
Glu Phe Leu Thr Val Asn Met Gly Ala Thr Ala Ile Gly Thr Gly Ile
225      230      235
tgc gcc cag ccg aac tat gcc gaa tac tgc ata gag gct ctt cgt gaa      768
Cys Ala Gln Pro Asn Tyr Ala Glu Tyr Cys Ile Glu Ala Leu Arg Glu
245      250      255
gtc acc ggc tgg gac att cgt ctc agt gcc gat ctg gta ggg gca acg      816
Val Thr Gly Trp Asp Ile Arg Leu Ser Ala Asp Leu Val Gly Ala Thr
260      265      270
agc gac act tcc gtg atg gta gga tat tcg tct gcc ttg cgc cgt atc      864
Ser Asp Thr Ser Val Met Val Gly Tyr Ser Ser Ala Leu Arg Arg Ile
275      280      285
tgt gtg aag gtg aac aag att tgc aac gac ctg cgt ctc ctt gcc agc      912
Cys Val Lys Val Asn Lys Ile Cys Asn Asp Leu Arg Leu Leu Ala Ser
290      295      300
ggc cct cgt tgc ggt ttg cac gaa ttc aat ctg cct gcc atg cag ccg      960
Gly Pro Arg Cys Gly Leu His Glu Phe Asn Leu Pro Ala Met Gln Pro
305      310      315
ggc tcg tcc atc atg ccg ggt aag gtg aat cct gtg att ccg gaa gta      1008
Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val
325      330      335
atg aat cag atc tgc tat aag gtg atg ggc aac gac ctg acc gta acg      1056
Met Asn Gln Ile Cys Tyr Lys Val Met Gly Asn Asp Leu Thr Val Thr
340      345      350
atg gca ggc gat gca gcc caa atg gag ctg aac gct atg gag cct gtg      1104
Met Ala Gly Asp Ala Ala Gln Met Glu Leu Asn Ala Met Glu Pro Val

```

PF59083SeqList PF59083.txt

atg	gca	caa	tgc	tgc	ttc	gaa	agt	tcg	gat	ctg	ctc	atg	aac	gga	ttc	1152
Met	Ala	Gln	Cys	Cys	Phe	Glu	Ser	Ser	Asp	Leu	Leu	Met	Asn	Gly	Phe	
	370					375				380						
gat	acg	ctg	cgt	aca	ctc	tgt	atc	gat	ggc	atc	acg	gcc	aac	gag	gac	1200
Asp	Thr	Leu	Arg	Thr	Leu	Cys	Ile	Asp	Gly	Ile	Thr	Ala	Asn	Glu	Asp	
	385				390					395					400	
gaa	tgc	cgt	ggg	tat	atc	cgc	aac	agc	atc	ggg	atc	ggt	acg	gct	ctg	1248
Glu	Cys	Arg	Gly	Tyr	Ile	Arg	Asn	Ser	Ile	Gly	Ile	Val	Thr	Ala	Leu	
				405					410					415		
aat	ccg	atc	atc	ggc	tat	aag	aat	tcg	acc	aag	atc	gcc	aag	gaa	gcg	1296
Asn	Pro	Ile	Ile	Gly	Tyr	Lys	Asn	Ser	Thr	Lys	Ile	Ala	Lys	Glu	Ala	
				420				425					430			
atg	gaa	acg	gga	cgt	ggc	gtt	tac	gac	ctc	gtt	ttg	gaa	cac	gac	atc	1344
Met	Glu	Thr	Gly	Arg	Gly	Val	Tyr	Asp	Leu	Val	Leu	Glu	His	Asp	Ile	
				435			440						445			
ctg	tcg	aaa	gag	gat	ctg	gat	acg	ata	ctc	tca	ccg	gag	aat	atg	atc	1392
Leu	Ser	Lys	Glu	Asp	Leu	Asp	Thr	Ile	Leu	Ser	Pro	Glu	Asn	Met	Ile	
				450		455					460					
aag	ccg	gtc	aag	ctc	gac	atc	aaa	ccg	cgt	cgc	tga					1428
Lys	Pro	Val	Lys	Leu	Asp	Ile	Lys	Pro	Arg	Arg						
	465				470					475						

<210> 9612

<211> 475

<212> PRT

<213> Porphyromonas gingivalis w83

<400> 9612

Met	Glu	Leu	Lys	Lys	Thr	Thr	Arg	Ile	Glu	Ser	Asp	Leu	Ile	Gly	Glu	
1				5					10					15		
Arg	Glu	Ile	Pro	Gly	His	Ile	Leu	Tyr	Gly	Val	Gln	Thr	Leu	Arg	Gly	
			20					25					30			
Ile	Glu	Asn	Phe	Pro	Ile	Ser	Asn	Phe	His	Leu	Asn	Asp	Tyr	Pro	Leu	
		35					40					45				
Phe	Ile	Asn	Gly	Leu	Ala	Met	Thr	Lys	Trp	Ala	Ala	Ala	Val	Ala	Asn	
	50					55				60						
His	Arg	Leu	Gly	Leu	Leu	Thr	Asp	Ala	Gln	Lys	Asp	Gly	Ile	Val	Lys	
65				70					75					80		
Ala	Cys	Lys	Glu	Ile	Leu	Glu	Gly	Lys	His	Glu	His	Phe	Pro	Val		
			85					90					95			
Asp	Met	Ile	Gln	Gly	Gly	Ala	Gly	Thr	Thr	Thr	Asn	Met	Asn	Ala	Asn	
			100				105					110				
Glu	Val	Ile	Cys	Asn	Arg	Ala	Leu	Gln	Ile	Met	Gly	His	Glu	Ala	Gly	
		115					120					125				
Glu	Phe	Ala	His	Leu	Ser	Pro	Asn	Asp	His	Val	Asn	Cys	Ser	Gln	Ser	
	130					135					140					
Thr	Asn	Asp	Ala	Tyr	Pro	Thr	Ala	Ile	His	Leu	Gly	Leu	Tyr	Ala	Thr	
145				150					155					160		
Tyr	Leu	Lys	Phe	Arg	Pro	His	Leu	Leu	Asp	Leu	Ile	Glu	Ser	Leu	Arg	
			165					170					175			
Ala	Lys	Ser	Arg	Glu	Phe	Ala	His	Val	Leu	Lys	Met	Gly	Arg	Thr	Gln	
			180				185					190				
Leu	Glu	Asp	Ala	Val	Pro	Met	Ser	Leu	Gly	Gln	Thr	Phe	Gly	Gly	Phe	
		195					200					205				
Ala	Ser	Ile	Leu	Gln	Asp	Glu	Ile	Lys	Asn	Leu	Asp	Phe	Ala	Ala	Glu	
	210					215					220					
Glu	Phe	Leu	Thr	Val	Asn	Met	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	
225				230					235						240	
Cys	Ala	Gln	Pro	Asn	Tyr	Ala	Glu	Tyr	Cys	Ile	Glu	Ala	Leu	Arg	Glu	
			245					250						255		
Val	Thr	Gly	Trp	Asp	Ile	Arg	Leu	Ser	Ala	Asp	Leu	Val	Gly	Ala	Thr	
			260					265					270			
Ser	Asp	Thr	Ser	Val	Met	Val	Gly	Tyr	Ser	Ser	Ala	Leu	Arg	Arg	Ile	
		275					280					285				
Cys	Val	Lys	Val	Asn	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ala	Ser	
	290					295					300					
Gly	Pro	Arg	Cys	Gly	Leu	His	Glu	Phe	Asn	Leu	Pro	Ala	Met	Gln	Pro	
	305				310					315				320		

PF59083SeqList PF59083.txt

Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val
 325 330 335
 Met Asn Gln Ile Cys Tyr Lys Val Met Gly Asn Asp Leu Thr Val Thr
 340 345 350
 Met Ala Gly Asp Ala Ala Gln Met Glu Leu Asn Ala Met Glu Pro Val
 355 360 365
 Met Ala Gln Cys Cys Phe Glu Ser Ser Asp Leu Leu Met Asn Gly Phe
 370 375 380
 Asp Thr Leu Arg Thr Leu Cys Ile Asp Gly Ile Thr Ala Asn Glu Asp
 385 390 400
 Glu Cys Arg Gly Tyr Ile Arg Asn Ser Ile Gly Ile Val Thr Ala Leu
 405 410 415
 Asn Pro Ile Ile Gly Tyr Lys Asn Ser Thr Lys Ile Ala Lys Glu Ala
 420 425 430
 Met Glu Thr Gly Arg Gly Val Tyr Asp Leu Val Leu Glu His Asp Ile
 435 440 445
 Leu Ser Lys Glu Asp Leu Asp Thr Ile Leu Ser Pro Glu Asn Met Ile
 450 455 460
 Lys Pro Val Lys Leu Asp Ile Lys Pro Arg Arg
 465 470 475

<210> 9613

<211> 1410

<212> DNA

<213> Gloeobacter violaceus PCC 7421

<220>

<221> CDS

<222> (1)..(1410)

<223> transl_table=11

<400> 9613

atg	caa	cca	aga	acc	gag	cgc	gac	tcg	atg	ggc	gag	cgc	acc	ctg	gag	48
Met	Gln	Pro	Arg	Thr	Glu	Arg	Asp	Ser	Met	Gly	Glu	Arg	Thr	Leu	Glu	
1				5				10						15		
gcc	gga	gcc	tat	tac	ggc	atc	cag	acc	ctg	cgc	gcc	gtc	gag	aat	ttc	96
Ala	Gly	Ala	Tyr	Tyr	Gly	Ile	Gln	Thr	Leu	Arg	Ala	Val	Glu	Asn	Phe	
			20					25					30			
ccg	att	agc	ggc	atc	ggc	ccg	ctg	ccc	gac	ttc	gtg	cgc	gcc	tgc	acc	144
Pro	Ile	Ser	Gly	Ile	Gly	Pro	Leu	Pro	Asp	Phe	Val	Arg	Ala	Cys	Thr	
		35					40					45				
ctc	atc	aaa	cgg	gcc	gcc	gcc	cgg	gtg	aac	gcc	gag	ctt	gaa	tgc	atc	192
Leu	Ile	Lys	Arg	Ala	Ala	Ala	Arg	Val	Asn	Ala	Glu	Leu	Glu	Cys	Ile	
	50				55					60						
ccc	aaa	gac	gtg	gcc	cag	gcg	atc	att	ggc	gcc	gag	ctt	gaa	tgc	atc	240
Pro	Lys	Asp	Val	Ala	Gln	Ala	Ile	Ile	Gly	Ala	Ser	Asp	Glu	Val	Leu	
65				70					75						80	
gcg	ggc	cag	tgg	agc	gat	cag	ttc	gtg	gtc	gat	atc	ttt	cag	gcg	ggc	288
Ala	Gly	Gln	Trp	Ser	Asp	Gln	Phe	Val	Val	Asp	Ile	Phe	Gln	Ala	Gly	
			85					90						95		
gcc	ggc	acc	tcc	cac	cac	atg	aat	atc	aac	gag	gtg	ctc	gcc	aac	cgc	336
Ala	Gly	Thr	Ser	His	His	Met	Asn	Ile	Asn	Glu	Val	Leu	Ala	Asn	Arg	
			100					105					110			
gcc	ctc	gag	ctg	ctg	ggt	tac	gcg	cgg	ggc	gac	tac	aag	cag	gtc	aac	384
Ala	Leu	Glu	Leu	Leu	Gly	Tyr	Ala	Arg	Gly	Asp	Tyr	Lys	Gln	Val	Asn	
		115					120					125				
ccc	aac	gat	cac	gtc	aac	tac	ggc	cag	tcc	acc	aac	gac	gtg	atc	ccc	432
Pro	Asn	Asp	His	Val	Asn	Tyr	Gly	Gln	Ser	Thr	Asn	Asp	Val	Ile	Pro	
	130					135					140					
act	gcc	atc	cgt	ctg	gga	gcg	ctc	ttt	gca	agc	gcg	ccg	ctg	ttg	gag	480
Thr	Ala	Ile	Arg	Leu	Gly	Ala	Leu	Phe	Ala	Ser	Ala	Pro	Leu	Leu	Glu	
145				150					155						160	
gcg	cta	agc	acc	ctg	caa	caa	agt	ttc	gag	gcc	aag	ggc	aac	gag	ttt	528
Ala	Leu	Ser	Thr	Leu	Gln	Gln	Ser	Phe	Glu	Ala	Lys	Gly	Asn	Glu	Phe	
			165					170						175		
ttg	ccc	atc	gtc	aaa	tcc	ggg	cgc	acc	cac	ctg	cag	gac	gcg	gtg	ccc	576
Leu	Pro	Ile	Val	Lys	Ser	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Val	Pro	
			180					185					190			
ata	agg	ctt	ggg	gat	gaa	ttt	ctg	gcc	tat	gcc	cag	atc	gtc	ggc	gag	624

PF59083SeqList PF59083.txt

Ile	Arg	Leu	Gly	Asp	Glu	Phe	Leu	Ala	Tyr	Ala	Gln	Ile	Val	Gly	Glu	
195		195					200					205				
cac	cg	gcc	cg	atc	gaa	acc	gcc	tgc	cg	gag	cta	ttg	gtg	ctg	ggc	672
His	Arg	Ala	Arg	Ile	Glu	Thr	Ala	Cys	Arg	Glu	Leu	Leu	Val	Leu	Gly	
210						215					220					
ctg	ggg	ggc	agc	gcc	gcc	ggg	acc	ggc	ctc	aac	acc	cat	ccc	cag	tac	720
Leu	Gly	Gly	Ser	Ala	Ala	Gly	Thr	Gly	Leu	Asn	Thr	His	Pro	Gln	Tyr	
225					230					235					240	
cg	gtg	cg	gtc	gtc	gcc	gaa	ctg	gcc	cg	ctg	aca	ggg	cac	ccc	ctc	768
Arg	Val	Arg	Val	Val	Ala	Glu	Leu	Ala	Arg	Leu	Thr	Gly	His	Pro	Leu	
				245				250						255		
acc	ccc	gcc	ccc	cga	ccg	atg	gcg	gca	atg	cag	agc	atg	gcg	ccc	ttc	816
Thr	Pro	Ala	Pro	Arg	Pro	Met	Ala	Ala	Met	Gln	Ser	Met	Ala	Pro	Phe	
				260			265							270		
gtg	gcc	gtc	tcc	ggc	agc	ctg	cg	aat	ctg	gcc	cag	gat	ctg	gtc	aag	864
Val	Ala	Val	Ser	Gly	Ser	Leu	Arg	Asn	Leu	Ala	Gln	Asp	Leu	Val	Lys	
				275			280									
atc	gcg	ggc	gat	ctg	cg	ctg	atg	gat	tcc	ggc	ccc	aag	acg	ggc	ctg	912
Ile	Ala	Gly	Asp	Leu	Arg	Leu	Met	Asp	Ser	Gly	Pro	Lys	Thr	Gly	Leu	
290						295					300					
cgt	gag	atc	gaa	ctg	ccg	gtg	cag	ccg	ggg	tcg	tcg	atc	atg	ccc		960
Arg	Glu	Ile	Glu	Leu	Pro	Pro	Val	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	
305					310					315					320	
ggc	aag	tac	aac	ccg	gtg	ctg	tgc	gag	atg	ctc	acg	atg	gtc	gcc	ttt	1008
Gly	Lys	Tyr	Asn	Pro	Val	Leu	Cys	Glu	Met	Leu	Thr	Met	Val	Ala	Phe	
				325				330						335		
cag	gtg	atg	ggc	tac	gac	cag	gcg	att	gcc	ttg	gcc	gcc	cag	gcg	ggc	1056
Gln	Val	Met	Gly	Tyr	Asp	Gln	Ala	Ile	Ala	Leu	Ala	Ala	Gln	Ala	Gly	
				340			345							350		
caa	ctg	gaa	ttg	aac	gtg	atg	atg	ccg	ctg	atc	gcc	tac	gac	ttg	ctc	1104
Gln	Leu	Glu	Leu	Asn	Val	Met	Met	Pro	Leu	Ile	Ala	Tyr	Asp	Leu	Leu	
				355			360									
cac	agc	ttc	acg	atc	ctc	acc	aac	gcc	ctc	acg	gtc	ttt	cga	gcg	cg	1152
His	Ser	Phe	Thr	Ile	Leu	Thr	Asn	Ala	Leu	Thr	Val	Phe	Arg	Ala	Arg	
						375					380					
tgc	atc	gac	ggc	atc	cag	gcc	caa	ccc	gag	cg	tcg	ctg	gcc	tac	gcc	1200
Cys	Ile	Asp	Gly	Ile	Gln	Ala	Gln	Pro	Glu	Arg	Cys	Leu	Ala	Tyr	Ala	
385					390					395					400	
gag	ggc	tcg	atc	gcc	ctg	gtg	acc	gct	ctc	aat	ccc	cac	atc	ggc	tat	1248
Glu	Gly	Ser	Ile	Ala	Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	
				405				410						415		
ctc	aac	gcc	gcc	gcc	gtc	gcc	aaa	gaa	tcg	ctc	gcg	acc	ggc	cg	tcc	1296
Leu	Asn	Ala	Ala	Ala	Val	Ala	Lys	Glu	Ser	Leu	Ala	Thr	Gly	Arg	Ser	
				420			425							430		
ctg	cg	gag	atc	gtt	ctc	gag	cg	ggg	cta	ctg	acc	gaa	gcg	caa	ctc	1344
Leu	Arg	Glu	Ile	Val	Leu	Glu	Arg	Gly	Leu	Leu	Thr	Glu	Ala	Gln	Leu	
				435			440									
gcc	gag	atc	ctc	gac	ctt	gaa	gcg	atg	agc	cg	ttg	ccg	gag	acg	cag	1392
Ala	Glu	Ile	Leu	Asp	Leu	Glu	Ala	Met	Ser	Arg	Leu	Pro	Glu	Thr	Gln	
						455					460					
gcc	gcc	tca	gac	cg	tag											1410
Ala	Ala	Ser	Asp	Arg												
465																

<210> 9614

<211> 469

<212> PRT

<213> Gloeobacter violaceus PCC 7421

<400> 9614

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

PF59083SeqList PF59083.txt

```

65      70      75      80
Ala Gly Gln Trp Ser Asp Gln Phe Val Val Asp Ile Phe Gln Ala Gly
      85      90      95
Ala Gly Thr Ser His His Met Asn Ile Asn Glu Val Leu Ala Asn Arg
      100      105      110
Ala Leu Glu Leu Leu Gly Tyr Ala Arg Gly Asp Tyr Lys Gln Val Asn
      115      120      125
Pro Asn Asp His Val Asn Tyr Gly Gln Ser Thr Asn Asp Val Ile Pro
      130      135      140
Thr Ala Ile Arg Leu Gly Ala Leu Phe Ala Ser Ala Pro Leu Leu Glu
      145      150      155
Ala Leu Ser Thr Leu Gln Gln Ser Phe Glu Ala Lys Gly Asn Glu Phe
      160      165      170
Leu Pro Ile Val Lys Ser Gly Arg Thr His Leu Gln Asp Ala Val Pro
      175      180      185
Ile Arg Leu Gly Asp Glu Phe Leu Ala Tyr Ala Gln Ile Val Gly Glu
      190      195      200
His Arg Ala Arg Ile Glu Thr Ala Cys Arg Glu Leu Leu Val Leu Gly
      205      210      215
Leu Gly Gly Ser Ala Ala Gly Thr Gly Leu Asn Thr His Pro Gln Tyr
      220      225      230
Arg Val Arg Val Val Ala Glu Leu Ala Arg Leu Thr Gly His Pro Leu
      235      240      245
Thr Pro Ala Pro Arg Pro Met Ala Ala Met Gln Ser Met Ala Pro Phe
      250      255      260
Val Ala Val Ser Gly Ser Leu Arg Asn Leu Ala Gln Asp Leu Val Lys
      265      270      275
Ile Ala Gly Asp Leu Arg Leu Met Asp Ser Gly Pro Lys Thr Gly Leu
      280      285      290
Arg Glu Ile Glu Leu Pro Pro Val Gln Pro Gly Ser Ser Ile Met Pro
      295      300      305
Gly Lys Tyr Asn Pro Val Leu Cys Glu Met Leu Thr Met Val Ala Phe
      310      315      320
Gln Val Met Gly Tyr Asp Gln Ala Ile Ala Leu Ala Ala Gln Ala Gly
      325      330      335
Gln Leu Glu Leu Asn Val Met Met Pro Leu Ile Ala Tyr Asp Leu Leu
      340      345      350
His Ser Phe Thr Ile Leu Thr Asn Ala Leu Thr Val Phe Arg Ala Arg
      355      360      365
Cys Ile Asp Gly Ile Gln Ala Gln Pro Glu Arg Cys Leu Ala Tyr Ala
      370      375      380
Glu Gly Ser Ile Ala Leu Val Thr Ala Leu Asn Pro His Ile Gly Tyr
      385      390      395
Leu Asn Ala Ala Val Ala Lys Glu Ser Leu Ala Thr Gly Arg Ser
      400      405      410
Leu Arg Glu Ile Val Leu Glu Arg Gly Leu Leu Thr Glu Ala Gln Leu
      415      420      425
Ala Glu Ile Leu Asp Leu Glu Ala Met Ser Arg Leu Pro Glu Thr Gln
      430      435      440
Ala Ala Ser Asp Arg
      445      450      455
465

```

<210> 9615

<211> 1425

<212> DNA

<213> Photorhabdus luminescens subsp. laumondii TT01

<220>

<221> CDS

<222> (1)..(1425)

<223> transl_table=11

<400> 9615

```

atg tca aac aac att cgt atc gaa gaa gac ctg tta ggt aaa cga gaa
Met Ser Asn Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Lys Arg Glu
1      5      10
gtc cct gct gaa gcc tat tat ggt att cac acc tta cgt gcg att gaa
Val Pro Ala Glu Ala Tyr Tyr Gly Ile His Thr Leu Arg Ala Ile Glu
20      25      30

```

48

96

PF59083SeqList PF59083.txt

aac	ttc	cat	atc	agt	aac	aac	acc	att	aat	gat	gta	ccc	gaa	ttc	atc	144
Asn	Phe	His	Ile	Ser	Asn	Asn	Thr	Ile	Asn	Asp	Val	Pro	Glu	Phe	Ile	
		35					40					45				
cgt	ggc	atg	gtg	atg	gta	aaa	aaa	gcc	gca	gcc	tta	gct	aac	aaa	gag	192
Arg	Gly	Met	Val	Met	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Lys	Glu	
	50					55					60					
cta	caa	act	att	cct	aaa	aaa	att	gct	gac	atc	atc	atc	aaa	gca	tgt	240
Leu	Gln	Thr	Ile	Pro	Lys	Lys	Ile	Ala	Asp	Ile	Ile	Ile	Lys	Ala	Cys	
65					70					75					80	
gac	gaa	gtg	ctc	tat	acc	ggc	aga	tgc	atg	gat	cag	ttt	ccg	gtc	gat	288
Asp	Glu	Val	Leu	Tyr	Thr	Gly	Arg	Cys	Met	Asp	Gln	Phe	Pro	Val	Asp	
				85					90					95		
gtg	ttt	caa	ggc	ggg	gcc	ggg	act	tca	ctc	aac	atg	aat	acc	aat	gag	336
Val	Phe	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Leu	Asn	Met	Asn	Thr	Asn	Glu	
			100					105					110			
gtt	ctg	gca	aac	att	ggg	ctg	gaa	ctg	tta	ggc	cat	aaa	aaa	ggc	gaa	384
Val	Leu	Ala	Asn	Ile	Gly	Leu	Glu	Leu	Leu	Gly	His	Lys	Lys	Gly	Glu	
		115					120					125				
tat	gag	tac	ctg	aat	ccc	aat	gac	cat	ctg	aat	aaa	agc	cag	tca	act	432
Tyr	Glu	Tyr	Leu	Asn	Pro	Asn	Asp	His	Leu	Asn	Lys	Ser	Gln	Ser	Thr	
	130					135					140					
aac	gac	gcc	tac	cca	act	ggc	ttc	cgc	atc	gcg	gtt	tat	aac	tcc	atc	480
Asn	Asp	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Ile	Ala	Val	Tyr	Asn	Ser	Ile	
145					150					155					160	
ctg	aaa	ctg	atc	gag	tct	att	gag	ctg	tta	att	gtg	ggg	ttc	gat	aaa	528
Leu	Lys	Leu	Ile	Glu	Ser	Ile	Glu	Leu	Leu	Ile	Val	Gly	Phe	Asp	Lys	
				165					170					175		
aaa	tcc	aga	gaa	ttt	aat	gac	att	cta	aaa	atg	ggg	cgt	acc	caa	tta	576
Lys	Ser	Arg	Glu	Phe	Asn	Asp	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	
			180					185					190			
cag	gat	gct	gtt	ccc	atg	aca	ctg	ggg	cag	gaa	ttc	aac	gca	ttc	tct	624
Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Asn	Ala	Phe	Ser	
		195					200					205				
atc	ctg	ttg	aaa	gaa	gaa	gtt	aaa	aac	ctc	aac	cga	acc	tct	gaa	tta	672
Ile	Leu	Leu	Lys	Glu	Glu	Val	Lys	Asn	Leu	Asn	Arg	Thr	Ser	Glu	Leu	
	210					215					220					
ctg	ctg	gaa	att	aac	ctt	ggc	gct	act	gct	atc	ggg	acc	cgc	ttg	aat	720
Leu	Leu	Glu	Ile	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Arg	Leu	Asn	
225					230					235					240	
aca	gca	cca	ggg	tat	cag	aaa	ttg	gcg	gtt	gaa	aaa	ctg	gcg	gaa	gtt	768
Thr	Ala	Pro	Gly	Tyr	Gln	Lys	Leu	Ala	Val	Glu	Lys	Leu	Ala	Glu	Val	
				245					250					255		
tca	ggg	tta	cct	tgc	gta	cca	gcc	gaa	gac	ctg	att	gaa	gcc	act	tct	816
Ser	Gly	Leu	Pro	Cys	Val	Pro	Ala	Glu	Asp	Leu	Ile	Glu	Ala	Thr	Ser	
			260					265					270			
gac	tgt	ggg	gct	tac	gtt	atg	gtc	cac	ggg	gct	ctg	aag	cgc	ctg	gct	864
Asp	Cys	Gly	Ala	Tyr	Val	Met	Val	His	Gly	Ala	Leu	Lys	Arg	Leu	Ala	
		275					280					285				
gtc	aaa	ctg	tct	aaa	att	tgt	aat	gac	ctg	cgt	ttg	ctt	tct	tct	ggc	912
Val	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	
	290					295					300					
cct	cgt	gct	ggc	ctg	aat	gaa	atc	aac	cta	cca	gaa	tta	cag	gca	ggc	960
Pro	Arg	Ala	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	Ala	Gly	
305					310					315					320	
tct	tct	att	atg	ccg	gca	aaa	gtg	aac	ccg	gtt	att	cca	gaa	gtt	gtg	1008
Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	
				325					330					335		
aat	cag	gtt	tgc	ttc	aaa	gtt	att	ggg	aac	gat	att	tgt	gtt	act	atg	1056
Asn	Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Ile	Cys	Val	Thr	Met	
			340					345					350			
gcg	tcc	gaa	gca	ggc	cag	tta	cag	ctc	aat	gta	atg	gaa	cct	gct	atc	1104
Ala	Ser	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Ala	Ile	
		355					360					365				
ggg	cag	gcc	atg	ttt	gaa	tct	atc	tcc	ctg	cta	agc	aac	gct	tgc	cgc	1152
Gly	Gln	Ala	Met	Phe	Glu	Ser	Ile	Ser	Leu	Leu	Ser	Asn	Ala	Cys	Arg	
		370				375					380					
aac	ctg	gta	gaa	aaa	tgc	gtt	aat	ggc	atc	acg	gct	aac	aaa	gaa	gtt	1200
Asn	Leu	Val	Glu	Lys	Cys	Val	Asn	Gly	Ile	Thr	Ala	Asn	Lys	Glu	Val	
385					390					395					400	

PF59083SeqList PF59083.txt

tgc	gaa	aat	ttc	gta	ttc	aac	tcg	atc	ggg	atc	gtg	aca	tat	ctg	aac	1248
Cys	Glu	Asn	Phe	Val	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	
			405						410					415		
cca	ttc	atc	ggg	cac	cat	aat	ggg	gac	att	gtt	ggg	aaa	att	tgt	gct	1296
Pro	Phe	Ile	Gly	His	His	Asn	Gly	Asp	Ile	Val	Gly	Lys	Ile	Cys	Ala	
			420					425					430			
gaa	acc	ggg	aaa	agt	gtt	cgt	gaa	gtc	gtt	ctg	gaa	cga	ggc	tta	ctg	1344
Glu	Thr	Gly	Lys	Ser	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gly	Leu	Leu	
		435				440					445					
acc	gaa	act	caa	ttg	gat	gac	atc	ttc	tct	gta	gag	aac	cta	aaa	tgc	1392
Thr	Glu	Thr	Gln	Leu	Asp	Asp	Ile	Phe	Ser	Val	Glu	Asn	Leu	Lys	Cys	
	450				455						460					
cca	tct	tac	aag	gca	aaa	cgt	ttt	gac	gat	taa						1425
Pro	Ser	Tyr	Lys	Ala	Lys	Arg	Phe	Asp	Asp							
465				470												

<210> 9616

<211> 474

<212> PRT

<213> Photorhabdus luminescens subsp. laumondii TT01

<400> 9616

Met	Ser	Asn	Asn	Ile	Arg	Ile	Glu	Glu	Asp	Leu	Leu	Gly	Lys	Arg	Glu
1				5					10					15	
Val	Pro	Ala	Glu	Ala	Tyr	Tyr	Gly	Ile	His	Thr	Leu	Arg	Ala	Ile	Glu
			20					25					30		
Asn	Phe	His	Ile	Ser	Asn	Asn	Thr	Ile	Asn	Asp	Val	Pro	Glu	Phe	Ile
		35					40					45			
Arg	Gly	Met	Val	Met	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Lys	Glu
	50					55					60				
Leu	Gln	Thr	Ile	Pro	Lys	Lys	Ile	Ala	Asp	Ile	Ile	Ile	Lys	Ala	Cys
65					70				75					80	
Asp	Glu	Val	Leu	Tyr	Thr	Gly	Arg	Cys	Met	Asp	Gln	Phe	Pro	Val	Asp
				85					90					95	
Val	Phe	Gln	Gly	Ala	Gly	Thr	Ser	Leu	Asn	Met	Asn	Thr	Asn	Glu	
		100					105						110		
Val	Leu	Ala	Asn	Ile	Gly	Leu	Glu	Leu	Leu	Gly	His	Lys	Lys	Gly	Glu
		115					120					125			
Tyr	Glu	Tyr	Leu	Asn	Pro	Asn	Asp	His	Leu	Asn	Lys	Ser	Gln	Ser	Thr
	130					135					140				
Asn	Asp	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Ile	Ala	Val	Tyr	Asn	Ser	Ile
145					150					155					160
Leu	Lys	Leu	Ile	Glu	Ser	Ile	Glu	Leu	Leu	Ile	Val	Gly	Phe	Asp	Lys
				165					170					175	
Lys	Ser	Arg	Glu	Phe	Asn	Asp	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu
			180					185					190		
Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Asn	Ala	Phe	Ser
		195					200					205			
Ile	Leu	Leu	Lys	Glu	Glu	Val	Lys	Asn	Leu	Asn	Arg	Thr	Ser	Glu	Leu
	210					215					220				
Leu	Leu	Glu	Ile	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Arg	Leu	Asn
225					230					235				240	
Thr	Ala	Pro	Gly	Tyr	Gln	Lys	Leu	Ala	Val	Glu	Lys	Leu	Ala	Glu	Val
			245						250					255	
Ser	Gly	Leu	Pro	Cys	Val	Pro	Ala	Glu	Asp	Leu	Ile	Glu	Ala	Thr	Ser
			260					265					270		
Asp	Cys	Gly	Ala	Tyr	Val	Met	Val	His	Gly	Ala	Leu	Lys	Arg	Leu	Ala
		275					280					285			
Val	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly
	290					295					300				
Pro	Arg	Ala	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	Ala	Gly
305					310					315					320
Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val
				325					330					335	
Asn	Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Ile	Cys	Val	Thr	Met
			340					345					350		
Ala	Ser	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Ala	Ile
		355				360						365			
Gly	Gln	Ala	Met	Phe	Glu	Ser	Ile	Ser	Leu	Leu	Ser	Asn	Ala	Cys	Arg

PF59083SeqList PF59083.txt

```

370          375          380
Asn Leu Val Glu Lys Cys Val Asn Gly Ile Thr Ala Asn Lys Glu Val
385          390          395
Cys Glu Asn Phe Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn
405
Pro Phe Ile Gly His His Asn Gly Asp Ile Val Gly Lys Ile Cys Ala
420
Glu Thr Gly Lys Ser Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu
435
Thr Glu Thr Gln Leu Asp Asp Ile Phe Ser Val Glu Asn Leu Lys Cys
450
Pro Ser Tyr Lys Ala Lys Arg Phe Asp Asp
465          470

```

<210> 9617

<211> 1452

<212> DNA

<213> Vibrio vulnificus YJ016

<220>

<221> CDS

<222> (1)..(1452)

<223> transl_table=11

<400> 9617

```

atg gct acc cta act gaa gct cca aaa gca tca act ccg gcc act cgt      48
Met Ala Thr Leu Thr Glu Ala Pro Lys Ala Ser Thr Pro Ala Thr Arg
  1          5          10          15
att gaa gaa gat cta tta ggc caa cgt cac gtt ccg gct gac gct tac      96
Ile Glu Glu Asp Leu Leu Gly Gln Arg His Val Pro Ala Asp Ala Tyr
20
tac ggt att cac acg ctg cgc gcc atc gaa aac ttc aac atc tca aat      144
Tyr Gly Ile His Thr Leu Arg Ala Ile Glu Asn Phe Asn Ile Ser Asn
35
gtc act att tct gac gta cca gaa ttc gtt cgt ggc atg gtt atg acc      192
Val Thr Ile Ser Asp Val Pro Glu Phe Val Arg Gly Met Val Met Thr
50
aaa aaa gcc gct gcg ctt gct aac aaa gaa ttg ggc gca att cct aag      240
Lys Lys Ala Ala Ala Leu Ala Asn Lys Glu Leu Gly Ala Ile Pro Lys
65
aat gtc gcg gat tac atc att caa gcg tgt gac cta atg ttg gaa act      288
Asn Val Ala Asp Tyr Ile Ile Gln Ala Cys Asp Leu Met Leu Glu Thr
85
ggc aaa tgc atg gat cag ttc cca tca gac gta ttc caa ggc ggt gcg      336
Gly Lys Cys Met Asp Gln Phe Pro Ser Asp Val Phe Gln Gly Gly Ala
100
ggc act tct gtg aac atg aac acc aac gaa gta ctt gcc aac att gct      384
Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Leu Ala Asn Ile Ala
115
cta gaa tta atg ggc aaa gag aaa ggc gat tac gac gtg gtg aac cca      432
Leu Glu Leu Met Gly Lys Glu Lys Gly Asp Tyr Asp Val Val Asn Pro
130
aac gat cac gtg aac aag agc caa tca acc aac tgt gcc tac cca aca      480
Asn Asp His Val Asn Lys Ser Gln Ser Thr Asn Cys Ala Tyr Pro Thr
145
ggc ttc cgt atc gcg gtt tac aac agc atc cat aaa ttg atg gaa gcg      528
Gly Phe Arg Ile Ala Val Tyr Asn Ser Ile His Lys Leu Met Glu Ala
165
att gaa tac cta aaa ggt gcg ttt gag ctg aaa tct caa gag ttt aac      576
Ile Glu Tyr Leu Lys Gly Ala Phe Glu Leu Lys Ser Gln Glu Phe Asn
180
gac atc cta aaa atg ggc cgt act cag ttg caa gat gca gtt cca atg      624
Asp Ile Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met
195
act gtc ggt caa gag ttc cac gct tgg gca gtg aca cta aac gaa gag      672
Thr Val Gly Gln Glu Phe His Ala Trp Ala Val Thr Leu Asn Glu Glu
210
atc cgt gcg cta gac tac acc tcg aag cta ctt ctt gaa gtg aac cta      720
Ile Arg Ala Leu Asp Tyr Thr Ser Lys Leu Leu Leu Glu Val Asn Leu

```

PF59083SeqList PF59083.txt

225	230	235	240	
ggt gca acg gca atc ggt act ggc tta aac aca cct cct ggt tac caa				768
Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr Pro Pro Gly Tyr Gln				
	245	250	255	
gca ctt gcc gtg aaa cac cta gcg gaa gta act ggc cta gaa gtg gtt				816
Ala Leu Ala Val Lys His Leu Ala Glu Val Thr Gly Leu Glu Val Val				
	260	265	270	
cca gca gaa gac ctt atc gaa gca act tca gac tgt ggt gct tac gta				864
Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser Asp Cys Gly Ala Tyr Val				
	275	280	285	
atg gca cac ggc gct cta aaa cgc cta gcg gtg aaa ttg tct aag atc				912
Met Ala His Gly Ala Leu Lys Arg Leu Ala Val Lys Leu Ser Lys Ile				
	290	295	300	
tgt aac gac ttg cgt ctg ctt tct tct ggt cct cgc gct ggt ttg aac				960
Cys Asn Asp Leu Arg Leu Ser Ser Gly Pro Arg Ala Gly Leu Asn				
	305	310	315	
gaa ctt aac ttg cca gaa atg caa gcc ggt tct tca atc atg cca gca				1008
Glu Leu Asn Leu Pro Glu Met Gln Ala Gly Ser Ser Ile Met Pro Ala				
	325	330	335	
aaa gtt aac cca gtt atc cca gaa gtg gtt aac caa gtg tgt ttc aaa				1056
Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Val Cys Phe Lys				
	340	345	350	
gta ctg ggt aac gac aac acg att tct ttc gca gcc gaa ggc ggt cag				1104
Val Leu Gly Asn Asp Asn Thr Ile Ser Phe Ala Ala Glu Gly Gly Gln				
	355	360	365	
cta cag ctg aac gta atg gag cct gtg att ggt caa gcg atg ttt gaa				1152
Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Gln Ala Met Phe Glu				
	370	375	380	
tcg att tca cta cta caa aac gcg tgt gtg aac cta cgt gac aag tgt				1200
Ser Ile Ser Leu Leu Gln Asn Ala Cys Val Asn Leu Arg Asp Lys Cys				
	385	390	395	
atc gac ggc atc act gtg aac aaa gag atc tgt gaa aac tac gtt tac				1248
Ile Asp Gly Ile Thr Val Asn Lys Glu Ile Cys Glu Asn Tyr Val Tyr				
	405	410	415	
aac tct atc ggt atc gtt act tac cta aac cca tac atc ggc cac cac				1296
Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro Tyr Ile Gly His His				
	420	425	430	
gaa ggt gac atc gtt ggt aag atc tgt gcg gaa acc ggt aag agc gtc				1344
Glu Gly Asp Ile Val Gly Lys Ile Cys Ala Glu Thr Gly Lys Ser Val				
	435	440	445	
cgt gaa gta gtg ctt gag cgt ggc ttg ctg aca tct gaa gag ttg gat				1392
Arg Glu Val Val Leu Glu Arg Gly Leu Leu Thr Ser Glu Glu Leu Asp				
	450	455	460	
gac atc ctg tct gtg cag aac ttc atg cac cca act tac aaa gca aaa				1440
Asp Ile Leu Ser Val Gln Asn Phe Met His Pro Thr Tyr Lys Ala Lys				
	465	470	475	
cgt tac gaa taa				1452
Arg Tyr Glu				

<210> 9618

<211> 483

<212> PRT

<213> Vibrio vulnificus YJ016

<400> 9618

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

PF59083SeqList PF59083.txt

```

      100      105      110
Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Leu Ala Asn Ile Ala
      115      120      125
Leu Glu Leu Met Gly Lys Glu Lys Gly Asp Tyr Asp Val Val Asn Pro
      130      135      140
Asn Asp His Val Asn Lys Ser Gln Ser Thr Asn Cys Ala Tyr Pro Thr
      145      150      155
Gly Phe Arg Ile Ala Val Tyr Asn Ser Ile His Lys Leu Met Glu Ala
      165      170      175
Ile Glu Tyr Leu Lys Gly Ala Phe Glu Leu Lys Ser Gln Glu Phe Asn
      180      185      190
Asp Ile Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met
      195      200      205
Thr Val Gly Gln Glu Phe His Ala Trp Ala Val Thr Leu Asn Glu Glu
      210      215      220
Ile Arg Ala Leu Asp Tyr Thr Ser Lys Leu Leu Glu Val Asn Leu
      225      230      235
Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr Pro Pro Gly Tyr Gln
      245      250      255
Ala Leu Ala Val Lys His Leu Ala Glu Val Thr Gly Leu Glu Val Val
      260      265      270
Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser Asp Cys Gly Ala Tyr Val
      275      280      285
Met Ala His Gly Ala Leu Lys Arg Leu Ala Val Lys Leu Ser Lys Ile
      290      295      300
Cys Asn Asp Leu Arg Leu Ser Ser Gly Pro Arg Ala Gly Leu Asn
      305      310      315
Glu Leu Asn Leu Pro Glu Met Gln Ala Gly Ser Ser Ile Met Pro Ala
      325      330      335
Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Val Cys Phe Lys
      340      345      350
Val Leu Gly Asn Asp Asn Thr Ile Ser Phe Ala Ala Glu Gly Gly Gln
      355      360      365
Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Gln Ala Met Phe Glu
      370      375      380
Ser Ile Ser Leu Leu Gln Asn Ala Cys Val Asn Leu Arg Asp Lys Cys
      385      390      395
Ile Asp Gly Ile Thr Val Asn Lys Glu Ile Cys Glu Asn Tyr Val Tyr
      405      410      415
Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro Tyr Ile Gly His His
      420      425      430
Glu Gly Asp Ile Val Gly Lys Ile Cys Ala Glu Thr Gly Lys Ser Val
      435      440      445
Arg Glu Val Val Leu Glu Arg Gly Leu Leu Thr Ser Glu Glu Leu Asp
      450      455      460
Asp Ile Leu Ser Val Gln Asn Phe Met His Pro Thr Tyr Lys Ala Lys
      465      470      475
Arg Tyr Glu

```

<210> 9619
 <211> 1575
 <212> DNA
 <213> Corynebacterium diphtheriae NCTC 13129

<220>
 <221> CDS
 <222> (1)..(1575)
 <223> transl_table=11

```

<400> 9619
atg gct tcc caa gct aaa aac aca aag ggc tcg aaa aac gcc gag gta
Met Ala Ser Gln Ala Lys Asn Thr Lys Gly Ser Lys Asn Ala Glu Val
1 5 10 15
acc aat gat gtt ctc gac gga aaa acc gaa ggc acc gcg gag aaa gta
Thr Asn Asp Val Leu Asp Gly Lys Thr Glu Gly Thr Ala Glu Lys Val
20 25 30
aac gat gcc ccc att gca tca gat gta aca aca aag cac gcc act aag
Asn Asp Ala Pro Ile Ala Ser Asp Val Thr Thr Lys His Ala Thr Lys
144

```

PF59083SeqList PF59083.txt

35																40																45																192
aaa Lys	gct Ala	gca Ala	cca Pro	gga Gly	ttc Phe	cgt Arg	atc Ile	gaa Glu	gaa Glu	gac Asp	ctc Leu	ttg Leu	ggt Gly	gag Glu	atg Met																																	
50																55																60																240
gaa Glu	ggt Val	ccc Pro	gac Asp	gag Glu	gtt Val	tat Tyr	tat Tyr	ggc Gly	gtc Val	cat His	act Thr	ctt Leu	cgt Arg	gcc Ala	atc Ile																																	
65																70																75																288
gac Asp	aat Asn	tac Tyr	aag Lys	atc Ile	tct Ser	agc Ser	acc Thr	acc Thr	att Ile	aat Asn	gat Asp	gtg Val	cca Pro	gag Glu	ttc Phe																																	
80																85																90																336
att Ile	cgt Arg	ggc Gly	atg Met	gtt Val	cag Gln	gta Val	aaa Lys	aag Lys	gcc Ala	acc Thr	gcg Ala	ctt Leu	gcc Ala	aac Asn	cga Arg																																	
95																100																105																384
cga Arg	ctc Leu	cat His	act Thr	ctg Leu	ccg Pro	aaa Lys	gac Asp	aag Lys	tgc Cys	gat Asp	gcc Ala	att Ile	gta Val	tggt Trp	gct Ala																																	
110																115																120																432
tgc Cys	gat Asp	caa Gln	atc Ile	ttg Leu	gat Asp	cac His	ggt Gly	cgt Arg	tgc Cys	atg Met	gat Asp	cag Gln	ttc Phe	cca Pro	atc Ile																																	
125																130																135																480
gat Asp	gtg Val	ttc Phe	caa Gln	gga Gly	ggc Gly	gct Ala	ggc Gly	aca Thr	agc Ser	gtc Val	aac Asn	atg Met	aac Asn	act Thr	aat Asn																																	
140																145																150																528
gag Glu	gta Val	atc Ile	gcc Ala	aac Asn	ctc Leu	gca Ala	ctg Leu	gag Glu	cat His	ctg Leu	ggt Gly	aag Lys	cca Pro	aag Lys	gga Gly																																	
155																160																165																576
tcc Ser	tat Tyr	gac Asp	atc Ile	atc Ile	aac Asn	cca Pro	aac Asn	gat Asp	gac Asp	gtc Val	aac Asn	atg Met	agc Ser	caa Gln	tca Ser																																	
170																175																180																624
act Thr	aac Asn	gat Asp	gcc Ala	tac Tyr	cca Pro	act Thr	gga Gly	ttc Phe	cgt Arg	ttg Leu	ggt Gly	gtc Val	tat Tyr	gag Glu	gcg Ala																																	
185																190																195																672
atg Met	cag Gln	gaa Glu	ctg Leu	atc Ile	act Thr	cgt Arg	att Ile	gac Asp	aat Asn	cta Leu	cag Gln	ttc Phe	gca Ala	ttc Phe	cat His																																	
200																205																210																720
gcc Ala	aaa Lys	ggt Gly	gat Asp	gag Glu	ttc Phe	acc Thr	gat Asp	att Ile	ctg Leu	aag Lys	atg Met	ggt Gly	cgc Arg	aca Thr	cag Gln																																	
215																220																225																768
ctc Leu	caa Gln	gat Asp	gct Ala	gta Val	ccg Pro	atg Met	act Thr	tta Leu	ggc Gly	gag Glu	gaa Glu	ttc Phe	cag Gln	gca Ala	ttc Phe																																	
230																235																240																816
gct Ala	cat His	aac Asn	ttg Leu	gct Ala	gag Glu	gag Glu	caa Gln	agc Ser	ggt Val	ctg Leu	cgt Arg	atg Met	gct Ala	tcc Ser	gac Asp																																	
245																250																255																864
cggt Arg	ctc Leu	aag Lys	gaa Glu	gtt Val	aac Asn	ttg Leu	ggc Gly	gca Ala	acc Thr	gct Ala	atc Ile	ggt Gly	act Thr	ggc Gly	ttg Leu																																	
260																265																270																912
aac Asn	acc Thr	cca Pro	gcc Ala	ggt Gly	tac Tyr	cgt Arg	tat Tyr	cag Gln	ggt Val	gta Val	gcc Ala	gca Ala	ttg Leu	tcc Ser	gag Glu																																	
275																280																285																960
tgc Cys	acc Thr	ggc Gly	ttg Leu	gaa Glu	att Ile	aag Lys	tct Ser	gca Ala	cggt Arg	gat Asp	ctt Leu	att Ile	gaa Glu	gct Ala	act Thr																																	
290																295																300																1008
tca Ser	gac Asp	act Thr	ggt Gly	gcg Ala	tat Tyr	gtc Val	ctt Leu	gcc Ala	cat His	gca Ala	gct Ala	gtt Val	aag Lys	cgt Arg	act Thr																																	
305																310																315																1056
gcgt Ala	atg Met	aag Lys	ctt Leu	tct Ser	aag Lys	atc Ile	tgc Cys	aat Asn	gat Asp	ctt Leu	cga Arg																																					

PF59083SeqList PF59083.txt

atc	ggc	caa	gcc	405	ttg	ttt	gag	tcg	att	410	cga	att	ctc	ggt	aat	415	gct	gca	1296
Ile	Gly	Gln	Ala	420	Leu	Phe	Glu	Ser	Ile	425	Arg	Ile	Leu	Gly	Asn	430	Ala	Ala	
gtc	acc	ctt	cag	435	cac	aag	tgt	gtc	gaa	440	ggg	att	acc	gca	aat	445	gct	gac	1344
Val	Thr	Leu	Gln	435	His	Lys	Cys	Val	Glu	440	Gly	Ile	Thr	Ala	Asn	445	Ala	Asp	
gta	tgt	cgc	gcc	450	tac	gta	gat	aat	tcc	455	att	ggt	atc	gtt	acc	460	tat	ctc	1392
Val	Cys	Arg	Ala	450	Tyr	Val	Asp	Asn	Ser	455	Ile	Gly	Ile	Val	Thr	460	Tyr	Leu	
aac	cct	ttc	att	465	ggt	cac	cat	atg	ggt	470	gac	gtg	att	ggc	aag	475	gaa	gct	1440
Asn	Pro	Phe	Ile	465	Gly	His	His	Met	Gly	470	Asp	Val	Ile	Gly	Lys	475	Glu	Ala	
gct	gag	acc	ggc	485	aag	tcc	gta	cgt	gag	490	ctt	gta	ttg	gaa	aag	495	gga	cta	1488
Ala	Glu	Thr	Gly	485	Lys	Ser	Val	Arg	Glu	490	Leu	Val	Leu	Glu	Lys	495	Gly	Leu	
atg	gat	gaa	gag	500	act	ttg	aac	caa	atc	505	ctg	tcc	aag	gaa	aat	510	cta	atg	1536
Met	Asp	Glu	Glu	500	Thr	Leu	Asn	Gln	Ile	505	Leu	Ser	Lys	Glu	Asn	510	Leu	Met	
cac	cct	tcg	ttt	515	cgt	gga	acc	ctc	tac	520	cta	gat	aac	tag					1575
His	Pro	Ser	Phe	515	Arg	Gly	Thr	Leu	Tyr	520	Leu	Asp	Asn						

<210> 9620

<211> 524

<212> PRT

<213> *Corynebacterium diphtheriae* NCTC 13129

<400> 9620

Met 1	Ala	Ser	Gln	Ala 5	Lys	Asn	Thr	Lys	Gly 10	Ser	Lys	Asn	Ala	Glu 15	Val
Thr	Asn	Asp	Val 20	Leu	Asp	Gly	Lys	Thr 25	Glu	Gly	Thr	Ala	Glu 30	Lys	Val
Asn	Asp	Ala 35	Pro	Ile	Ala	Ser	Asp 40	Val	Thr	Thr	Lys	His 45	Ala	Thr	Lys
Lys	Ala 50	Ala	Pro	Gly	Phe	Arg 55	Ile	Glu	Glu	Asp	Leu 60	Leu	Gly	Glu	Met
Glu 65	Val	Pro	Asp	Glu 70	Val	Tyr	Tyr	Gly	Val	His 75	Thr	Leu	Arg	Ala	Ile 80
Asp	Asn	Tyr	Lys	Ile 85	Ser	Ser	Thr	Thr	Ile 90	Asn	Asp	Val	Pro	Glu 95	Phe
Ile	Arg	Gly	Met 100	Val	Gln	Val	Lys	Lys 105	Ala	Thr	Ala	Leu	Ala 110	Asn	Arg
Arg	Leu	His 115	Thr	Leu	Pro	Lys	Asp 120	Lys	Cys	Asp	Ala	Ile 125	Val	Trp	Ala
Cys	Asp 130	Gln	Ile	Leu	Asp	His 135	Gly	Arg	Cys	Met	Asp 140	Gln	Phe	Pro	Ile
Asp 145	Val	Phe	Gln	Gly	Gly 150	Ala	Gly	Thr	Ser	Val 155	Asn	Met	Asn	Thr	Asn 160
Glu	Val	Ile	Ala	Asn 165	Leu	Ala	Leu	Glu	His 170	Leu	Gly	Lys	Pro	Lys 175	Gly
Ser	Tyr	Asp	Ile 180	Ile	Asn	Pro	Asn	Asp 185	Asp	Val	Asn	Met	Ser 190	Gln	Ser
Thr	Asn	Asp 195	Ala	Tyr	Pro	Thr	Gly 200	Phe	Arg	Leu	Gly	Val 205	Tyr	Glu	Ala
Met	Gln 210	Glu	Leu	Ile	Thr	Arg 215	Ile	Asp	Asn	Leu	Gln 220	Phe	Ala	Phe	His
Ala 225	Lys	Gly	Asp	Glu	Phe 230	Thr	Asp	Ile	Leu	Lys 235	Met	Gly	Arg	Thr	Gln 240
Leu	Gln	Asp	Ala 245	Val	Pro	Met	Thr	Leu	Gly 250	Glu	Glu	Phe	Gln	Ala 255	Phe
Ala	His	Asn	Leu 260	Ala	Glu	Glu	Gln	Ser 265	Val	Leu	Arg	Met	Ala 270	Ser	Asp
Arg	Leu	Lys 275	Glu	Val	Asn	Leu	Gly 280	Ala	Thr	Ala	Ile	Gly 285	Thr	Gly	Leu
Asn	Thr 290	Pro	Ala	Gly	Tyr	Arg 295	Tyr	Gln	Val	Val	Ala 300	Ala	Leu	Ser	Glu
Cys 305	Thr	Gly	Leu	Glu	Ile 310	Lys	Ser	Ala	Arg	Asp 315	Leu	Ile	Glu	Ala	Thr 320

PF59083SeqList PF59083.txt

Ser Asp Thr Gly Ala Tyr Val Leu Ala His Ala Ala Val Lys Arg Thr
 325 330 335
 Ala Met Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser
 340 345 350
 Gly Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Ala Arg Ala Ala
 355 360 365
 Gly Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val
 370 375 380
 Val Asn Gln Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr Val Thr
 385 390 400
 Met Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val
 405 410 415
 Ile Gly Gln Ala Leu Phe Glu Ser Ile Arg Ile Leu Gly Asn Ala Ala
 420 425 430
 Val Thr Leu Gln His Lys Cys Val Glu Gly Ile Thr Ala Asn Ala Asp
 435 440 445
 Val Cys Arg Ala Tyr Val Asp Asn Ser Ile Gly Ile Val Thr Tyr Leu
 450 455 460
 Asn Pro Phe Ile Gly His His Met Gly Asp Val Ile Gly Lys Glu Ala
 465 470 475 480
 Ala Glu Thr Gly Lys Ser Val Arg Glu Leu Val Leu Glu Lys Gly Leu
 485 490 495
 Met Asp Glu Glu Thr Leu Asn Gln Ile Leu Ser Lys Glu Asn Leu Met
 500 505 510
 His Pro Ser Phe Arg Gly Thr Leu Tyr Leu Asp Asn
 515 520

<210> 9621

<211> 1392

<212> DNA

<213> Geobacter sulfurreducens PCA

<220>

<221> CDS

<222> (1)..(1392)

<223> transl_table=11

<400> 9621

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

PF59083SeqList PF59083.txt

Ala	Leu	Glu	Gly	Leu	Val	Ala	Ala	Leu	Arg	Lys	Lys	Ser	Ala	Glu	Phe	
gac	ggc	att	ctc	aag	agc	ggc	cgg	act	cac	ctg	cag	gat	gcg	gtg	ccg	576
Asp	Gly	Ile	Leu	Lys	Ser	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Val	Pro	
			180					185					190			
atc	cgt	ctc	ggc	cag	gag	ttc	gag	gcg	tgg	gcc	gtg	gcg	ctg	gag	aag	624
Ile	Arg	Leu	Gly	Gln	Glu	Phe	Glu	Ala	Trp	Ala	Val	Ala	Leu	Glu	Lys	
		195					200					205				
aac	ctg	gcc	gcc	atc	gag	ggg	gcg	gtg	ccg	ggc	ctt	gcg	gaa	ctg	ggt	672
Asn	Leu	Ala	Ala	Ile	Glu	Gly	Ala	Val	Pro	Gly	Leu	Ala	Glu	Leu	Gly	
	210					215					220					
atc	ggc	ggc	acc	gcg	gca	ggt	acc	ggc	atg	aac	gcc	gag	ccg	gcc	tac	720
Ile	Gly	Gly	Thr	Ala	Ala	Gly	Thr	Gly	Met	Asn	Ala	Glu	Pro	Ala	Tyr	
	225				230			235							240	
atc	gat	ctt	gtg	gtg	gca	gag	ctc	gcc	cgg	gaa	acc	ggc	ttt	ccc	ctc	768
Ile	Asp	Leu	Val	Val	Ala	Glu	Leu	Ala	Arg	Glu	Thr	Gly	Phe	Pro	Leu	
				245				250						255		
gta	cgg	ggt	gcg	aac	ctg	gtt	gag	cgg	atg	cag	aac	atg	gac	ccc	ttc	816
Val	Arg	Gly	Ala	Asn	Leu	Val	Glu	Arg	Met	Gln	Asn	Met	Asp	Pro	Phe	
			260				265						270			
gtg	gcc	ctc	tcc	tcc	gct	ctc	aag	gga	ctt	gcc	gta	aac	ctc	gcc	cgt	864
Val	Ala	Leu	Ser	Ser	Ala	Leu	Lys	Gly	Leu	Ala	Val	Asn	Leu	Ala	Arg	
		275					280					285				
atc	gcc	aac	gac	ctg	cgg	ctc	ctt	tcc	tct	ggc	ccc	cgg	acc	ggg	ctg	912
Ile	Ala	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Thr	Gly	Leu	
	290					295					300					
gcc	gag	atc	gcg	ctg	ccg	gcg	ctg	cag	ccc	ggc	tcc	tct	atc	atg	ccg	960
Ala	Glu	Ile	Ala	Leu	Pro	Ala	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	
	305				310					315					320	
ggg	aag	gtc	aac	ccg	gtc	atg	gcc	gag	gtg	acc	gac	atg	gtc	gcc	ttt	1008
Gly	Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Val	Thr	Asp	Met	Val	Ala	Phe	
				325					330					335		
caa	gtg	atg	ggt	gcg	gac	acg	aca	atc	atg	ctc	gcc	gcc	cag	gca	ggg	1056
Gln	Val	Met	Gly	Ala	Asp	Thr	Thr	Ile	Met	Leu	Ala	Ala	Gln	Ala	Gly	
			340				345						350			
cag	ctg	gag	ctt	aac	gtc	atg	atg	ccg	gtc	atc	gcg	ttc	aac	ctt	ctg	1104
Gln	Leu	Glu	Leu	Asn	Val	Met	Met	Pro	Val	Ile	Ala	Phe	Asn	Leu	Leu	
		355				360						365				
ttc	agc	ctt	gaa	atc	ctg	aag	aac	acg	gtg	ccc	aag	ctg	gct	gat	gcc	1152
Phe	Ser	Leu	Glu	Ile	Leu	Lys	Asn	Thr	Val	Pro	Lys	Leu	Ala	Asp	Ala	
	370					375					380					
tgc	atc	gcc	ggc	atc	act	gcg	gac	cgg	gag	cgc	tgc	ctc	cgg	tac	ctg	1200
Cys	Ile	Ala	Gly	Ile	Thr	Ala	Asp	Arg	Glu	Arg	Cys	Leu	Arg	Tyr	Leu	
	385				390				395						400	
gag	cag	tcg	gta	gga	ctg	gcc	acg	gtg	ctc	gcg	ccc	tac	atc	ggc	tat	1248
Glu	Gln	Ser	Val	Gly	Leu	Ala	Thr	Val	Leu	Ala	Pro	Tyr	Ile	Gly	Tyr	
			405					410						415		
gcc	gcg	gcc	gcg	gag	gtg	gcc	aag	gaa	tcg	act	gcc	acg	ggc	cgg	agt	1296
Ala	Ala	Ala	Ala	Glu	Val	Ala	Lys	Glu	Ser	Thr	Ala	Thr	Gly	Arg	Ser	
			420				425						430			
atc	cgg	cag	atc	gtg	gaa	gac	cgg	cag	ctc	ctg	tcg	gcc	ggg	cgt	ctg	1344
Ile	Arg	Gln	Ile	Val	Glu	Asp	Arg	Gln	Leu	Leu	Ser	Ala	Gly	Arg	Leu	
		435				440						445				
gcg	gag	atc	ctc	gac	ccc	ttc	cct	ctc	acc	agc	cct	ggc	gtt	ccg		1389
Ala	Glu	Ile	Leu	Asp	Pro	Phe	Pro	Leu	Thr	Ser	Pro	Gly	Val	Pro		
	450					455					460					
tga																1392

<210> 9622

<211> 463

<212> PRT

<213> Geobacter sulfurreducens PCA

<400> 9622

Met Thr Phe Arg Val Glu Lys Asp Thr Leu Gly Glu Val Arg Val Pro
1 5 10 15

Ala Asp Ala Tyr Tyr Gly Ala Gln Thr Val Arg Ala Val Glu Asn Phe
Seite 10080

PF59083SeqList PF59083.txt

```

      20      25      30
Pro Ile Ser Gly Leu Arg Pro His Pro Ala Leu Val Arg Ala Thr Val
      35      40      45
Leu Val Lys Met Cys Ala Ala Arg Ala Asn Met Ala Thr Gly Arg Leu
      50      55      60
Asp Ser Arg Leu Gly Asp Ala Ile Val Arg Ala Asp Glu Cys Leu
      65      70      75
Ala Gly Ala Phe Asp Ala His Phe Val Val Asp Pro Phe Gln Ala Gly
      85      90      95
Ala Gly Thr Ser His Asn Met Asn Val Asn Glu Val Leu Ala Asn Arg
      100      105      110
Ala Asn Glu Leu Leu Gly Glu Glu Arg Gly Arg Tyr Ala Pro Val His
      115      120      125
Pro Asn Asp His Val Asn Met Ala Gln Ser Thr Asn Asp Val Phe Pro
      130      135      140
Thr Ala Met Arg Leu Ala Leu Arg Val Ala Gly Asp Leu Arg Pro
      145      150      155
Ala Leu Glu Gly Leu Val Ala Ala Leu Arg Lys Lys Ser Ala Glu Phe
      165      170      175
Asp Gly Ile Leu Lys Ser Gly Arg Thr His Leu Gln Asp Ala Val Pro
      180      185      190
Ile Arg Leu Gly Gln Glu Phe Glu Ala Trp Ala Val Ala Leu Glu Lys
      195      200      205
Asn Leu Ala Ala Ile Glu Gly Ala Val Pro Gly Leu Ala Glu Leu Gly
      210      215      220
Ile Gly Gly Thr Ala Ala Gly Thr Gly Met Asn Ala Glu Pro Ala Tyr
      225      230      235
Ile Asp Leu Val Val Ala Glu Leu Ala Arg Glu Thr Gly Phe Pro Leu
      245      250      255
Val Arg Gly Ala Asn Leu Val Glu Arg Met Gln Asn Met Asp Pro Phe
      260      265      270
Val Ala Leu Ser Ser Ala Leu Lys Gly Leu Ala Val Asn Leu Ala Arg
      275      280      285
Ile Ala Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Thr Gly Leu
      290      295      300
Ala Glu Ile Ala Leu Pro Ala Leu Gln Pro Gly Ser Ser Ile Met Pro
      305      310      315
Gly Lys Val Asn Pro Val Met Ala Glu Val Thr Asp Met Val Ala Phe
      325      330      335
Gln Val Met Gly Ala Asp Thr Thr Ile Met Leu Ala Ala Gln Ala Gly
      340      345      350
Gln Leu Glu Leu Asn Val Met Met Pro Val Ile Ala Phe Asn Leu Leu
      355      360      365
Phe Ser Leu Glu Ile Leu Lys Asn Thr Val Pro Lys Leu Ala Asp Ala
      370      375      380
Cys Ile Ala Gly Ile Thr Ala Asp Arg Glu Arg Cys Leu Arg Tyr Leu
      385      390      395
Glu Gln Ser Val Gly Leu Ala Thr Val Leu Ala Pro Tyr Ile Gly Tyr
      405      410      415
Ala Ala Ala Ala Glu Val Ala Lys Glu Ser Thr Ala Thr Gly Arg Ser
      420      425      430
Ile Arg Gln Ile Val Glu Asp Arg Gln Leu Leu Ser Ala Gly Arg Leu
      435      440      445
Ala Glu Ile Leu Asp Pro Phe Pro Leu Thr Ser Pro Gly Val Pro
      450      455      460

```

<210> 9623

<211> 1395

<212> DNA

<213> Wolbachia endosymbiont of Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1395)

<223> transl_table=11

<400> 9623

```

atg gat aga aag acg aga ata gaa tca gac agc tta ggg gaa gta aaa
Met Asp Arg Lys Thr Arg Ile Glu Ser Asp Ser Leu Gly Glu Val Lys

```

PF59083SeqList PF59083.txt

1	5	10	15	
gta cca agt gaa cat tac tgg gga gca cag act cag cgt tct tta gaa	20	25	30	96
Val Pro Ser Glu His Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Glu				
aat ttt aag att ggc aca gaa aaa atg cca gag cct ctg att aaa gca	35	40	45	144
Asn Phe Lys Ile Gly Thr Glu Lys Met Pro Glu Pro Leu Ile Lys Ala				
tta gca ata gta aaa ctt gca gca gcg cgt gtt aat atg aaa cat ggt	50	55	60	192
Leu Ala Ile Val Lys Leu Ala Ala Ala Arg Val Asn Met Lys His Gly				
gtt ata gat gat agg gta ggg gac gca att tgc aca gcc gcg agg gaa	65	70	75	240
Val Ile Asp Asp Arg Val Gly Asp Ala Ile Cys Thr Ala Ala Arg Glu				
gta ata gat ggc aaa ttt aat aat gaa ttt ccg ctt gtt gtt tgg caa	85	90	95	288
Val Ile Asp Gly Lys Phe Asn Asn Glu Phe Pro Leu Val Val Trp Gln				
acc gga tcc gga acg cag act aat atg aat atg aat gaa gtg atc agc	100	105	110	336
Thr Gly Ser Gly Thr Gln Thr Asn Met Asn Met Asn Glu Val Ile Ser				
aat cgt gca ata gag att tta ggt ggt aat ttg ggt agt aaa tct cca	115	120	125	384
Asn Arg Ala Ile Glu Ile Leu Gly Gly Asn Leu Gly Ser Lys Ser Pro				
ata cat cca aat gat cat gtg aat tat ggt cag tcg tca aat gac acc	130	135	140	432
Ile His Pro Asn Asp His Val Asn Tyr Gly Gln Ser Ser Asn Asp Thr				
ttt cca aca gca atg cat ata gca gca gca gag caa ata aac tgc ttg	145	150	155	480
Phe Pro Thr Ala Met His Ile Ala Ala Ala Glu Gln Ile Asn Cys Leu				
ctt att cca aat ctt gaa aaa ttg cat aag gtg ctg gat aat aag gtt	165	170	175	528
Leu Ile Pro Asn Glu Lys Leu His Val Leu Asp Asn Lys Val Val				
cag gaa ttt aaa gat ata ata aaa gta gga cgt act cat ctg caa gat	180	185	190	576
Gln Glu Phe Lys Asp Ile Ile Lys Val Gly Arg Thr His Leu Gln Asp				
gca acg ccc cta aca cta gga cag gag ttt tct ggc tat gca gcc cag	195	200	205	624
Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Ala Ala Gln				
att aaa aag ggg ata gag aga gta aaa tca act tta agt ggt ata tac	210	215	220	672
Ile Lys Lys Gly Ile Glu Arg Val Lys Ser Thr Leu Ser Gly Ile Tyr				
gag ctt gca caa ggt ggc act gcg gtt ggc acg gga ctc aat act aaa	225	230	235	720
Glu Leu Ala Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Lys				
aag ggt ttt gct gaa gat ttt gca aag caa gtt gca gga att act aac	245	250	255	768
Lys Gly Phe Ala Glu Asp Phe Ala Lys Val Val Ala Gly Ile Thr Asn				
ctt cca ttt act tca gca ggc aat aaa ttt gaa gcg cta gca gca aat	260	265	270	816
Leu Pro Phe Thr Ser Ala Gly Asn Lys Phe Glu Ala Leu Ala Ala Asn				
gat gct tta gtt gag ctc agt gga aca ctc aat aca gta gca gtc agt	275	280	285	864
Asp Ala Leu Val Glu Leu Ser Gly Thr Leu Asn Thr Val Ala Val Ser				
tta atg aaa att gca aat gat ata agg ttg ctt ggt tct ggt cca aga	290	295	300	912
Leu Met Lys Ile Ala Asn Asp Ile Arg Leu Leu Gly Ser Gly Pro Arg				
tgc gga att ggg gaa ata atg tta ccg gaa aat gag cct ggt tct tca	305	310	315	960
Cys Gly Ile Gly Glu Ile Met Leu Pro Glu Asn Glu Pro Gly Ser Ser				
att atg cca ggt aaa gtg aat cca act cag tgt gaa gcg gtg act atg	325	330	335	1008
Ile Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Val Thr Met				
gta tgc act caa gtt atg gga aat cat gtt gct gta acc att agt ggt	340	345	350	1056
Val Cys Thr Gln Val Met Gly Asn His Val Ala Val Thr Ile Ser Gly				
tca aac ggt cat ttt gaa ttg aat gtg ttt aag cca gtg ata att tac	355	360	365	1104
Ser Asn Gly His Phe Glu Leu Asn Val Phe Lys Pro Val Ile Ile Tyr				
aat gtt ttg cag tct ata aga ctt tta gct gac gca agt tta aat ttt				1152
Asn Val Leu Gln Ser Ile Arg Leu Leu Ala Asp Ala Ser Leu Asn Phe				

PF59083SeqList PF59083.txt

370	375	380	
aca gaa aaa tgt gta gtt ggt att aaa gca aat gaa gag agg ata aaa			1200
Thr Glu Lys Cys Val Val Gly Ile Lys Ala Asn Glu Glu Arg Ile Lys			
385	390	395	400
gat tta ctg aat cag tcg ttg atg ttg gtc act ata tta aat acg cat			1248
Asp Leu Leu Asn Gln Ser Leu Met Leu Val Thr Ile Leu Asn Thr His			
	405	410	415
ata ggg tac gac aat gca gca aaa ata gcg aag ctt gct tat aaa gaa			1296
Ile Gly Tyr Asp Asn Ala Ala Lys Ile Ala Lys Leu Ala Tyr Lys Glu			
	420	425	430
aat atc act cta aag gaa gca gca gca aaa ctt caa ctg ctc act gag			1344
Asn Ile Thr Leu Lys Glu Ala Ala Ala Lys Leu Gln Leu Leu Thr Glu			
	435	440	445
gaa gag ttt gaa agg ata gtg aaa cca gaa gaa atg gta aat tat ttg			1392
Glu Glu Phe Glu Arg Ile Val Lys Pro Glu Glu Met Val Asn Tyr Leu			
	450	455	460
taa			1395

<210> 9624

<211> 464

<212> PRT

<213> Wolbachia endosymbiont of Drosophila melanogaster

<400> 9624

Met Asp Arg Lys Thr Arg Ile Glu Ser Asp Ser Leu Gly Glu Val Lys	
1 5 10 15	
Val Pro Ser Glu His Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Glu	
20 25 30	
Asn Phe Lys Ile Gly Thr Glu Lys Met Pro Glu Pro Leu Ile Lys Ala	
35 40 45	
Leu Ala Ile Val Lys Leu Ala Ala Arg Val Asn Met Lys His Gly	
50 55 60	
Val Ile Asp Asp Arg Val Gly Asp Ala Ile Cys Thr Ala Ala Arg Glu	
65 70 75 80	
Val Ile Asp Gly Lys Phe Asn Asn Glu Phe Pro Leu Val Val Trp Gln	
85 90 95	
Thr Gly Ser Gly Thr Gln Thr Asn Met Asn Met Asn Glu Val Ile Ser	
100 105 110	
Asn Arg Ala Ile Glu Ile Leu Gly Gly Asn Leu Gly Ser Lys Ser Pro	
115 120 125	
Ile His Pro Asn Asp His Val Asn Tyr Gly Gln Ser Ser Asn Asp Thr	
130 135 140	
Phe Pro Thr Ala Met His Ile Ala Ala Ala Glu Gln Ile Asn Cys Leu	
145 150 155 160	
Leu Ile Pro Asn Leu Glu Lys Leu His Lys Val Leu Asp Asn Lys Val	
165 170 175	
Gln Glu Phe Lys Asp Ile Ile Lys Val Gly Arg Thr His Leu Gln Asp	
180 185 190	
Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Ala Ala Gln	
195 200 205	
Ile Lys Lys Gly Ile Glu Arg Val Lys Ser Thr Leu Ser Gly Ile Tyr	
210 215 220	
Glu Leu Ala Gln Gly Gly Thr Ala Val Gly Thr Leu Asn Thr Lys	
225 230 235 240	
Lys Gly Phe Ala Glu Asp Phe Ala Lys Gln Val Ala Gly Ile Thr Asn	
245 250 255	
Leu Pro Phe Thr Ser Ala Gly Asn Lys Phe Glu Ala Leu Ala Ala Asn	
260 265 270	
Asp Ala Leu Val Glu Leu Ser Gly Thr Leu Asn Thr Val Ala Val Ser	
275 280 285	
Leu Met Lys Ile Ala Asn Asp Ile Arg Leu Leu Gly Ser Gly Pro Arg	
290 295 300	
Cys Gly Ile Gly Glu Ile Met Leu Pro Glu Asn Glu Pro Gly Ser Ser	
305 310 315 320	
Ile Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Val Thr Met	
325 330 335	
Val Cys Thr Gln Val Met Gly Asn His Val Ala Val Thr Ile Ser Gly	

PF59083SeqList PF59083.txt

```

          340          345          350
Ser Asn Gly His Phe Glu Leu Asn Val Phe Lys Pro Val Ile Ile Tyr
          355          360          365
Asn Val Leu Gln Ser Ile Arg Leu Leu Ala Asp Ala Ser Leu Asn Phe
          370          375          380
Thr Glu Lys Cys Val Val Gly Ile Lys Ala Asn Glu Glu Arg Ile Lys
          385          390          395
Asp Leu Leu Asn Gln Ser Leu Met Leu Val Thr Ile Leu Asn Thr His
          400          405          410
Ile Gly Tyr Asp Asn Ala Ala Lys Ile Ala Lys Leu Ala Tyr Lys Glu
          415          420          425
Asn Ile Thr Leu Lys Glu Ala Ala Ala Lys Leu Gln Leu Leu Thr Glu
          430          435          440
Glu Glu Phe Glu Arg Ile Val Lys Pro Glu Glu Met Val Asn Tyr Leu
          445          450          455          460

```

<210> 9625

<211> 1431

<212> DNA

<213> Bdellovibrio bacteriovorus HD100

<220>

<221> CDS

<222> (1)..(1431)

<223> transl_table=11

<400> 9625

```

ttg gag tta gtg atg gaa aag ttc cgc gta gaa aaa gat ttg ctg ggt      48
Met Glu Leu Val Met Glu Lys Phe Arg Val Glu Lys Asp Leu Leu Gly
1          5          10          15
gaa aag aaa gtc cct gcg gaa gct tat tac ggc att cat acc ctg cgg      96
Glu Lys Lys Val Pro Ala Glu Ala Tyr Tyr Gly Ile His Thr Leu Arg
          20          25          30
gcg atg gag aac ttt cag atc tcg ggc atc cct gtc gga gcc aat caa      144
Ala Met Glu Asn Phe Gln Ile Ser Gly Ile Pro Val Gly Ala Asn Gln
          35          40          45
agt ttc gtg cgt ggt ctg gca ctg gtg aaa aaa gcc tgc gcg ttg gcc      192
Ser Phe Val Arg Gly Leu Ala Leu Val Lys Lys Ala Cys Ala Leu Ala
          50          55          60
aat ggt gaa ctg ggc aca atc ccg gcg gat gtt tcc aag tcc ttg gtt      240
Asn Gly Glu Leu Gly Thr Ile Pro Ala Asp Val Ser Lys Ser Leu Val
          65          70          75          80
gaa gcc tgt gac atc gtt ttg cag gac ccg aaa aaa tgg ggt cag cag      288
Glu Ala Cys Asp Ile Val Leu Gln Asp Pro Lys Lys Trp Gly Gln Gln
          85          90          95
ttc cca tcc gac gtt tat cag ggc ggc gcg ggg act tcg atc aac atg      336
Phe Pro Ser Asp Val Tyr Gln Gly Gly Ala Gly Thr Ser Ile Asn Met
          100          105          110
aat gcc aac gaa gtg att gcc aat atc gca ttg gaa aaa cgc ggt ctg      384
Asn Ala Asn Glu Val Ile Ala Asn Ile Ala Leu Glu Lys Arg Gly Leu
          115          120          125
caa aaa ggc acc tac gcg gtg atc aac cct aat gat cac gtg aat aag      432
Gln Lys Gly Thr Tyr Ala Val Ile Asn Pro Asn Asp His Val Asn Lys
          130          135          140
tgc cag tcc acg aat gat gct tat ccg acc gct ttc cga gtg gcg ctg      480
Cys Gln Ser Thr Asn Asp Ala Tyr Pro Thr Ala Phe Arg Val Ala Leu
          145          150          155          160
tat gaa cac ctg aac gga act ttg gcg gcg ctg gat tct ttg gct ttg      528
Tyr Glu His Leu Asn Gly Thr Leu Ala Ala Leu Asp Ser Leu Ala Leu
          165          170          175
gcc ttc gag aaa aaa ggc aaa gaa ttc cag agc gtt ttg aaa atg ggc      576
Ala Phe Glu Lys Lys Gly Lys Glu Phe Gln Ser Val Leu Lys Met Gly
          180          185          190
cgc acg cag ttg cag gat gca gtt ccc atg tct ttg ggg cag gag ttt      624
Arg Thr Gln Leu Gln Asp Ala Val Pro Met Ser Leu Gly Gln Glu Phe
          195          200          205          210
aac gct ttt gcc act tta cta aaa gaa gac ggt cgt ctg atc cgc act      672
Asn Ala Phe Ala Thr Leu Leu Lys Glu Asp Gly Arg Leu Ile Arg Thr
          210          215          220

```

PF59083SeqList PF59083.txt

gtt	cag	aaa	ttc	atg	ctg	gaa	gtg	aac	ttg	ggg	gcc	acc	gcg	att	ggg	720
Val	Gln	Lys	Phe	Met	Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	
225					230					235					240	
act	ggc	atc	aac	aca	cct	ccg	ggt	tat	gcg	tct	ttg	gcg	gtg	caa	aag	768
Thr	Gly	Ile	Asn	Thr	Pro	Pro	Gly	Tyr	Ala	Ser	Leu	Ala	Val	Gln	Lys	
				245					250					255		
ctg	gct	gag	gtc	acc	ggg	cat	ccg	ttt	gtt	cag	tcg	gaa	gat	tac	atc	816
Leu	Ala	Glu	Val	Thr	Gly	His	Pro	Phe	Val	Gln	Ser	Glu	Asp	Tyr	Ile	
			260					265					270			
gaa	gcc	acc	agc	gac	tgt	ggt	gcc	tac	atc	att	atc	tct	ggc	gca	ctg	864
Glu	Ala	Thr	Ser	Asp	Cys	Gly	Ala	Tyr	Ile	Ile	Ile	Ser	Gly	Ala	Leu	
		275					280					285				
aaa	cgc	acg	gca	gtg	aaa	ctt	tcg	aaa	atc	tgc	aac	gac	ttg	cgc	ttg	912
Lys	Arg	Thr	Ala	Val	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	
	290					295					300					
ctt	agt	tct	ggt	ccg	cgt	ggc	ttg	aaa	gaa	atc	aac	ctg	cct	gaa		960
Leu	Ser	Ser	Gly	Pro	Arg	Gly	Leu	Lys	Glu	Ile	Asn	Leu	Pro	Glu		
305					310				315					320		
atg	cag	gcg	ggt	tct	tcc	atc	atg	ccg	gca	aaa	gtg	aat	ccg	gtg	att	1008
Met	Gln	Ala	Gly	Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	
				325					330					335		
ccg	gaa	gtt	gtg	aat	cag	gtc	agc	ttc	aaa	atc	atc	ggc	aat	gac	ctg	1056
Pro	Glu	Val	Val	Asn	Gln	Val	Ser	Phe	Lys	Ile	Ile	Gly	Asn	Asp	Leu	
			340					345					350			
gcg	atc	acc	ctg	gcg	gcc	gaa	gca	ggg	cag	ctg	cag	ctg	aat	gtg	atg	1104
Ala	Ile	Thr	Leu	Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	
		355					360					365				
gaa	cct	gtg	atc	gcc	tcc	agt	ctg	ttt	gag	tct	ttg	gat	ctt	ttg	aag	1152
Glu	Pro	Val	Ile	Ala	Ser	Ser	Leu	Phe	Glu	Ser	Leu	Asp	Leu	Leu	Lys	
	370					375					380					
aat	gcc	tgt	gaa	acc	ctg	gaa	cat	aaa	tgt	gtg	aag	ggt	att	acg	gcc	1200
Asn	Ala	Cys	Glu	Thr	Leu	Glu	His	Lys	Cys	Val	Lys	Gly	Ile	Thr	Ala	
385					390				395					400		
aat	gca	gaa	cgc	tgc	cgg	gac	tac	gtc	atg	aac	agc	atc	ggt	att	gtg	1248
Asn	Ala	Glu	Arg	Cys	Arg	Asp	Tyr	Val	Met	Asn	Ser	Ile	Gly	Ile	Val	
				405				410						415		
act	tat	ctg	gat	ccg	atc	atc	ggt	cac	gat	gaa	ggc	gac	cgt	atc	gga	1296
Thr	Tyr	Leu	Asp	Pro	Ile	Ile	Gly	His	Asp	Glu	Gly	Asp	Arg	Ile	Gly	
			420				425						430			
aaa	atc	tgt	gcg	gag	acc	ggt	cgc	aac	gtg	gct	gaa	gtg	gcc	ctg	gag	1344
Lys	Ile	Cys	Ala	Glu	Thr	Gly	Arg	Asn	Val	Ala	Glu	Val	Ala	Leu	Glu	
		435					440					445				
cga	ggc	gtg	gtg	act	cag	gcg	caa	ctg	gat	gaa	ctg	ttc	tca	atg	gaa	1392
Arg	Gly	Val	Val	Thr	Gln	Ala	Gln	Leu	Asp	Glu	Leu	Phe	Ser	Met	Glu	
	450					455					460					
aat	ctg	ctg	aac	ccg	aaa	tac	gtc	ggc	aag	aag	cac	tag				1431
Asn	Leu	Leu	Asn	Pro	Lys	Tyr	Val	Gly	Lys	Lys	His					
465					470				475							

<210> 9626

<211> 476

<212> PRT

<213> Bdellovibrio bacteriovorus HD100

<400> 9626

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

PF59083SeqList PF59083.txt

Asn Ala Asn Glu Val Ile Ala Asn Ile Ala Leu Glu Lys Arg Gly Leu
115 120 125
Gln Lys Gly Thr Tyr Ala Val Ile Asn Pro Asn Asp His Val Asn Lys
130 135 140
Cys Gln Ser Thr Asn Asp Ala Tyr Pro Thr Ala Phe Arg Val Ala Leu
145 150 155 160
Tyr Glu His Leu Asn Gly Thr Leu Ala Ala Leu Asp Ser Leu Ala Leu
165 170 175
Ala Phe Glu Lys Lys Gly Lys Glu Phe Gln Ser Val Leu Lys Met Gly
180 185 190
Arg Thr Gln Leu Gln Asp Ala Val Pro Met Ser Leu Gly Gln Glu Phe
195 200 205
Asn Ala Phe Ala Thr Leu Leu Lys Glu Asp Gly Arg Leu Ile Arg Thr
210 215 220
Val Gln Lys Phe Met Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly
225 230 235 240
Thr Gly Ile Asn Thr Pro Pro Gly Tyr Ala Ser Leu Ala Val Gln Lys
245 250 255
Leu Ala Glu Val Thr Gly His Pro Phe Val Gln Ser Glu Asp Tyr Ile
260 265 270
Glu Ala Thr Ser Asp Cys Gly Ala Tyr Ile Ile Ile Ser Gly Ala Leu
275 280 285
Lys Arg Thr Ala Val Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu
290 295 300
Leu Ser Ser Gly Pro Arg Ala Gly Leu Lys Glu Ile Asn Leu Pro Glu
305 310 315 320
Met Gln Ala Gly Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile
325 330 335
Pro Glu Val Val Asn Gln Val Ser Phe Lys Ile Ile Gly Asn Asp Leu
340 345 350
Ala Ile Thr Leu Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met
355 360 365
Glu Pro Val Ile Ala Ser Ser Leu Phe Glu Ser Leu Asp Leu Leu Lys
370 375 380
Asn Ala Cys Glu Thr Leu Glu His Lys Cys Val Lys Gly Ile Thr Ala
385 390 395 400
Asn Ala Glu Arg Cys Arg Asp Tyr Val Met Asn Ser Ile Gly Ile Val
405 410 415
Thr Tyr Leu Asp Pro Ile Ile Gly His Asp Glu Gly Asp Arg Ile Gly
420 425 430
Lys Ile Cys Ala Glu Thr Gly Arg Asn Val Ala Glu Val Ala Leu Glu
435 440 445
Arg Gly Val Val Thr Gln Ala Gln Leu Asp Glu Leu Phe Ser Met Glu
450 455 460
Asn Leu Leu Asn Pro Lys Tyr Val Gly Lys Lys His
465 470 475

<210> 9627

<211> 1392

<212> DNA

<213> Treponema denticola ATCC 35405

<220>

<221> CDS

<222> (1)..(1392)

<223> transl_table=11

<400> 9627

atg cga agg gaa cat gac tta ctc gga gaa ttg gat att ccg gaa gat	48
Met Arg Arg Glu His Asp Leu Leu Gly Glu Leu Asp Ile Pro Glu Asp	
1 5 10	
gct tat tat gga att caa aca ttc cgc agt gtt gaa aat ttt caa att	96
Ala Tyr Tyr Gly Ile Gln Thr Phe Arg Ser Val Glu Asn Phe Gln Ile	
20 25 30	
aca gga tta agg ctc tgt gat ttt ccc gat ttt att aag ggt ctt gct	144
Thr Gly Leu Arg Leu Cys Asp Phe Pro Asp Phe Ile Lys Gly Leu Ala	
35 40 45	
tat aca aag cag gct gca gcc gaa gcc aac cat gaa ctc ggc tat tta	192
Tyr Thr Lys Gln Ala Ala Ala Glu Ala Asn His Glu Leu Gly Tyr Leu	

PF59083SeqList PF59083.txt

50	55	60	
agc gat gaa gtt tac aag gct atg att cag gct tgt aaa gaa gtt gcc			240
Ser Asp Glu Val Tyr Lys Ala Met Ile Gln Ala Cys Lys Glu Val Ala			
65	70	75	80
gaa ggc aaa ttc gat aag gaa ttt gta gtc gat atg att cag ggc gga			288
Glu Gly Lys Phe Asp Lys Glu Phe Val Val Asp Met Ile Gln Gly Gly			
85	90	95	
gca gga act tct acc aat atg aat gca aat gaa gtt atc gcc aac cgc			336
Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu Val Ile Ala Asn Arg			
100	105	110	
gca aac gaa atc tta gga aag gcc aag gga act tat tcg ccc tgc cat			384
Ala Asn Glu Ile Leu Gly Lys Ala Lys Gly Thr Tyr Ser Pro Cys His			
115	120	125	
ccc aat aat cac gta aac ttt gct caa tct aca aac gac gct tat cct			432
Pro Asn Asn His Val Asn Phe Ala Gln Ser Thr Asn Asp Ala Tyr Pro			
130	135	140	
aca gct gca aag ctc ggc atc tcg tta aat aca ccg gct ctt ata gat			480
Thr Ala Ala Lys Leu Gly Ile Ser Leu Asn Thr Pro Ala Leu Ile Asp			
145	150	155	160
gaa ctc aaa tct ctt gtt gct tct ttt aga aaa aag gcc caa gaa ctt			528
Glu Leu Lys Ser Leu Val Ala Ser Phe Arg Lys Lys Ala Gln Glu Leu			
165	170	175	
gga gaa aat atc aag atg gga aga acc cag ctt caa gat gcc gta ccc			576
Gly Glu Asn Ile Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro			
180	185	190	
atg acc ctc ggc caa gag ttt gaa tcc tat gcc gct tct ttg gaa aac			624
Met Thr Leu Gly Gln Glu Phe Glu Ser Tyr Ala Ala Ser Leu Glu Asn			
195	200	205	
gaa att cct cag att cag ttt gca agg gaa aat ctt cac acc ata aac			672
Glu Ile Pro Gln Ile Gln Phe Ala Arg Glu Asn Leu His Thr Ile Asn			
210	215	220	
atg gga gct acc gct atc gga aca ggt atc aac tcg gat cct aac tat			720
Met Gly Ala Thr Ala Ile Gly Thr Gly Ile Asn Ser Asp Pro Asn Tyr			
225	230	235	240
aca ccg aaa gta acc tct cat ctg gca aaa att tcg ggt ctt gat cta			768
Thr Pro Lys Val Thr Ser His Leu Ala Lys Ile Ser Gly Leu Asp Leu			
245	250	255	
aag gct gca aaa aac atg ata gct gcc acg aac gat aca tcc gac ttt			816
Lys Ala Ala Lys Asn Met Ile Ala Ala Thr Asn Asp Thr Ser Asp Phe			
260	265	270	
gta aca tat tct tca caa tta aag cgc ctt tct gca aag ctt tca aag			864
Val Thr Tyr Ser Ser Gln Leu Lys Arg Leu Ser Ala Lys Leu Ser Lys			
275	280	285	
ata tgc agc gat tta cgc ctt ctt tct tcg ggc ccc aga aca gga ctt			912
Ile Cys Ser Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Thr Gly Leu			
290	295	300	
tac gat ata agt ctt cct ccg atg cag ccc ggt tct tct atc atg ccc			960
Tyr Asp Ile Ser Leu Pro Pro Met Gln Pro Gly Ser Ser Ile Met Pro			
305	310	315	320
gga aag gta aac ccg gtt att cct gag gtt gtc aat cag gtt tgc tac			1008
Gly Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Val Cys Tyr			
325	330	335	
agg gtt atc gga aat gat act gcc gtt atc ttg gct gca gaa tca ggc			1056
Arg Val Ile Gly Asn Asp Thr Ala Val Ile Leu Ala Ala Glu Ser Gly			
340	345	350	
cag ctt gaa ctc aac gtt ttt gaa ccc gtt ata att tat tct atc ttt			1104
Gln Leu Glu Leu Asn Val Phe Glu Pro Val Ile Ile Tyr Ser Ile Phe			
355	360	365	
gag tcg att aag ctt ctt ata aat gca atg aag act ttg agg gaa cga			1152
Glu Ser Ile Lys Leu Leu Ile Asn Ala Met Lys Thr Leu Arg Glu Arg			
370	375	380	
tgc gtt acg ggc att gta gga aac tat gag cat tgt aag gaa agc gtt			1200
Cys Val Thr Gly Ile Val Gly Asn Tyr Glu His Cys Lys Glu Ser Val			
385	390	395	400
cac cga agt atc ggc ttg gtt acg gcc tta aat ccc gtc atc ggt tat			1248
His Arg Ser Ile Gly Leu Val Thr Ala Leu Asn Pro Val Ile Gly Tyr			
405	410	415	
gag gct tct tcc gat att gca aag act gcc ttg cgc gat aac cgc agc			1296
Glu Ala Ser Ser Asp Ile Ala Lys Thr Ala Leu Arg Asp Asn Arg Ser			

PF59083SeqList PF59083.txt

<div> <div>420</div> <div>425</div> <div>430</div> </div>																
gtt	tat	gac	ctt	gtt	ttg	gaa	aga	ggg	ctt	ctt	tca	aaa	gaa	aaa	ttg	1344
Val	Tyr	Asp	Leu	Val	Leu	Glu	Arg	Gly	Leu	Leu	Ser	Lys	Glu	Lys	Leu	
<div> <div>435</div> <div>440</div> <div>445</div> </div>																
gat	gag	gtt	tta	aaa	ccc	gaa	aac	atg	aca	aag	ccc	aga	aag	ctt	1389	
Asp	Glu	Val	Leu	Lys	Pro	Glu	Asn	Met	Thr	Lys	Pro	Arg	Lys	Leu		
<div> <div>450</div> <div>455</div> <div>460</div> </div>																
tag															1392	

<210> 9628
<211> 463
<212> PRT
<213> Treponema denticola ATCC 35405

<400>	9628																		
Met	Arg	Arg	Glu	His	Asp	Leu	Leu	Gly	Glu	Leu	Asp	Ile	Pro	Glu	Asp				
1				5					10					15					
Ala	Tyr	Tyr	Gly	Ile	Gln	Thr	Phe	Arg	Ser	Val	Glu	Asn	Phe	Gln	Ile				
			20					25					30						
Thr	Gly	Leu	Arg	Leu	Cys	Asp	Phe	Pro	Asp	Phe	Ile	Lys	Gly	Leu	Ala				
		35					40					45							
Tyr	Thr	Lys	Gln	Ala	Ala	Ala	Glu	Ala	Asn	His	Glu	Leu	Gly	Tyr	Leu				
	50					55					60								
Ser	Asp	Glu	Val	Tyr	Lys	Ala	Met	Ile	Gln	Ala	Cys	Lys	Glu	Val	Ala				
65					70					75					80				
Glu	Gly	Lys	Phe	Asp	Lys	Glu	Phe	Val	Val	Asp	Met	Ile	Gln	Gly	Gly				
				85					90					95					
Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg				
			100					105					110						
Ala	Asn	Glu	Ile	Leu	Gly	Lys	Ala	Lys	Gly	Thr	Tyr	Ser	Pro	Cys	His				
	115						120					125							
Pro	Asn	Asn	His	Val	Asn	Phe	Ala	Gln	Ser	Thr	Asn	Asp	Ala	Tyr	Pro				
	130					135					140								
Thr	Ala	Ala	Lys	Leu	Gly	Ile	Ser	Leu	Asn	Thr	Pro	Ala	Leu	Ile	Asp				
145					150					155				160					
Glu	Leu	Lys	Ser	Leu	Val	Ala	Ser	Phe	Arg	Lys	Lys	Ala	Gln	Glu	Leu				
				165					170				175						
Gly	Glu	Asn	Ile	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro				
			180					185					190						
Met	Thr	Leu	Gly	Gln	Glu	Phe	Glu	Ser	Tyr	Ala	Ala	Ser	Leu	Glu	Asn				
	195						200					205							
Glu	Ile	Pro	Gln	Ile	Gln	Phe	Ala	Arg	Glu	Asn	Leu	His	Thr	Ile	Asn				
	210					215					220								
Met	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Ser	Asp	Pro	Asn	Tyr				
225				230						235				240					
Thr	Pro	Lys	Val	Thr	Ser	His	Leu	Ala	Lys	Ile	Ser	Gly	Leu	Asp	Leu				
				245					250				255						
Lys	Ala	Ala	Lys	Asn	Met	Ile	Ala	Ala	Thr	Asn	Asp	Thr	Ser	Asp	Phe				
			260					265				270							
Val	Thr	Tyr	Ser	Ser	Gln	Leu	Lys	Arg	Leu	Ser	Ala	Lys	Leu	Ser	Lys				
		275					280					285							
Ile	Cys	Ser	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Thr	Gly					

PF59083SeqList PF59083.txt

Glu Ala Ser Ser Asp Ile Ala Lys Thr Ala Leu Arg Asp Asn Arg Ser
 Val Tyr Asp Leu Val Leu Glu Arg Gly Leu Leu Ser Lys Glu Lys Leu
 Asp Glu Val Leu Lys Pro Glu Asn Met Thr Lys Pro Arg Lys Leu
 420 425 430 435 440 445 450 455 460

<210> 9629
 <211> 1434
 <212> DNA
 <213> Bacillus cereus ATCC 10987

<220>
 <221> CDS
 <222> (1)..(1434)
 <223> transl_table=11

<400> 9629
 atg ata gca acg aag gat ata cgt ata gaa aaa gat ttt tta ggt gaa 48
 Met Ile Ala Thr Lys Asp Ile Arg Ile Glu Lys Asp Phe Leu Gly Glu
 1 5 10 15
 aag gaa gta cca agt aga gct tat tat ggt gta caa aca tta cgt gcg 96
 Lys Glu Val Pro Ser Arg Ala Tyr Tyr Gly Val Gln Thr Leu Arg Ala
 20 25 30
 gta gaa aat ttc ccg att aca ggg tat tat cgc att cat cca tca ctc att 144
 Val Glu Asn Phe Pro Ile Thr Gly Tyr Arg Ile His Pro Ser Leu Ile
 35 40 45
 acg gca atg gca att gtg aaa aaa gcg gcg gca ctt gca aat atg gat 192
 Thr Ala Met Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met Asp
 50 55 60
 act ggt tac tta gcg aaa gac att gga cac gaa att gca gag gca gca 240
 Thr Gly Tyr Leu Ala Lys Asp Ile Gly His Glu Ile Ala Glu Ala Ala
 65 70 75 80
 caa gaa att gtt gat ggg aaa ttt cat gat caa ttt att gta gat cca 288
 Gln Glu Ile Val Asp Gly Lys Phe His Asp Gln Phe Ile Val Asp Pro
 85 90 95
 att cag ggc ggt gct gga act tct att aat atg aat aca aat gaa gta 336
 Ile Gln Gly Gly Ala Gly Thr Ser Ile Asn Met Asn Thr Asn Glu Val
 100 105 110
 atc gct aat cga gcg tta gaa cgt atg gga tat gaa aaa ggc gag tat 384
 Ile Ala Asn Arg Ala Leu Glu Arg Met Gly Tyr Glu Lys Gly Glu Tyr
 115 120 125
 gca aaa att agc cca aat acg cat gta aac atg gct cag tca acg aat 432
 Ala Lys Ile Ser Pro Asn Thr His Val Asn Met Ala Gln Ser Thr Asn
 130 135 140
 gat gcg ttt cca aca gga att cat att gca act ctt atg atg tta gaa 480
 Asp Ala Phe Pro Thr Gly Ile His Ile Ala Thr Leu Met Met Leu Glu
 145 150 155 160
 gaa ctt ctt att aca atg gaa gaa ctt cat gct gct ttc ctt gca aaa 528
 Glu Leu Leu Ile Thr Met Glu Glu Leu His Ala Ala Phe Leu Ala Lys
 165 170 175
 gca aaa gag ttc gat cac gtc att aaa atg gga cgt acg cat tta caa 576
 Ala Lys Glu Phe Asp His Val Ile Lys Met Gly Arg Thr His Leu Gln
 180 185 190
 gat gct gtt ccg att cgt ctt gga caa gaa ttt gaa gcg tat agc aga 624
 Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser Arg
 195 200 205
 gtg ctt gcg cgt gat ata aaa aga att aaa caa tct cgc caa cat tta 672
 Val Leu Ala Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His Leu
 210 215 220
 tat gaa gtg aat atg ggg gcg aca gct gtt ggt acg gga tta aat gca 720
 Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn Ala
 225 230 235 240
 aac cct acc tac att gaa caa gtg gtt aaa cac tta cga aca ttt agc 768
 Asn Pro Thr Tyr Ile Glu Gln Val Val Lys His Leu Arg Thr Phe Ser
 245 250 255
 gga ttc cca ctt gtt ggt gca gag cat tta gtt gat gca aca caa aat 816
 Gly Phe Pro Leu Val Gly Ala Glu His Leu Val Asp Ala Thr Gln Asn
 260 265 270

PF59083SeqList PF59083.txt

aca	gat	gca	tac	aca	gaa	gta	tct	gca	gca	tta	aaa	gta	tgt	atg	atg	864
Thr	Asp	Ala	Tyr	Thr	Glu	Val	Ser	Ala	Ala	Leu	Lys	Val	Cys	Met	Met	
		275					280					285				
aat	atg	tct	aaa	att	gcg	aac	gac	ctt	cgt	att	atg	gca	tct	ggt	cca	912
Asn	Met	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Ile	Met	Ala	Ser	Gly	Pro	
		290					295					300				
cgt	gtt	gga	ttg	gcg	gaa	att	caa	tta	cca	gct	cgt	caa	cca	ggt	tca	960
Arg	Val	Gly	Leu	Ala	Glu	Ile	Gln	Leu	Pro	Ala	Arg	Gln	Pro	Gly	Ser	
		305			310					315					320	
tct	att	atg	cca	ggt	aaa	gta	aat	cct	gtt	atg	gca	gaa	gta	att	aat	1008
Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Val	Ile	Asn	
				325					330					335		
caa	gtc	gct	ttc	caa	gta	att	ggt	aat	gat	cac	aca	att	tgc	tta	gcg	1056
Gln	Val	Ala	Phe	Gln	Val	Ile	Gly	Asn	Asp	His	Thr	Ile	Cys	Leu	Ala	
			340					345					350			
tca	gaa	gca	gga	caa	ctg	gag	ctc	aac	gta	atg	gag	cct	gtg	ctt	gta	1104
Ser	Glu	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Leu	Val	
		355				360						365				
ttt	aat	tta	att	caa	tct	atc	agt	att	atg	aat	aac	gga	ttc	cgt	gta	1152
Phe	Asn	Leu	Ile	Gln	Ser	Ile	Ser	Ile	Met	Asn	Asn	Gly	Phe	Arg	Val	
		370				375						380				
ttc	cgt	gaa	tat	tgt	att	aaa	gga	att	aca	gca	aat	gaa	gaa	ctg	ctg	1200
Phe	Arg	Glu	Tyr	Cys	Ile	Lys	Gly	Ile	Thr	Ala	Asn	Glu	Glu	Leu	Leu	
		385			390				395					400		
aag	caa	tat	gtt	gag	aaa	agt	gtt	gga	att	att	aca	gca	gtt	aac	cct	1248
Lys	Gln	Tyr	Val	Glu	Lys	Ser	Val	Gly	Ile	Ile	Thr	Ala	Val	Asn	Pro	
				405				410						415		
cat	att	ggt	tat	gaa	gta	gca	tca	cgt	att	gca	cgt	gaa	gca	att	gaa	1296
His	Ile	Gly	Tyr	Glu	Val	Ala	Ser	Arg	Ile	Ala	Arg	Glu	Ala	Ile	Glu	
			420					425					430			
aca	gga	aaa	tct	gtt	cgg	gag	tta	tgt	tta	gaa	cat	ggt	gta	ctg	aca	1344
Thr	Gly	Lys	Ser	Val	Arg	Glu	Leu	Cys	Leu	Glu	His	Gly	Val	Leu	Thr	
		435				440						445				
gaa	gaa	gaa	tta	gat	att	att	tta	gat	cca	ttc	gaa	atg	acg	cat	cct	1392
Glu	Glu	Glu	Leu	Asp	Ile	Ile	Leu	Asp	Pro	Phe	Glu	Met	Thr	His	Pro	
		450				455					460					
gaa	att	gct	ggt	gct	tct	tta	cta	aag	aat	aag	aag	atg	taa			1434
Glu	Ile	Ala	Gly	Ala	Ser	Leu	Leu	Lys	Asn	Lys	Lys	Met				
		465			470					475						

<210> 9630

<211> 477

<212> PRT

<213> Bacillus cereus ATCC 10987

<400> 9630

Met	Ile	Ala	Thr	Lys	Asp	Ile	Arg	Ile	Glu	Lys	Asp	Phe	Leu	Gly	Glu	
1				5					10					15		
Lys	Glu	Val	Pro	Ser	Arg	Ala	Tyr	Tyr	Gly	Val	Gln	Thr	Leu	Arg	Ala	
			20					25					30			
Val	Glu	Asn	Phe	Pro	Ile	Thr	Gly	Tyr	Arg	Ile	His	Pro	Ser	Leu	Ile	
		35					40					45				
Thr	Ala	Met	Ala	Ile	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Met	Asp	
		50				55					60					
Thr	Gly	Tyr	Leu	Ala	Lys	Asp	Ile	Gly	His	Glu	Ile	Ala	Glu	Ala	Ala	
65				70				75						80		
Gln	Glu	Ile	Val	Asp	Gly	Lys	Phe	His	Asp	Gln	Phe	Ile	Val	Asp	Pro	
				85				90						95		
Ile	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Ile	Asn	Met	Asn	Thr	Asn	Glu	Val	
		100					105					110				
Ile	Ala	Asn	Arg	Ala	Leu	Glu	Arg	Met	Gly	Tyr	Glu	Lys	Gly	Glu	Tyr	
		115				120						125				
Ala	Lys	Ile	Ser	Pro	Asn	Thr	His	Val	Asn	Met	Ala	Gln	Ser	Thr	Asn	
		130				135					140					
Asp	Ala	Phe	Pro	Thr	Gly	Ile	His	Ile	Ala	Thr	Leu	Met	Met	Leu	Glu	
145				150				155						160		
Glu	Leu	Leu	Ile	Thr	Met	Glu	Glu	Leu	His	Ala	Ala	Phe	Leu	Ala	Lys	
			165					170						175		
Ala	Lys	Glu	Phe	Asp	His	Val	Ile	Lys	Met	Gly	Arg	Thr	His	Leu	Gln	

PF59083SeqList PF59083.txt

180 185 190
 Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser Arg
 195 200 205
 Val Leu Ala Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His Leu
 210 215 220
 Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn Ala
 225 230 235
 Asn Pro Thr Tyr Ile Glu Gln Val Val Lys His Leu Arg Thr Phe Ser
 240 245 250 255
 Gly Phe Pro Leu Val Gly Ala Glu His Leu Val Asp Ala Thr Gln Asn
 260 265 270
 Thr Asp Ala Tyr Thr Glu Val Ser Ala Ala Leu Lys Val Cys Met Met
 275 280 285
 Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Ile Met Ala Ser Gly Pro
 290 295 300
 Arg Val Gly Leu Ala Glu Ile Gln Leu Pro Ala Gln Pro Gly Ser
 305 310 315 320
 Ser Ile Met Pro Gly Lys Val Asn Pro Val Met Ala Glu Val Ile Asn
 325 330 335
 Gln Val Ala Phe Gln Val Ile Gly Asn Asp His Thr Ile Cys Leu Ala
 340 345 350
 Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu Val
 355 360 365
 Phe Asn Leu Ile Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg Val
 370 375 380
 Phe Arg Glu Tyr Cys Ile Lys Gly Ile Thr Ala Asn Glu Glu Leu Leu
 385 390 395 400
 Lys Gln Tyr Val Glu Lys Ser Val Gly Ile Ile Thr Ala Val Asn Pro
 405 410 415
 His Ile Gly Tyr Glu Val Ala Ser Arg Ile Ala Arg Glu Ala Ile Glu
 420 425 430
 Thr Gly Lys Ser Val Arg Glu Leu Cys Leu Glu His Gly Val Leu Thr
 435 440 445
 Glu Glu Glu Leu Asp Ile Ile Leu Asp Pro Phe Glu Met Thr His Pro
 450 455 460
 Glu Ile Ala Gly Ala Ser Leu Leu Lys Asn Lys Lys Met
 465 470 475

<210> 9631

<211> 1422

<212> DNA

<213> Nasonia vitripennis

<220>

<221> CDS

<222> (1)..(1422)

<400> 9631

atg gca ttc aac gca ctg aga cag cgg gtg acg agc gtc ggg ctt cgc	48
Met Ala Phe Asn Ala Leu Arg Gln Arg Val Thr Ser Val Gly Leu Arg	
1 5 10 15	
cgt cag ccg agg gaa atc agc gcc ttc ctc ggg ccg cgg ctc gtc atg	96
Arg Gln Pro Arg Glu Ile Ser Ala Phe Leu Gly Pro Arg Leu Val Met	
20 25 30	
tgc gag ccc aag tgc cga gcg gcc tcc aag gcc agc ggc gag tac agg	144
Cys Glu Pro Lys Cys Arg Ala Ala Ser Lys Ala Ser Gly Glu Tyr Arg	
35 40 45	
ctc gag agg gac acc ttc ggg gag ctg aag gtg ccg gct gat aag tat	192
Leu Glu Arg Asp Thr Phe Gly Glu Leu Lys Val Pro Ala Asp Lys Tyr	
50 55 60	
tat gga gcc cag acg atg cga tcg gta atg aac ttc ccg atc ggc gac	240
Tyr Gly Ala Gln Thr Met Arg Ser Val Met Asn Phe Pro Ile Gly Asp	
65 70 75 80	
cag gcc gag cgc atg ccg aaa ggc gtc atc gtg gct atg ggt atc ctg	288
Gln Ala Glu Arg Met Pro Lys Gly Val Ile Val Ala Met Gly Ile Leu	
85 90 95	
aag aaa gcc gcc gcc gag gtg aac aag gaa ttc ggc ctc gac gcg aaa	336
Lys Lys Ala Ala Ala Glu Val Asn Lys Glu Phe Gly Leu Asp Ala Lys	
100 105 110	

PF59083SeqList PF59083.txt																
gtc	gcg	gat	gcc	atc	agc	aaa	gtg	atc	tcg	aac	cga	gcg	atc	gag	ctg	384
Val	Ala	Asp	Ala	Ile	Ser	Lys	Val	Ile	Ser	Asn	Arg	Ala	Ile	Glu	Leu	
		115					120					125				
ctt	ggt	ggt	cag	ctg	ggc	tcc	aag	aac	ccg	gtc	cat	ccc	aac	gac	cac	432
Leu	Gly	Gly	Gln	Leu	Gly	Ser	Lys	Asn	Pro	Val	His	Pro	Asn	Asp	His	
	130					135					140					
gtg	aac	aag	tcc	cag	agc	tcg	aac	gac	acc	ttc	cct	acg	gcg	atg	cac	480
Val	Asn	Lys	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Met	His	
145					150					155					160	
atc	gcc	gta	gcc	ctg	gaa	atc	aac	aag	atc	ctc	atc	ccc	ggc	ctc	cag	528
Ile	Ala	Val	Ala	Leu	Glu	Ile	Asn	Lys	Ile	Leu	Ile	Pro	Gly	Leu	Gln	
				165					170					175		
cag	ctg	cac	tcg	gca	ctt	aag	gaa	aaa	tct	cag	gca	tgg	aag	gac	atc	576
Gln	Leu	His	Ser	Ala	Leu	Lys	Glu	Lys	Ser	Gln	Ala	Trp	Lys	Asp	Ile	
			180					185					190			
atc	aag	atc	ggc	agg	acg	cac	acg	cag	gac	gcc	gtg	ccg	ctg	act	ctc	624
Ile	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Val	Pro	Leu	Thr	Leu	
		195					200					205				
ggc	cag	gaa	ttt	tcc	gct	tac	gcg	aca	cag	gtg	gag	aac	gga	atc	gcc	672
Gly	Gln	Glu	Phe	Ser	Ala	Tyr	Ala	Thr	Gln	Val	Glu	Asn	Gly	Ile	Ala	
	210					215					220					
cga	gtg	aag	gac	acg	ctg	ccg	agg	ctc	tac	cag	ctg	gcc	ctt	gga	ggt	720
Arg	Val	Lys	Asp	Thr	Leu	Pro	Arg	Leu	Tyr	Gln	Leu	Ala	Leu	Gly	Gly	
225					230					235					240	
acc	gcc	gta	ggt	act	ggt	ttg	aac	acg	agg	ata	ggc	ttc	gct	gag	aaa	768
Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Arg	Ile	Gly	Phe	Ala	Glu	Lys	
				245					250					255		
gcc	gct	gcg	aga	atc	gct	tcc	ctc	aca	ggt	ctg	ccc	ttc	ggt	acg	gct	816
Ala	Ala	Ala	Arg	Ile	Ala	Ser	Leu	Thr	Gly	Leu	Pro	Phe	Val	Thr	Ala	
			260					265					270			
ccc	aac	aag	ttc	gaa	gcg	ctg	gct	gct	cac	gat	gcg	ctc	ggt	gag	gtc	864
Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Leu	Val	Glu	Val	
		275				280					285					
cac	ggt	gcg	ctc	aac	act	gtc	gct	gtc	tct	ctg	atg	aag	atc	gcc	aac	912
His	Gly	Ala	Leu	Asn	Thr	Val	Ala	Val	Ser	Leu	Met	Lys	Ile	Ala	Asn	
	290					295					300					
gac	atc	cga	ttc	ctg	ggc	agc	gga	ccc	cgc	tgt	ggt	ctt	ggc	gag	ctc	960
Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	
305					310					315					320	
ttc	ctg	ccc	gaa	aac	gag	cct	ggt	agc	tcc	atc	atg	cct	gga	aag	gtg	1008
Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	
				325					330					335		
aac	cca	act	cag	tgc	gag	gcc	ctg	acg	atg	gtg	tgt	gcc	cag	gtg	atg	1056
Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	Gln	Val	Met	
			340					345					350			
ggt	aac	cac	gtc	gcg	acg	acg	atc	ggc	ggc	agc	aac	ggc	cac	ttc	gag	1104
Gly	Asn	His	Val	Ala	Thr	Thr	Ile	Gly	Gly	Ser	Asn	Gly	His	Phe	Glu	
		355					360					365				
ctc	aac	gtc	ttc	aag	ccc	gtc	atc	gtc	gcc	aac	gtc	ctc	agg	tcg	gcc	1152
Leu	Asn	Val	Phe	Lys	Pro	Val	Ile	Val	Ala	Asn	Val	Leu	Arg	Ser	Ala	
		370				375						380				
aga	ctt	ctt	ggt	gac	gcc	tct	gct	acg	ttc	acc	aag	aac	tgc	gtc	gtc	1200
Arg	Leu	Leu	Gly	Asp	Ala	Ser	Ala	Thr	Phe	Thr	Lys	Asn	Cys	Val	Val	
385					390					395					400	
gga	att	cag	ccc	aac	atc	gac	gcc	atc	aac	aag	atc	atg	aac	gag	agt	1248
Gly	Ile	Gln	Pro	Asn	Ile	Asp	Ala	Ile	Asn	Lys	Ile	Met	Asn	Glu	Ser	
				405					410					415		
ctt	atg	cta	gtc	acg	gcc	ctt	aat	cct	cat	atc	ggt	tac	gat	aag	gct	1296
Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	Asp	Lys	Ala	
			420					425					430			
gct	gcg	ata	gcg	aag	caa	gca	cac	aaa	gag	aag	ctg	acg	ctg	aag	gaa	1344
Ala	Ala	Ile	Ala	Lys	Gln	Ala	His	Lys	Glu	Lys	Leu	Thr	Leu	Lys	Glu	
		435				440						445				
tcg	gca	ttg	aag	aac	ggc	ctc	acc	gag	gaa	caa	ttc	aac	cag	tgg	gtc	1392
Ser	Ala	Leu	Lys	Asn	Gly	Leu	Thr	Glu	Glu	Gln	Phe	Asn	Gln	Trp	Val	
		450				455					460					
aaa	ccc	gag	gag	atg	ctt	gga	cct	aag	taa							1422
Lys	Pro	Glu	Glu	Met	Leu	Gly	Pro	Lys								
465					470											

PF59083SeqList PF59083.txt

<210> 9632
 <211> 473
 <212> PRT
 <213> Nasonia vitripennis

<400> 9632
 Met Ala Phe Asn Ala Leu Arg Gln Arg Val Thr Ser Val Gly Leu Arg
 1 5 10 15
 Arg Gln Pro Arg Glu Ile Ser Ala Phe Leu Gly Pro Arg Leu Val Met
 20 25 30
 Cys Glu Pro Lys Cys Arg Ala Ala Ser Lys Ala Ser Gly Glu Tyr Arg
 35 40 45
 Leu Glu Arg Asp Thr Phe Gly Glu Leu Lys Val Pro Ala Asp Lys Tyr
 50 55 60
 Tyr Gly Ala Gln Thr Met Arg Ser Val Met Asn Phe Pro Ile Gly Asp
 65 70 75 80
 Gln Ala Glu Arg Met Pro Lys Gly Val Ile Val Ala Met Gly Ile Leu
 85 90 95
 Lys Lys Ala Ala Glu Val Asn Lys Glu Phe Gly Leu Asp Ala Lys
 100 105 110
 Val Ala Asp Ala Ile Ser Lys Val Ile Ser Asn Arg Ala Ile Glu Leu
 115 120 125
 Leu Gly Gly Gln Leu Gly Ser Lys Asn Pro Val His Pro Asn Asp His
 130 135 140
 Val Asn Lys Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr Ala Met His
 145 150 155 160
 Ile Ala Val Ala Leu Glu Ile Asn Lys Ile Leu Ile Pro Gly Leu Gln
 165 170 175
 Gln Leu His Ser Ala Leu Lys Glu Lys Ser Gln Ala Trp Lys Asp Ile
 180 185 190
 Ile Lys Ile Gly Arg Thr His Thr Gln Asp Ala Val Pro Leu Thr Leu
 195 200 205
 Gly Gln Glu Phe Ser Ala Tyr Ala Thr Gln Val Glu Asn Gly Ile Ala
 210 215 220
 Arg Val Lys Asp Thr Leu Pro Arg Leu Tyr Gln Leu Ala Leu Gly Gly
 225 230 235 240
 Thr Ala Val Gly Thr Gly Leu Asn Thr Arg Ile Gly Phe Ala Glu Lys
 245 250 255
 Ala Ala Ala Arg Ile Ala Ser Leu Thr Gly Leu Pro Phe Val Thr Ala
 260 265 270
 Pro Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Leu Val Glu Val
 275 280 285
 His Gly Ala Leu Asn Thr Val Ala Val Ser Leu Met Lys Ile Ala Asn
 290 295 300
 Asp Ile Arg Phe Leu Gly Ser Gly Pro Arg Cys Gly Leu Gly Glu Leu
 305 310 315 320
 Ser Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys Val
 325 330 335
 Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys Ala Gln Val Met
 340 345 350
 Gly Asn His Val Ala Thr Thr Ile Gly Gly Ser Asn Gly His Phe Glu
 355 360 365
 Leu Asn Val Phe Lys Pro Val Ile Val Ala Asn Val Leu Arg Ser Ala
 370 375 380
 Arg Leu Leu Gly Asp Ala Ser Ala Thr Phe Thr Lys Asn Cys Val Val
 385 390 395 400
 Gly Ile Gln Pro Asn Ile Asp Ala Ile Asn Lys Ile Met Asn Glu Ser
 405 410 415
 Leu Met Leu Val Thr Ala Leu Asn Pro His Ile Gly Tyr Asp Lys Ala
 420 425 430
 Ala Ala Ile Ala Lys Gln Ala His Lys Glu Lys Leu Thr Leu Lys Glu
 435 440 445
 Ser Ala Leu Lys Asn Gly Leu Thr Glu Glu Gln Phe Asn Gln Trp Val
 450 455 460
 Lys Pro Glu Glu Met Leu Gly Pro Lys
 465 470

<210> 9633

PF59083SeqList PF59083.txt

<211> 1638

<212> DNA

<213> Magnaporthe grisea 70-15

<220>

<221> CDS

<222> (1)..(1638)

<400> 9633

atg	cga	cag	gtg	cag	gcn	gct	gcg	gcc	agg	tct	ttt	cag	aca	tgt	ggg	48
Met	Arg	Gln	Val	Gln	Ala	Ala	Ala	Ala	Arg	Ser	Phe	Gln	Thr	Cys	Gly	
1				5					10					15		
ccg	agg	tta	ggt	gct	tca	att	aac	ccc	tcc	gca	gct	gta	acg	agg	agg	96
Pro	Arg	Leu	Gly	Ala	Ser	Ile	Asn	Pro	Ser	Ala	Ala	Val	Thr	Arg	Arg	
			20					25						30		
gca	ttg	agc	agc	tcc	agt	aga	tgg	act	agc	tcc	cct	cgt	tgt	acc	atc	144
Ala	Leu	Ser	Ser	Ser	Ser	Arg	Trp	Thr	Ser	Ser	Pro	Arg	Cys	Thr	Ile	
			35				40					45				
atc	gca	tct	tca	cct	ttc	tcc	aac	act	cag	acg	cat	atc	tcc	cgc	agc	192
Ile	Ala	Ser	Ser	Pro	Phe	Ser	Asn	Thr	Gln	Thr	His	Ile	Ser	Arg	Ser	
			50			55					60					
tcc	agg	ctg	ttc	cac	tcc	aca	cca	gtt	acc	atg	tcc	gcg	aac	act	agg	240
Ser	Arg	Leu	Phe	His	Ser	Thr	Pro	Val	Thr	Met	Ser	Ala	Asn	Thr	Arg	
					70				75					80		
gct	gag	acc	gat	gcc	ttt	ggc	gag	gtt	cag	gtg	cct	gcc	gac	aag	tac	288
Ala	Glu	Thr	Asp	Ala	Phe	Gly	Glu	Val	Gln	Val	Pro	Ala	Asp	Lys	Tyr	
				85					90					95		
tgg	ggc	gcc	cag	aca	cag	cgc	tcg	ctc	ggc	aac	ttc	gac	atc	aac	cag	336
Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Gly	Asn	Phe	Asp	Ile	Asn	Gln	
			100					105					110			
cct	cag	gat	cgc	atg	ccc	ccg	cca	att	gtc	aag	gct	ctg	ggg	atc	ctc	384
Pro	Gln	Asp	Arg	Met	Pro	Pro	Pro	Ile	Val	Lys	Ala	Leu	Gly	Ile	Leu	
			115			120						125				
aag	ggc	gcc	gcc	gcc	acg	gtg	aac	atg	aac	tat	ggc	ctt	gac	ccc	acc	432
Lys	Gly	Ala	Ala	Ala	Thr	Val	Asn	Met	Asn	Tyr	Gly	Leu	Asp	Pro	Thr	
			130			135					140					
atc	ggc	aag	gcc	att	cag	cag	gcg	gcc	aag	gag	gtc	gct	gac	ctg	aag	480
Ile	Gly	Lys	Ala	Ile	Gln	Gln	Ala	Ala	Lys	Glu	Val	Ala	Asp	Leu	Lys	
					150					155				160		
ctg	ctc	gac	cac	ttc	ttg	gtc	gtc	tgg	cag	acc	ggc	tct	ggc	act	thr	528
Leu	Leu	Asp	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr	
				165				170						175		
cag	tcc	aac	atg	aac	gcg	aac	gag	gtc	atc	tcc	aac	cga	gcc	atc	gag	576
Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ser	Asn	Arg	Ala	Ile	Glu	
			180					185					190			
atc	ctg	ggc	ggc	gag	aag	ggc	agc	aag	aaa	ccc	gtc	cac	ccc	aac	gac	624
Ile	Leu	Gly	Gly	Glu	Lys	Gly	Ser	Lys	Lys	Pro	Val	His	Pro	Asn	Asp	
			195			200						205				
cac	gtc	aac	cgc	agc	gcc	tcc	tct	aac	gac	acc	ttc	ccc	acc	gtc	atg	672
His	Val	Asn	Arg	Ser	Ala	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val	Met	
			210			215					220					
cac	atc	gcc	gcc	gtc	ctc	gag	atc	gag	ggg	gag	ctg	att	cct	tcc	ctg	720
His	Ile	Ala	Ala	Val	Leu	Glu	Ile	Glu	Gly	Glu	Leu	Ile	Pro	Ser	Leu	
					230					235					240	
cg	agc	ctg	cga	gac	gcc	ctg	cag	gcc	aag	gtg	gac	gag	ttc	gag	gcc	768
Arg	Ser	Leu	Arg	Asp	Ala	Leu	Gln	Ala	Lys	Val	Asp	Glu	Phe	Glu	Ala	
				245					250					255		
aag	aag	att	atc	aag	att	ggc	cgc	aca	cat	ctc	cag	gac	gcc	acg	cct	816
Lys	Lys	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	
			260					265					270			
ctg	act	ctg	gct	cag	gag	ttc	tct	ggc	tac	gtc	gcc	cag	ctt	gac	ttt	864
Leu	Thr	Leu	Ala	Gln	Glu	Phe	Ser	Gly	Tyr	Val	Ala	Gln	Leu	Asp	Phe	
			275			280						285				
ggc	atc	aag	cgc	gtc	gag	gct	acc	ctg	ccg	gac	ctg	agg	ctg	ctc	gct	912
Gly	Ile	Lys	Arg	Val	Glu	Ala	Thr	Leu	Pro	Asp	Leu	Arg	Leu	Leu	Ala	
						295					300					
cag	ggc	ggt	acc	gct	gtc	ggc	acc	ggc	att	aac	acc	ttt	gag	ggc	ttt	960
Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Thr	Phe	Glu	Gly	Phe	
					310					315					320	

PF59083SeqList PF59083.txt

gct	gag	ggc	atc	gcc	gag	gag	gtc	agc	cgc	atg	act	ggc	acc	gag	ttc	1008
Ala	Glu	Gly	Ile	Ala	Glu	Glu	Val	Ser	Arg	Met	Thr	Gly	Thr	Glu	Phe	
				325					330					335		
aag	acg	gcc	ccc	aac	aag	ttc	gag	gcc	ctt	gct	gcg	cat	gac	gcg	ctt	1056
Lys	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Leu	
			340					345					350			
gtg	cat	gcc	tcg	ggc	gct	ctc	aac	act	ctc	gcc	acc	tcg	ctg	acc	aag	1104
Val	His	Ala	Ser	Gly	Ala	Leu	Asn	Thr	Leu	Ala	Thr	Ser	Leu	Thr	Lys	
		355				360						365				
gtt	gct	cag	gac	atc	cgc	tac	ctg	ggc	agc	ggc	ccg	cgc	tgc	ggc	ctg	1152
Val	Ala	Gln	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	
	370					375					380					
ggc	gag	ctc	ggt	ctg	cct	gag	aac	gag	ccg	ggc	agc	agc	atc	atg	cct	1200
Gly	Glu	Leu	Val	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
	385				390					395					400	
gga	aag	gtc	aat	ccg	acc	cag	tgc	gag	gcc	ctg	acc	atg	ggt	tgc	gcg	1248
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	
			405					410						415		
cag	gtc	atg	ggc	aac	cat	gtt	gct	gct	acc	att	ggt	ggc	atg	aac	ggc	1296
Gln	Val	Met	Gly	Asn	His	Val	Ala	Ala	Thr	Ile	Gly	Gly	Met	Asn	Gly	
			420				425						430			
cag	ttt	gag	ctt	aac	gtc	tac	aag	ccc	ctc	atc	atc	cgc	aac	gtc	ctg	1344
Gln	Phe	Glu	Leu	Asn	Val	Tyr	Lys	Pro	Leu	Ile	Ile	Arg	Asn	Val	Leu	
		435				440						445				
cac	agc	gtc	agg	ctg	ctg	tca	gat	ggc	atg	cgg	tcg	ttt	gag	aag	cac	1392
His	Ser	Val	Arg	Leu	Leu	Ser	Asp	Gly	Met	Arg	Ser	Phe	Glu	Lys	His	
	450					455					460					
ctc	gtc	gag	ggc	ctc	aag	gcc	aac	gag	gag	aag	att	gcc	agc	att	atg	1440
Leu	Val	Glu	Gly	Leu	Lys	Ala	Asn	Glu	Glu	Lys	Ile	Ala	Ser	Ile	Met	
	465				470					475					480	
aag	gag	tct	ctc	atg	ctt	gtc	acc	tgc	ctt	aac	ccc	aag	att	ggc	tat	1488
Lys	Glu	Ser	Leu	Met	Leu	Val	Thr	Cys	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	
			485					490						495		
gac	atg	gct	agc	aag	gtc	gca	aag	aac	gcc	cac	aag	aag	ggt	ctg	acc	1536
Asp	Met	Ala	Ser	Lys	Val	Ala	Lys	Asn	Ala	His	Lys	Lys	Gly	Leu	Thr	
			500					505					510			
cta	aag	gaa	agc	gcc	ctc	gag	ctc	aat	gct	ctg	act	gag	gaa	gag	ttt	1584
Leu	Lys	Glu	Ser	Ala	Leu	Glu	Leu	Asn	Ala	Leu	Thr	Glu	Glu	Glu	Phe	
		515				520						525				
gac	acc	ttg	gtc	aag	ccc	gag	ctc	atg	atc	act	ccc	aag	ccc	tac	aag	1632
Asp	Thr	Leu	Val	Lys	Pro	Glu	Leu	Met	Ile	Thr	Pro	Lys	Pro	Tyr	Lys	
	530					535					540					
gcc	tag															1638
Ala																
545																

<210> 9634

<211> 545

<212> PRT

<213> Magnaporthe grisea 70-15

<400> 9634

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

PF59083SeqList PF59083.txt

130 135 140
 Ile Gly Lys Ala Ile Gln Gln Ala Ala Lys Glu Val Ala Asp Leu Lys
 145 150 155 160
 Leu Leu Asp His Phe Pro Leu Val Val Trp Gln Thr Gly Ser Gly Thr
 165 170 175
 Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ser Asn Arg Ala Ile Glu
 180 185 190
 Ile Leu Gly Gly Glu Lys Gly Ser Lys Lys Pro Val His Pro Asn Asp
 195 200 205
 His Val Asn Arg Ser Ala Ser Ser Asn Asp Thr Phe Pro Thr Val Met
 210 215 220
 His Ile Ala Ala Val Leu Glu Ile Glu Gly Glu Leu Ile Pro Ser Leu
 225 230 235 240
 Arg Ser Leu Arg Asp Ala Leu Gln Ala Lys Val Asp Glu Phe Glu Ala
 245 250 255
 Lys Lys Ile Ile Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr Pro
 260 265 270
 Leu Thr Leu Ala Gln Glu Phe Ser Gly Tyr Val Ala Gln Leu Asp Phe
 275 280 285
 Gly Ile Lys Arg Val Glu Ala Thr Leu Pro Asp Leu Arg Leu Leu Ala
 290 295 300
 Gln Gly Gly Thr Ala Val Gly Thr Gly Ile Asn Thr Phe Glu Gly Phe
 305 310 315 320
 Ala Glu Gly Ile Ala Glu Glu Val Ser Arg Met Thr Gly Thr Glu Phe
 325 330 335
 Lys Thr Ala Pro Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Leu
 340 345 350
 Val His Ala Ser Gly Ala Leu Asn Thr Leu Ala Thr Ser Leu Thr Lys
 355 360 365
 Val Ala Gln Asp Ile Arg Tyr Leu Gly Ser Gly Pro Arg Cys Gly Leu
 370 375 380
 Gly Glu Leu Val Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro
 385 390 395 400
 Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys Ala
 405 410 415
 Gln Val Met Gly Asn His Val Ala Ala Thr Ile Gly Gly Met Asn Gly
 420 425 430
 Gln Phe Glu Leu Asn Val Tyr Lys Pro Leu Ile Ile Arg Asn Val Leu
 435 440 445
 His Ser Val Arg Leu Leu Ser Asp Gly Met Arg Ser Phe Glu Lys His
 450 455 460
 Leu Val Glu Gly Leu Lys Ala Asn Glu Glu Lys Ile Ala Ser Ile Met
 465 470 475 480
 Lys Glu Ser Leu Met Leu Val Thr Cys Leu Asn Pro Lys Ile Gly Tyr
 485 490 495
 Asp Met Ala Ser Lys Val Ala Lys Asn Ala His Lys Lys Gly Leu Thr
 500 505 510
 Leu Lys Glu Ser Ala Leu Glu Leu Asn Ala Leu Thr Glu Glu Glu Phe
 515 520 525
 Asp Thr Leu Val Lys Pro Glu Leu Met Ile Thr Pro Lys Pro Tyr Lys
 530 535 540
 Ala
 545

<210> 9635

<211> 1590

<212> DNA

<213> Gibberella zeae PH-1

<220>

<221> CDS

<222> (1)..(1590)

<400> 9635

atg ctt cga tct gtc acg gga cgc gct gcc gcc tcg ggc ctt atg aag
 Met Leu Arg Ser Val Thr Gly Arg Ala Ala Ala Ser Gly Leu Met Lys
 1 5 10 15
 tca gct ctg cct cgg gtc tcc caa gca gca gct ccc aca tgc tcg ctt
 Ser Ala Leu Pro Arg Val Ser Gln Ala Ala Ala Pro Thr Cys Ser Leu
 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95

48

96

PF59083SeqList PF59083.txt

					20						25						30	
gcc	ccg	cag	ctg	cga	ctc	caa	agc	aag	tct	tct	gtt	gct	ggg	ctt	cga	144		
Ala	Pro	Gln	Leu	Arg	Leu	Gln	Ser	Lys	Ser	Ser	Val	Ala	Gly	Leu	Arg			
ctc	tcc	aga	gct	att	cac	agc	acc	tca	gtc	agg	atg	tct	caa	aca	cga	192		
Leu	Ser	Arg	Ala	Ile	His	Ser	Thr	Ser	Val	Arg	Met	Ser	Gln	Thr	Arg			
aca	gaa	agc	gat	gcc	ttt	ggc	gag	atc	cag	gtc	ccc	gcc	gac	cgc	tac	240		
Thr	Glu	Ser	Asp	Ala	Phe	Gly	Glu	Ile	Gln	Val	Pro	Ala	Asp	Arg	Tyr			
tgg	gga	gct	cag	acg	gag	cga	tcc	ctc	gag	aac	ttc	cg	atc	aac	cag	288		
Trp	Gly	Ala	Gln	Thr	Glu	Arg	Ser	Leu	Glu	Asn	Phe	Arg	Ile	Asn	Gln			
ccc	cag	gac	cg	atg	ccc	cca	cct	att	gtc	aag	gcg	ttt	ggg	atc	ctg	336		
Pro	Gln	Asp	Arg	Met	Pro	Pro	Pro	Ile	Val	Lys	Ala	Phe	Gly	Ile	Leu			
aag	ggg	gct	gcc	gcc	act	gtt	aac	atg	aaa	tat	gga	ctt	gac	ccc	aag	384		
Lys	Gly	Ala	Ala	Ala	Thr	Val	Asn	Met	Lys	Tyr	Gly	Leu	Asp	Pro	Lys			
atc	ggg	gct	atc	cag	cag	gct	gcc	aag	gag	gtc	gct	gat	ggc	aag		432		
Ile	Gly	Ala	Ala	Ile	Gln	Gln	Ala	Ala	Lys	Glu	Val	Ala	Asp	Gly	Lys			
ctc	atc	gac	cac	ttc	cct	ctc	gtc	gtc	tgg	cag	act	ggc	tcc	ggg	act	480		
Leu	Ile	Asp	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr			
cag	tcc	aac	atg	aac	gcc	aac	gag	gtc	atc	tcc	aac	cg	gcc	att	gag	528		
Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ser	Asn	Arg	Ala	Ile	Glu			
att	ctt	ggc	ggg	acc	atg	ggc	agc	aag	aag	cct	gtc	cac	ccc	aat	gac	576		
Ile	Leu	Gly	Gly	Thr	Met	Gly	Ser	Lys	Lys	Pro	Val	His	Pro	Asn	Asp			
cac	gtc	aac	cg	agc	gct	tcc	tcc	aac	gac	act	ttt	cct	acc	gtc	atg	624		
His	Val	Asn	Arg	Ser	Ala	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val	Met			
cac	att	gct	gct	gtc	ctc	gac	att	gaa	agc	gag	ctc	ctg	cct	gct	ctc	672		
His	Ile	Ala	Ala	Val	Leu	Asp	Ile	Glu	Ser	Glu	Leu	Leu	Pro	Ala	Leu			
cg	agc	ctg	cg	gac	gct	atc	cag	aag	aag	gtc	gac	gag	ttc	gag	gcc	720		
Arg	Ser	Leu	Arg	Asp	Ala	Ile	Gln	Lys	Lys	Val	Asp	Glu	Phe	Glu	Ala			
aag	aag	atc	atc	aag	atc	ggc	cg	act	cac	ctt	cag	gac	gcc	act	cct	768		
Lys	Lys	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro			
ctc	act	ctc	gcc	cag	gag	ttc	tcc	ggg	tac	gtt	gcc	cag	ctc	gac	ttt	816		
Leu	Thr	Leu	Ala	Gln	Glu	Phe	Ser	Gly	Tyr	Val	Ala	Gln	Leu	Asp	Phe			
ggc	atc	aag	cg	gtc	gag	agc	tct	ctg	ccc	gac	cta	cga	ctc	ctc	gcc	864		
Gly	Ile	Lys	Arg	Val	Glu	Ser	Ser	Leu	Pro	Asp	Leu	Arg	Leu	Leu	Ala			
cag	ggg	ggg	acc	gct	gtc	ggg	act	ggc	atc	aac	act	ttc	cag	gga	ttt	912		
Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Thr	Phe	Gln	Gly	Phe			
gcc	gag	gct	atc	gct	gag	gag	gtc	aca	aag	atg	acc	ggg	act	gag	ttc	960		
Ala	Glu	Ala	Ile	Ala	Glu	Glu	Val	Thr	Lys	Met	Thr	Gly	Thr	Glu	Phe			
aag	act	gcc	ccc	aac	aag	ttc	gag	gcc	ctc	gcc	gcc	cac	gac	gct	att	1008		
Lys	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Ile			
gtc	cag	gcc	cac	ggc	tcc	ctc	aac	acc	ctg	gct	gct	tct	ctt	acc	aaa	1056		
Val	Gln	Ala	His	Gly	Ser	Leu	Asn	Thr	Leu	Ala	Ala	Ser	Leu	Thr	Lys			
atc	gca	caa	gac	gtc	cga	tac	ctt	ggg	agc	ggc	ccc	cg	tgc	ggg	ctt	1104		
Ile	Ala	Gln	Asp	Val	Arg	Tyr	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu			
ggg	gag	ctg	aac	ctg	ccc	gag	aac	gag	cct	ggc	agc	agt	atc	atg	cct	1152		
Gly	Glu	Leu	Asn	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro			
ggc	aag	gtc	aac	cct	acc	cag	tgt	gag	gcc	ttg	act	atg	gtc	tgc	gcc	1200		
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala			

PF59083SeqList PF59083.txt

385		390		395		400	
cag gtt atg ggc aac cac gtt gcc acc act atc gga ggc atg aac ggc							1248
Gln Val Met Gly Asn His Val Ala Thr Thr Ile Gly Gly Met Asn Gly							
		405		410		415	
cag ttt gaa ctc aac gtt tac aag cct ctg gtc att cgt aac ctg ctc							1296
Gln Phe Glu Leu Asn Val Tyr Lys Pro Leu Val Ile Arg Asn Leu Leu							
		420		425		430	
cac agc tcc cgt ctt ctg act gac ggc atg cgc tct ttc gag aag aac							1344
His Ser Ser Arg Leu Leu Thr Asp Gly Met Arg Ser Phe Glu Lys Asn							
		435		440		445	
ctg gtt gcc ggc ctc aac gct aac gag gag aag att gcc agc atc atg							1392
Leu Val Ala Gly Leu Asn Ala Asn Glu Glu Lys Ile Ala Ser Ile Met							
		450		455		460	
aag gag tcg ctt atg ctt gtc acc tgc ctg aac ccc aag att gga tac							1440
Lys Glu Ser Leu Met Leu Val Thr Cys Leu Asn Pro Lys Ile Gly Tyr							
		465		470		475	
gac atg gct agc aag gtt gcc aag aac gct cat aag aag ggc ctt acc							1488
Asp Met Ala Ser Lys Val Ala Lys Asn Ala His Lys Lys Gly Leu Thr							
		485		490		495	
ctc aag cag agt gct ctc gaa cta aac gct ctg act gag gag gaa ttt							1536
Leu Lys Gln Ser Ala Leu Glu Leu Asn Ala Leu Thr Glu Glu Glu Phe							
		500		505		510	
gac act ttg gtt aag cct gag ctg atg gtc ggt ccc agt cct tac aag							1584
Asp Thr Leu Val Lys Pro Glu Leu Met Val Gly Pro Ser Pro Tyr Lys							
		515		520		525	
ggt tag							1590
Gly							

<210> 9636

<211> 529

<212> PRT

<213> Gibberella zeae PH-1

<400> 9636

Met Leu Arg Ser Val Thr Gly Arg Ala Ala Ala Ser Gly Leu Met Lys	
1 5 10 15	
Ser Ala Leu Pro Arg Val Ser Gln Ala Ala Ala Pro Thr Cys Ser Leu	
20 25 30	
Ala Pro Gln Leu Arg Leu Gln Ser Ser Val Ala Gly Leu Arg	
35 40 45	
Leu Ser Arg Ala Ile His Ser Thr Ser Val Arg Met Ser Gln Thr Arg	
50 55 60	
Thr Glu Ser Asp Ala Phe Gly Glu Ile Gln Val Pro Ala Asp Arg Tyr	
65 70 75	
Trp Gly Ala Gln Thr Glu Arg Ser Leu Glu Asn Phe Arg Ile Asn Gln	
85 90 95	
Pro Gln Asp Arg Met Pro Pro Pro Ile Val Lys Ala Phe Gly Ile Leu	
100 105 110	
Lys Gly Ala Ala Thr Val Asn Met Lys Tyr Gly Leu Asp Pro Lys	
115 120 125	
Ile Gly Ala Ala Ile Gln Gln Ala Ala Lys Glu Val Ala Asp Gly Lys	
130 135 140	
Leu Ile Asp His Phe Pro Leu Val Val Trp Gln Thr Gly Ser Gly Thr	
145 150 155	
Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ser Asn Arg Ala Ile Glu	
165 170 175	
Ile Leu Gly Gly Thr Met Gly Ser Lys Lys Pro Val His Pro Asn Asp	
180 185 190	
His Val Asn Arg Ser Ala Ser Ser Asn Asp Thr Phe Pro Thr Val Met	
195 200 205	
His Ile Ala Ala Val Leu Asp Ile Glu Ser Glu Leu Leu Pro Ala Leu	
210 215 220	
Arg Ser Leu Arg Asp Ala Ile Gln Lys Lys Val Asp Glu Phe Glu Ala	
225 230 235	
Lys Lys Ile Ile Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr Pro	
245 250 255	
Leu Thr Leu Ala Gln Glu Phe Ser Gly Tyr Val Ala Gln Leu Asp Phe	
260 265 270	

PF59083SeqList PF59083.txt

Gly Ile Lys Arg Val Glu Ser Ser Leu Pro Asp Leu Arg Leu Leu Ala
 275 280 285
 Gln Gly Gly Thr Ala Val Gly Thr Gly Ile Asn Thr Phe Gln Gly Phe
 290 295 300
 Ala Glu Ala Ile Ala Glu Val Thr Lys Met Thr Gly Thr Glu Phe
 305 310 315 320
 Lys Thr Ala Pro Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Ile
 325 330 335
 Val Gln Ala His Gly Ser Leu Asn Thr Leu Ala Ala Ser Leu Thr Lys
 340 345 350
 Ile Ala Gln Asp Val Arg Tyr Leu Gly Ser Gly Pro Arg Cys Gly Leu
 355 360 365
 Gly Glu Leu Asn Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro
 370 375 380
 Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys Ala
 385 390 395 400
 Gln Val Met Gly Asn His Val Ala Thr Thr Ile Gly Gly Met Asn Gly
 405 410 415
 Gln Phe Glu Leu Asn Val Tyr Lys Pro Leu Val Ile Arg Asn Leu Leu
 420 425 430
 His Ser Ser Arg Leu Leu Thr Asp Gly Met Arg Ser Phe Glu Lys Asn
 435 440 445
 Leu Val Ala Gly Leu Asn Ala Asn Glu Glu Lys Ile Ala Ser Ile Met
 450 455 460
 Lys Glu Ser Leu Met Leu Val Thr Cys Leu Asn Pro Lys Ile Gly Tyr
 465 470 475 480
 Asp Met Ala Ser Lys Val Ala Lys Asn Ala His Lys Lys Gly Leu Thr
 485 490 495
 Leu Lys Gln Ser Ala Leu Glu Leu Asn Ala Leu Thr Glu Glu Glu Phe
 500 505 510
 Asp Thr Leu Val Lys Pro Glu Leu Met Val Gly Pro Ser Pro Tyr Lys
 515 520 525
 Gly

<210> 9637

<211> 1452

<212> DNA

<213> Candida glabrata CBS 138

<220>

<221> CDS

<222> (1)..(1452)

<400> 9637

atg ttg agg gct agc agt agg gca aag aca tcg ctc atc ggg tac agc	48
Met Leu Arg Ala Ser Ser Arg Ala Lys Thr Ser Leu Ile Gly Tyr Ser	
1 5 10 15	
gcg cgg atg atg cat tac aga gta gag acg gac act ttc ggc gag atc	96
Ala Arg Met Met His Tyr Arg Val Glu Thr Asp Thr Phe Gly Glu Ile	
20 25 30	
aag gta ccc gcg gac aag tac tgg ggc gcg cag acg cag cgg tcg ttc	144
Lys Val Pro Ala Asp Lys Tyr Trp Gly Ala Gln Thr Gln Arg Ser Phe	
35 40 45	
cag aac ttc aag atc ggc ggc gcg gag cgc atg ccg gag ccc atc	192
Gln Asn Phe Lys Ile Gly Gly Ala Arg Glu Arg Met Pro Glu Pro Ile	
50 55 60	
gtg agg gcg ttc ggt gtg ctg aag aag tca gcc gcc ata gtc aac gag	240
Val Arg Ala Phe Gly Val Leu Lys Lys Ser Ala Ala Ile Val Asn Glu	
65 70 75 80	
aag ctc ggg acg cta gac agc gag atc gcg ggg ccc atc cag cag gcc	288
Lys Leu Gly Thr Leu Asp Ser Glu Ile Ala Gly Pro Ile Gln Gln Ala	
85 90 95	
gct gac gag gtc gcc aag ggc aag ctc aac gac cac ttc ccc ttg gtg	336
Ala Asp Glu Val Ala Lys Gly Lys Leu Asn Asp His Phe Pro Leu Val	
100 105 110	
gtg ttc cag acc ggg tca ggc acg cag tct aac atg aac gcc aac gag	384
Val Phe Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu	
115 120 125	

PF59083SeqList PF59083.txt																
gtc	atc	tcc	aac	agg	gcg	att	gag	ctg	atc	ggc	ggc	gag	ctc	ggc	tcc	432
Val	Ile	Ser	Asn	Arg	Ala	Ile	Glu	Leu	Ile	Gly	Gly	Glu	Leu	Gly	Ser	
	130					135				140						
aag	aag	atc	cac	cca	aac	aac	cac	tgc	aat	cag	gcg	cag	tcc	tcc	aac	480
Lys	Lys	Ile	His	Pro	Asn	Asn	His	Cys	Asn	Gln	Ala	Gln	Ser	Ser	Asn	
	145				150					155					160	
gac	act	ttc	ccc	tcg	gtg	atg	cac	atc	gcc	gcg	gtc	acg	gag	atc	acc	528
Asp	Thr	Phe	Pro	Ser	Val	Met	His	Ile	Ala	Ala	Val	Thr	Glu	Ile	Thr	
				165					170					175		
aac	tcc	ctc	ttg	ccg	gag	atc	acc	cag	ctg	aag	gac	gcc	ctc	cac	aag	576
Asn	Ser	Leu	Leu	Pro	Glu	Ile	Thr	Gln	Leu	Lys	Asp	Ala	Leu	His	Lys	
			180					185					190			
aag	gcc	gag	gag	ttc	cag	gac	atc	gtc	aag	atc	ggc	aga	aca	cac	ctg	624
Lys	Ala	Glu	Glu	Phe	Gln	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Leu	
		195				200						205				
cag	gac	gcc	aca	ccg	ctg	acc	ctc	gga	cag	gaa	ttc	agc	ggc	tac	gtc	672
Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	
	210					215					220					
cag	cag	ctc	gtc	aac	ggc	atc	gca	aga	atc	gag	aac	acc	ctg	cca	cac	720
Gln	Gln	Leu	Val	Asn	Gly	Ile	Ala	Arg	Ile	Glu	Asn	Thr	Leu	Pro	His	
	225				230					235					240	
ctg	aag	tac	ctc	gca	caa	ggc	ggc	acc	gct	gtc	ggc	aca	ggg	ctg	aac	768
Leu	Lys	Tyr	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	
				245				250						255		
acg	aag	gag	ggc	ttc	gac	aag	ctg	atc	gcc	gag	cag	atc	tcc	aag	gaa	816
Thr	Lys	Glu	Gly	Phe	Asp	Lys	Leu	Ile	Ala	Glu	Gln	Ile	Ser	Lys	Glu	
			260					265					270			
acg	ggc	atc	gac	ttc	aaa	acc	gcc	cct	aac	aag	ttc	gaa	gct	ctc	gca	864
Thr	Gly	Ile	Asp	Phe	Lys	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	
		275				280						285				
gct	cac	gac	gag	atc	gtc	gag	gcc	agc	ggc	gcc	ctg	aac	acc	gtg	gct	912
Ala	His	Asp	Ala	Ile	Val	Glu	Ala	Ser	Gly	Ala	Leu	Asn	Thr	Val	Ala	
	290				295					300						
tgc	tct	ctg	ttc	aag	atc	gca	cag	gac	atc	agg	tac	ctg	ggc	tcc	ggc	960
Cys	Ser	Leu	Phe	Lys	Ile	Ala	Gln	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	
	305				310					315					320	
cct	cgt	tgc	ggc	tac	ggc	gaa	ctg	cac	ttg	cca	gag	aac	gag	cca	ggc	1008
Pro	Arg	Cys	Gly	Tyr	Gly	Glu	Leu	His	Leu	Pro	Glu	Asn	Glu	Pro	Gly	
				325					330					335		
tcc	tcc	atc	atg	cct	ggc	aag	gtc	aac	cca	aca	cag	aac	gag	gcc	atg	1056
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Asn	Glu	Ala	Met	
				340				345					350			
acc	cag	gtc	tgt	gtc	cag	gtc	atg	ggc	aac	aac	gca	gct	gtg	acc	ttc	1104
Thr	Gln	Val	Cys	Val	Gln	Val	Met	Gly	Asn	Asn	Ala	Ala	Val	Thr	Phe	
		355					360					365				
gag	ggc	gcc	aac	ggc	cag	ttc	gaa	ctg	aac	gtc	ttc	aag	ccg	gtc	atg	1152
Ala	Gly	Ala	Asn	Gly	Gln	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Met	
	370				375						380					
atc	tca	aac	ttg	ttg	agc	tcc	atc	aga	ttg	ctg	gca	gac	gct	tgc	cac	1200
Ile	Ser	Asn	Leu	Leu	Ser	Ile	Arg	Leu	Leu	Ala	Ala	Asp	Ala	Cys	His	
					390				395						400	
tcc	ttc	aga	gtc	cac	tgt	gtc	gaa	ggc	atc	gag	gca	aac	cgc	gag	aag	1248
Ser	Phe	Arg	Val	His	Cys	Val	Glu	Gly	Ile	Glu	Ala	Asn	Arg	Glu	Lys	
				405					410					415		
atc	aac	cac	aac	ttg	cac	aac	tca	ttg	atg	ctg	gtc	acc	gct	ctg	aac	1296
Ile	Asn	His	Asn	Leu	His	Asn	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	
			420				425					430				
cca	aag	atc	ggc	tac	gac	gcc	gcc	tcc	aag	atc	gca	aag	aac	gct	ttc	1344
Pro	Lys	Ile	Gly	Tyr	Asp	Ala	Ala	Ser	Lys	Ile	Ala	Lys	Asn	Ala	Phe	
		435				440						445				
aag	aag	aac	atc	acc	ttg	aaa	gag	tcc	gcc	ttg	gag	ttg	aaa	tac	ttg	1392
Lys	Lys	Asn	Ile	Thr	Leu	Lys	Glu	Ser	Ala	Leu	Glu	Leu	Lys	Tyr	Leu	
	450				455					460						
acc	tca	gaa	gag	ttc	gac	gaa	tgg	gtc	att	cct	gaa	aac	atg	gtt	gga	1440
Thr	Ser	Glu	Glu	Phe	Asp	Glu	Trp	Val	Ile	Pro	Glu	Asn	Met	Val	Gly	
					470					475					480	
cca	acc	aag	taa													1452
Pro	Thr	Lys														

PF59083SeqList PF59083.txt

<210> 9638
 <211> 483
 <212> PRT
 <213> Candida glabrata CBS 138

<400> 9638
 Met Leu Arg Ala Ser Ser Arg Ala Lys Thr Ser Leu Ile Gly Tyr Ser
 1 5 10 15
 Ala Arg Met Met His Tyr Arg Val Glu Thr Asp Thr Phe Gly Glu Ile
 20 25 30
 Lys Val Pro Ala Asp Lys Tyr Trp Gly Ala Gln Thr Gln Arg Ser Phe
 35 40 45
 Gln Asn Phe Lys Ile Gly Gly Ala Arg Glu Arg Met Pro Glu Pro Ile
 50 55 60
 Val Arg Ala Phe Gly Val Leu Lys Lys Ser Ala Ile Val Asn Glu
 65 70 75 80
 Lys Leu Gly Thr Leu Asp Ser Glu Ile Ala Gly Pro Ile Gln Gln Ala
 85 90 95
 Ala Asp Glu Val Ala Lys Gly Lys Leu Asn Asp His Phe Pro Leu Val
 100 105 110
 Val Phe Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu
 115 120 125
 Val Ile Ser Asn Arg Ala Ile Glu Leu Ile Gly Gly Glu Leu Gly Ser
 130 135 140
 Lys Lys Ile His Pro Asn Asn His Cys Asn Gln Ala Gln Ser Ser Asn
 145 150 155 160
 Asp Thr Phe Pro Ser Val Met His Ile Ala Ala Val Thr Glu Ile Thr
 165 170 175
 Asn Ser Leu Leu Pro Glu Ile Thr Gln Leu Lys Asp Ala Leu His Lys
 180 185 190
 Lys Ala Glu Glu Phe Gln Asp Ile Val Lys Ile Gly Arg Thr His Leu
 195 200 205
 Gln Asp Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Val
 210 215 220
 Gln Gln Leu Val Asn Gly Ile Ala Arg Ile Glu Asn Thr Leu Pro His
 225 230 235 240
 Leu Lys Tyr Leu Ala Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn
 245 250 255
 Thr Lys Glu Gly Phe Asp Lys Leu Ile Ala Glu Gln Ile Ser Lys Glu
 260 265 270
 Thr Gly Ile Asp Phe Lys Thr Ala Pro Asn Lys Phe Glu Ala Leu Ala
 275 280 285
 Ala His Asp Ala Ile Val Glu Ala Ser Gly Ala Leu Asn Thr Val Ala
 290 295 300
 Cys Ser Leu Phe Lys Ile Ala Gln Asp Ile Arg Tyr Leu Gly Ser Gly
 305 310 315 320
 Pro Arg Cys Gly Tyr Gly Glu Leu His Leu Pro Glu Asn Glu Pro Gly
 325 330 335
 Ser Ser Ile Met Pro Gly Lys Val Asn Pro Thr Gln Asn Glu Ala Met
 340 345 350
 Thr Gln Val Cys Val Gln Val Met Gly Asn Asn Ala Ala Val Thr Phe
 355 360 365
 Ala Gly Ala Asn Gly Gln Phe Glu Leu Asn Val Phe Lys Pro Val Met
 370 375 380
 Ile Ser Asn Leu Leu Ser Ser Ile Arg Leu Leu Ala Asp Ala Cys His
 385 390 395 400
 Ser Phe Arg Val His Cys Val Glu Gly Ile Glu Ala Asn Arg Glu Lys
 405 410 415
 Ile Asn His Asn Leu His Asn Ser Leu Met Leu Val Thr Ala Leu Asn
 420 425 430
 Pro Lys Ile Gly Tyr Asp Ala Ala Ser Lys Ile Ala Lys Asn Ala Phe
 435 440 445
 Lys Lys Asn Ile Thr Leu Lys Glu Ser Ala Leu Glu Leu Lys Tyr Leu
 450 455 460
 Thr Ser Glu Glu Phe Asp Glu Trp Val Ile Pro Glu Asn Met Val Gly
 465 470 475 480
 Pro Thr Lys

PF59083SeqList PF59083.txt

<210> 9639
 <211> 1479
 <212> DNA
 <213> Kluyveromyces lactis NRRL Y-1140

<220>
 <221> CDS
 <222> (1)..(1479)

<400> 9639
 atg ttg aga aat agc att gta tca cgt ggt cta gct caa acc cgc gtt 48
 Met Leu Arg Asn Ser Ile Val Ser Arg Gly Leu Ala Gln Thr Arg Val
 1 5 10 15
 agt gca aag gtt aac aga cta gca tcg tta aga atg gtt tcg tat aga 96
 Ser Ala Lys Val Asn Arg Leu Ala Ser Leu Arg Met Val Ser Tyr Arg
 20 25 30
 gtg gag acc gat gcg ttc ggt gag atc caa gtt cct tct gat aag tac 144
 Val Glu Thr Asp Ala Phe Gly Glu Ile Gln Val Pro Ser Asp Lys Tyr
 35 40 45
 tgg ggt gct caa acc caa cgt tct ttg caa aat ttc aag att ggt ggt 192
 Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn Phe Lys Ile Gly Gly
 50 55 60
 cct cgt gaa aga atg cct gag cca att gtc aag gct ttt ggt gtt ttg 240
 Pro Arg Glu Arg Met Pro Glu Pro Ile Val Lys Ala Phe Gly Val Leu
 65 70 75 80
 aag aag tcg gct gct gtg gtc aat gag cgt ctg ggg acg ttg gac cct 288
 Lys Lys Ser Ala Ala Val Val Asn Glu Arg Leu Gly Thr Leu Asp Pro
 85 90 95
 gaa atc gct aag cct atc aag caa gca gcc gat gaa gtt gct cag ggt 336
 Glu Ile Ala Lys Pro Ile Lys Gln Ala Ala Asp Glu Val Ala Gln Gly
 100 105 110
 aaa cta atg gaa cat ttt cca ttg gtt gtg ttc caa act ggg tct ggt 384
 Lys Leu Met Glu His Phe Pro Leu Val Val Phe Gln Thr Gly Ser Gly
 115 120 125
 act cag tcc aac atg aac gcc aac gaa gtt att tca aac agg gcc atc 432
 Thr Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ser Asn Arg Ala Ile
 130 135 140
 gaa ttg att ggt ggt gaa ttg ggt tct aag aag att cac cca aac aac 480
 Glu Leu Ile Gly Gly Glu Leu Gly Ser Lys Lys Ile His Pro Asn Asn
 145 150 155 160
 cac tgt aac caa gct caa tcc agt aac gat act ttc cca tct gtt atg 528
 His Cys Asn Gln Ala Gln Ser Ser Asn Asp Thr Phe Pro Ser Val Met
 165 170 175
 cat att gct gct gtc act gaa att aca cac cat ttg ttg cca gaa ttg 576
 His Ile Ala Ala Val Thr Glu Ile Thr His His Leu Leu Pro Glu Leu
 180 185 190
 gaa ggt ttg aaa gtt gct tta aag caa aaa tct gat gag ttc cag cat 624
 Glu Gly Leu Lys Val Ala Leu Lys Gln Lys Ser Asp Glu Phe Gln His
 195 200 205
 atc gtt aag atc ggt aga acc cat ttg caa gat gct act cca ttg acc 672
 Ile Val Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr Pro Leu Thr
 210 215 220
 cta ggt caa gag ttc agc gga tac gtg caa cag gtg gag aac ggt att 720
 Leu Gly Gln Glu Phe Ser Gly Tyr Val Gln Val Glu Asn Gly Ile
 225 230 235 240
 gct cgt gtt aaa caa tct cta tat cat ttg aag ttc ttg gca caa ggt 768
 Ala Arg Val Lys Gln Ser Leu Tyr His Leu Lys Phe Leu Ala Gln Gly
 245 250 255
 ggt act gcc gtt ggt act ggt ttg aat act aag gtc ggt ttt gct gaa 816
 Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Lys Val Gly Phe Ala Glu
 260 265 270
 gat atc gct gaa caa gtt tct aaa gaa act ggt atc gat ttc aag acc 864
 Asp Ile Ala Glu Gln Val Ser Lys Glu Thr Gly Ile Asp Phe Lys Thr
 275 280 285
 gct cca aac aag ttc gaa gca ttg gct gct cac gat gct gtc gtt gaa 912
 Ala Pro Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Val Val Glu
 290 295 300
 gcc tct ggt gcc cta aac act ctg gct gtc tct tta ttc aag att gct 960

PF59083SeqList PF59083.txt

Ala 305	Ser	Gly	Ala	Leu	Asn 310	Thr	Leu	Ala	Val	Ser 315	Leu	Phe	Lys	Ile	Ala 320	
aac	gat	atc	aga	tac	ttg	ggt	tct	gga	cct	cgt	tgc	ggt	tac	ggt	gaa	1008
Asn	Asp	Ile	Arg	Tyr 325	Leu	Gly	Ser	Gly	Pro 330	Arg	Cys	Gly	Tyr	Gly 335	Glu	
tta	agt	ttg	cca	gaa	aac	gaa	cca	ggt	tct	tct	atc	atg	cct	ggt	aaa	1056
Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	
			340					345					350			
gtg	aac	cct	act	cag	aat	gaa	gcc	atg	act	caa	gtg	tgt	ggt	caa	ggt	1104
Val	Asn	Pro	Thr	Gln	Asn	Glu	Ala	Met	Thr	Gln	Val	Cys	Val	Gln	Val	
			355					360					365			
atg	ggt	aac	cat	gcc	gct	atc	act	ttt	gca	ggt	gct	tct	ggt	caa	ttt	1152
Met	Gly	Asn	His	Ala	Ala	Ile	Thr	Phe	Ala	Gly	Ala	Ser	Gly	Gln	Phe	
			370			375							380			
gaa	ttg	aat	gtc	ttc	aag	cca	ggt	atg	atc	tgc	aac	ttg	ttg	agt	tca	1200
Glu	Leu	Asn	Val	Phe	Lys 390	Pro	Val	Met	Ile	Ser 395	Asn	Leu	Leu	Ser	Ser 400	
atc	aga	cta	ttg	gga	gat	gct	tct	aac	tct	ttc	aga	att	cac	tgt	ggt	1248
Ile	Arg	Leu	Leu	Gly 405	Asp	Ala	Ser	Asn	Ser 410	Phe	Arg	Ile	His	Cys 415	Val	
gaa	ggt	att	aag	gct	aac	gag	gac	aga	atc	gct	aaa	ttg	ttg	cat	gaa	1296
Glu	Gly	Ile	Lys	Ala	Asn	Glu	Asp	Arg	Ile	Ala	Lys	Leu	Leu	His	Glu	
			420					425					430			
tcc	tta	atg	ttg	gta	act	gca	ttg	aac	cca	aag	atc	ggt	tac	gat	gcc	1344
Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	Asp	Ala	
			435					440					445			
gct	tct	aag	gtc	gct	aag	aac	gct	cac	aag	aag	gga	atc	act	ttg	aag	1392
Ala	Ser	Lys	Val	Ala	Lys	Asn	Ala	His	Lys	Lys	Gly	Ile	Thr	Leu	Lys	
			450			455							460			
gaa	tct	gct	ttg	gaa	ttg	aag	ggt	cta	tca	agt	gaa	gaa	ttc	gac	caa	1440
Glu	Ser	Ala	Leu	Glu	Leu	Lys	Val	Leu	Ser	Ser 475	Glu	Glu	Phe	Asp	Gln 480	
465					470											
tgg	gtc	atc	cct	gaa	aag	atg	att	ggt	cca	aag	gag	taa				1479
Trp	Val	Ile	Pro	Glu	Lys	Met	Ile	Gly	Pro 490	Lys	Glu					
				485												

<210> 9640

<211> 492

<212> PRT

<213> Kluyveromyces lactis NRRL Y-1140

<400> 9640

Met 1	Leu	Arg	Asn	Ser 5	Ile	Val	Ser	Arg	Gly 10	Leu	Ala	Gln	Thr	Arg 15	Val	
Ser	Ala	Lys	Val	Asn 20	Arg	Leu	Ala	Ser 25	Leu	Arg	Met	Val	Ser	Tyr 30	Arg	
Val	Glu	Thr	Asp	Ala	Phe	Gly	Glu	Ile	Gln	Val	Pro	Ser	Asp	Lys	Tyr	
			35					40					45			
Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	Lys	Ile	Gly	Gly	
			50			55						60				
Pro	Arg	Glu	Arg	Met	Pro	Glu	Pro	Ile	Val	Lys 75	Ala	Phe	Gly	Val	Leu	
65					70										80	
Lys	Lys	Ser	Ala	Ala	Val	Val	Asn	Glu	Arg	Leu	Gly	Thr	Leu	Asp	Pro	
				85					90					95		
Glu	Ile	Ala	Lys	Pro	Ile	Lys	Gln	Ala	Ala	Asp	Glu	Val	Ala	Gln	Gly	
			100					105					110			
Lys	Leu	Met	Glu	His	Phe	Pro	Leu	Val	Val	Phe	Gln	Thr	Gly	Ser	Gly	
			115				120					125				
Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ser	Asn	Arg	Ala	Ile	
			130			135						140				
Glu	Leu	Ile	Gly	Gly	Glu	Leu	Gly	Ser	Lys	Lys	Ile	His	Pro	Asn	Asn	
145					150					155					160	
His	Cys	Asn	Gln	Ala	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Ser	Val	Met	
				165					170					175		
His	Ile	Ala	Ala	Val	Thr	Glu	Ile	Thr	His	His	Leu	Leu	Pro	Glu	Leu	
			180					185					190			
Glu	Gly	Leu	Lys	Val	Ala	Leu	Lys	Gln	Lys	Ser	Asp	Glu	Phe	Gln	His	
			195				200					205				
Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	Leu	Thr	

PF59083SeqList PF59083.txt

```

210          215          220
Leu Gly Gln Glu Phe Ser Gly Tyr Val Gln Gln Val Glu Asn Gly Ile
225 Ala Arg Val Lys Gln Ser Leu Tyr His Leu Lys Phe Leu Ala Gln Gly
245
Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Lys Val Gly Phe Ala Glu
260
Asp Ile Ala Glu Gln Val Ser Lys Glu Thr Gly Ile Asp Phe Lys Thr
275
Ala Pro Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Val Val Glu
290
Ala Ser Gly Ala Leu Asn Thr Leu Ala Val Ser Leu Phe Lys Ile Ala
305
Asn Asp Ile Arg Tyr Leu Gly Ser Gly Pro Arg Cys Gly Tyr Gly Glu
325
Leu Ser Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys
340
Val Asn Pro Thr Gln Asn Glu Ala Met Thr Gln Val Cys Val Gln Val
355
Met Gly Asn His Ala Ala Ile Thr Phe Ala Gly Ala Ser Gly Gln Phe
370
Glu Leu Asn Val Phe Lys Pro Val Met Ile Ser Asn Leu Leu Ser Ser
385
Ile Arg Leu Leu Gly Asp Ala Ser Asn Ser Phe Arg Ile His Cys Val
405
Glu Gly Ile Lys Ala Asn Glu Asp Arg Ile Ala Lys Leu Leu His Glu
420
Ser Leu Met Leu Val Thr Ala Leu Asn Pro Lys Ile Gly Tyr Asp Ala
435
Ala Ser Lys Val Ala Lys Asn Ala His Lys Lys Gly Ile Thr Leu Lys
450
Glu Ser Ala Leu Glu Leu Lys Val Leu Ser Ser Glu Glu Phe Asp Gln
465
Trp Val Ile Pro Glu Lys Met Ile Gly Pro Lys Glu
485          490

```

<210> 9641
 <211> 1479
 <212> DNA
 <213> Debaryomyces hansenii CBS767

<220>
 <221> CDS
 <222> (1)..(1479)

```

<400> 9641
atg tta aga tta acc agt aaa tat acc cca gtg gct aga tct att caa      48
Met Leu Arg Leu Thr Ser Lys Tyr Thr Pro Val Ala Arg Ser Ile Gln
1      5      10      15
tta aga tca tta tcg tca act tct gca tta tta agt tcg acc aga acc      96
Leu Arg Ser Leu Ser Thr Ser Ala Leu Leu Ser Ser Thr Arg Thr
20      25      30
gaa tca gat gct ttc ggt gaa atc gaa gtt gat tca gct aag tat tac      144
Glu Ser Asp Ala Phe Gly Glu Ile Glu Val Asp Ser Ala Lys Tyr Tyr
35      40      45
ggt gcc caa act gcc aga tcc aag cat aac ttc aag atc ggt ggt gaa      192
Gly Ala Gln Thr Ala Arg Ser Lys His Asn Phe Lys Ile Gly Gly Glu
50      55      60
gcc gca aga atg cca att ccg gtt gtg aga gca ttt ggt att tta aaa      240
Ala Ala Arg Met Pro Ile Pro Val Val Arg Ala Phe Gly Ile Leu Lys
65      70      75      80
aaa tct gct gct att gtg aac gaa ggt tta gga gct tta gat cct aaa      288
Lys Ser Ala Ala Ile Val Asn Glu Gly Leu Gly Ala Leu Asp Pro Lys
85      90      95
tta tcc aag gct atc caa caa gct gct act gaa gtt gcg gaa ggt aaa      336
Leu Ser Lys Ala Ile Gln Gln Ala Ala Thr Glu Val Ala Glu Gly Lys
100      105      110
ttg gat gac cac ttc cca ttg gtt gtg ttc caa act ggt tca ggt act      384
Leu Asp Asp His Phe Pro Leu Val Val Phe Gln Thr Gly Ser Gly Thr

```


PF59083SeqList PF59083.txt

caa	tct	aac	atg	aat	gct	aac	gaa	gtt	att	tcc	aac	aga	gcc	att	gaa	432
Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ser	Asn	Arg	Ala	Ile	Glu	
130						135					140					
atc	tta	ggt	ggt	gaa	ttg	ggt	tcc	aag	aag	cca	ggt	cat	cca	aac	gat	480
Ile	Leu	Gly	Gly	Glu	Leu	Gly	Ser	Lys	Lys	Pro	Val	His	Pro	Asn	Asp	
145					150					155					160	
cac	tgt	aac	atg	tct	caa	tca	tct	aat	gat	act	ttc	cca	aca	gtc	atg	528
His	Cys	Asn	Met	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val	Met	
				165					170					175		
cac	att	gct	gct	act	gaa	att	tct	aac	tct	ttg	att	ccg	gag	tta		576
His	Ile	Ala	Ala	Ala	Thr	Glu	Ile	Ser	Asn	Ser	Leu	Ile	Pro	Glu	Leu	
				180					185				190			
acc	aag	tta	cgt	gat	gcg	tta	caa	gct	aag	tct	gat	gaa	ttc	aag	gat	624
Thr	Lys	Leu	Arg	Asp	Ala	Leu	Gln	Ala	Lys	Ser	Asp	Glu	Phe	Lys	Asp	
		195					200					205				
atc	att	aag	att	ggt	aga	act	cat	tta	caa	gat	gct	act	cct	ttg	act	672
Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	Leu	Thr	
210					215					220						
tta	ggt	caa	gaa	ttt	tct	ggt	tac	gtt	caa	caa	tta	acc	aac	ggt	att	720
Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	Gln	Gln	Leu	Thr	Asn	Gly	Ile	
225					230				235						240	
gaa	aga	att	gaa	aag	act	tta	cca	aac	ttg	caa	ttc	tta	gct	caa	ggt	768
Glu	Arg	Ile	Glu	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Phe	Leu	Ala	Gln	Gly	
				245					250					255		
ggt	act	gct	gtt	ggt	act	ggt	tta	aac	acc	gtc	aaa	ggt	ttt	gac	tct	816
Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Val	Lys	Gly	Phe	Asp	Ser	
				260					265					270		
aag	att	gct	gaa	gaa	gtc	tct	aag	ttg	act	tct	att	cct	ttc	aag	act	864
Lys	Ile	Ala	Glu	Glu	Val	Ser	Lys	Leu	Thr	Ser	Ile	Pro	Phe	Lys	Thr	
		275					280					285				
gct	cct	aac	aag	ttc	gaa	gcc	tta	gct	gct	cat	gat	gcc	gtt	gtt	gaa	912
Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Val	Val	Glu	
290					295					300						
gct	tca	ggt	gcc	tta	aac	ggt	gct	gtt	tct	tta	ttc	aag	att	gcc		960
Ala	Ser	Gly	Ala	Leu	Asn	Thr	Val	Ala	Val	Ser	Leu	Phe	Lys	Ile	Ala	
305					310				315						320	
aac	gat	atc	aga	tac	ttg	ggt	tcc	ggt	cca	aga	tgt	ggt	tac	ggt	gaa	1008
Asn	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Tyr	Gly	Glu	
				325					330					335		
tta	tcc	ttg	cca	gaa	aac	gaa	cca	ggc	tcg	tca	att	atg	cct	ggt	aag	1056
Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	
				340				345					350			
gtt	aac	cca	acc	caa	aat	gaa	gcc	tta	aca	atg	gtc	gct	acc	caa	gtc	1104
Val	Asn	Pro	Thr	Gln	Asn	Glu	Ala	Leu	Thr	Met	Val	Ala	Thr	Gln	Val	
		355					360					365				
ttc	ggt	aac	cac	tct	gca	atc	act	ttt	gct	ggt	gca	tct	ggt	caa	ttc	1152
Phe	Gly	Asn	His	Ser	Ala	Ile	Thr	Phe	Ala	Gly	Ala	Ser	Gly	Gln	Phe	
370					375					380						
gaa	ttg	aat	gtc	ttc	aag	cct	gtc	atg	att	tct	aac	ttg	ttg	tct	tca	1200
Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Met	Ile	Ser	Asn	Leu	Leu	Ser	Ser	
385					390					395				400		
att	aga	tta	att	gct	gac	ggt	tct	gct	tct	ttc	aga	gag	cat	tgt	gtt	1248
Ile	Arg	Leu	Ile	Ala	Asp	Gly	Ser	Ala	Ser	Phe	Arg	Glu	His	Cys	Val	
				405					410					415		
gta	ggt	att	act	gcc	aat	gta	gac	aaa	atc	gag	aaa	act	tta	cac	gaa	1296
Val	Gly	Ile	Thr	Ala	Asn	Val	Asp	Lys	Ile	Glu	Lys	Thr	Leu	His	Glu	
				420				425					430			
tct	tta	atg	ttg	gtt	act	gct	tta	aac	cca	aag	att	ggt	tat	gat	gct	1344
Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	Asp	Ala	
		435					440					445				
gct	tca	aag	act	gcc	aag	aat	gct	cac	aag	aag	ggt	tta	act	ttg	aaa	1392
Ala	Ser	Lys	Thr	Ala	Lys	Asn	Ala	His	Lys	Lys	Gly	Leu	Thr	Leu	Lys	
450					455					460						
gaa	tct	gct	ttg	gaa	ttg	ggt	gtt	tta	aat	gaa	caa	gaa	ttc	gac	gaa	1440
Glu	Ser	Ala	Leu	Glu	Leu	Gly	Val	Leu	Asn	Glu	Gln	Glu	Phe	Asp	Glu	
465					470					475					480	
tggt	gtc	aga	cca	gaa	aag	atg	att	ggt	cca	aag	gat	tag				1479
Trp	Val	Arg	Pro	Glu	Lys	Met	Ile	Gly	Pro	Lys	Asp					

<210> 9642
<211> 492
<212> PRT
<213> Debaryomyces hansenii CBS767

<400> 9642

```

Met Leu Arg Leu Thr Ser Lys Tyr Thr Pro Val Ala Arg Ser Ile Gln
1      5      10      15
Leu Arg Ser Leu Ser Ser Thr Ser Ala Leu Leu Ser Ser Thr Arg Thr
      20      25      30
Glu Ser Asp Ala Phe Gly Glu Ile Glu Val Asp Ser Ala Lys Tyr Tyr
      35      40      45
Gly Ala Gln Thr Ala Arg Ser Lys His Asn Phe Lys Ile Gly Gly Glu
      50      55      60
Ala Ala Arg Met Pro Ile Pro Val Val Arg Ala Phe Gly Ile Leu Lys
65      70      75      80
Lys Ser Ala Ala Ile Val Asn Glu Gly Leu Gly Ala Leu Asp Pro Lys
      85      90      95
Leu Ser Lys Ala Ile Gln Gln Ala Ala Thr Glu Val Ala Glu Gly Lys
      100      105      110
Leu Asp Asp His Phe Pro Leu Val Val Phe Gln Thr Gly Ser Gly Thr
      115      120      125
Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ser Asn Arg Ala Ile Glu
130      135      140
Ile Leu Gly Gly Glu Leu Gly Ser Lys Lys Pro Val His Pro Asn Asp
145      150      155      160
His Cys Asn Met Ser Gln Ser Ser Asn Thr Phe Pro Thr Val Met
      165      170      175
His Ile Ala Ala Ala Thr Glu Ile Ser Asn Ser Leu Ile Pro Glu Leu
      180      185      190
Thr Lys Leu Arg Asp Ala Leu Gln Ala Lys Ser Asp Glu Phe Lys Asp
195      200      205
Ile Ile Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr Pro Leu Thr
210      215      220
Leu Gly Gln Glu Phe Ser Gly Tyr Val Gln Gln Leu Thr Asn Gly Ile
225      230      235      240
Glu Arg Ile Glu Lys Thr Leu Pro Asn Leu Gln Phe Leu Ala Gln Gly
      245      250      255
Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Val Lys Gly Phe Asp Ser
260      265      270
Lys Ile Ala Glu Glu Val Ser Lys Leu Thr Ser Ile Pro Phe Lys Thr
275      280      285
Ala Pro Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Val Val Glu
290      295      300
Ala Ser Gly Ala Leu Asn Thr Val Ala Val Ser Leu Phe Lys Ile Ala
305      310      315      320
Asn Asp Ile Arg Tyr Leu Gly Ser Gly Pro Arg Cys Gly Tyr Gly Glu
      325      330      335
Leu Ser Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys
340      345      350
Val Asn Pro Thr Gln Asn Glu Ala Leu Thr Met Val Ala Thr Gln Val
355      360      365
Phe Gly Asn His Ser Ala Ile Thr Phe Ala Gly Ala Ser Gly Gln Phe
370      375      380
Glu Leu Asn Val Phe Lys Pro Val Met Ile Ser Asn Leu Leu Ser Ser
385      390      395      400
Ile Arg Leu Ile Ala Asp Gly Ser Ala Ser Phe Arg Glu His Cys Val
405      410      415
Val Gly Ile Thr Ala Asn Val Asp Lys Ile Glu Lys Thr Leu His Glu
420      425      430
Ser Leu Met Leu Val Thr Ala Leu Asn Pro Lys Ile Gly Tyr Asp Ala
435      440      445
Ala Ser Lys Thr Ala Lys Asn Ala His Lys Lys Gly Leu Thr Leu Lys
450      455      460
Glu Ser Ala Leu Glu Leu Gly Val Leu Asn Glu Gln Glu Phe Asp Glu
465      470      475      480
Trp Val Arg Pro Glu Lys Met Ile Gly Pro Lys Asp

```

<210> 9643
<211> 1404
<212> DNA
<213> Debaryomyces hansenii CBS767

<220>
<221> CDS
<222> (1)..(1404)

```

<400> 9643
atg tca ggt aac aaa gct aac gaa agg gtc gaa agc gat gcg ttc gga      48
Met Ser Gly Asn Lys Ala Asn Glu Arg Val Glu Ser Asp Ala Phe Gly
  1      5      10      15
gaa atc tcc gtt cca aac gat aag tat tgg ggt gcc caa agt caa aga      96
Glu Ile Ser Val Pro Asn Asp Lys Tyr Trp Gly Ala Gln Ser Gln Arg
      20      25      30
tcg tta ggt aat ttt gat atc ggt gat att aga atg cca gaa tcc att      144
Ser Leu Gly Asn Phe Asp Ile Gly Asp Ile Arg Met Pro Glu Ser Ile
      35      40      45
gtt aaa tca ttt ggt att tta aag aag gct gct gcc att gtt aat gag      192
Val Lys Ser Phe Gly Ile Leu Lys Lys Ala Ala Ala Ile Val Asn Glu
      50      55      60
gaa atc ggt gcg tta gac cct ctg tta gct aag gct atc aaa gaa gct      240
Glu Ile Gly Ala Leu Asp Pro Leu Leu Ala Lys Ala Ile Lys Glu Ala
      65      70      75      80
gca act gaa gtt gcg gaa ggt aaa ttg acg gaa cat ttc cca tta gta      288
Ala Thr Glu Val Ala Glu Gly Lys Leu Thr Glu His Phe Pro Leu Val
      85      90      95
gtc tac cag aca gga tcc ggt act caa tca aac atg aat gcc aac gag      336
Val Tyr Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu
      100      105      110
gtt att tcg aac aga gca atc gag att tta ggc ggt gaa atg ggt tca      384
Val Ile Ser Asn Arg Ala Ile Glu Ile Leu Gly Gly Glu Met Gly Ser
      115      120      125
aag tcc cct gtt cat cca aat gat cac tgt aat atg tcc caa tct tca      432
Lys Ser Pro Val His Pro Asn Asp His Cys Asn Met Ser Gln Ser Ser
      130      135      140
aat gat act ttc cca aca gtt atg cat att gca gcc gtt act gag atc      480
Asn Asp Thr Phe Pro Thr Val Met His Ile Ala Ala Val Thr Glu Ile
      145      150      155      160
agc aac aag tta att cct tct tta aca cag ctt cgt gat gca ttt gat      528
Ser Asn Lys Leu Ile Pro Ser Leu Thr Gln Leu Arg Asp Ala Phe Asp
      165      170      175
gcc aag gca aaa gaa ttc gaa aag atc att aaa atc ggt aga act cat      576
Ala Lys Ala Lys Glu Phe Glu Lys Ile Ile Lys Ile Gly Arg Thr His
      180      185      190
ttg caa gat gct act cca tta act ttg ggt caa gaa ttc tca ggt tac      624
Leu Gln Asp Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr
      195      200      205
gtt caa caa tta agt ttt ggt att gaa cgt att caa caa acc ctt cca      672
Val Gln Gln Leu Ser Phe Gly Ile Glu Arg Ile Gln Gln Thr Leu Pro
      210      215      220
aga tta tca tac tta gct caa ggt ggt act gct gtt ggt act ggt ttg      720
Arg Leu Ser Tyr Leu Ala Gln Gly Gly Thr Ala Val Gly Thr Gly Leu
      225      230      235      240
aac act tca aag ggt ttt gat gtt aag att gcg aaa gag gtt tct aat      768
Asn Thr Ser Lys Gly Phe Asp Val Lys Ile Ala Lys Glu Val Ser Asn
      245      250      255
att act ggg ttg aaa ttc caa act gct cca aat aaa ttc gaa gcc tta      816
Ile Thr Gly Leu Lys Phe Gln Thr Ala Pro Asn Lys Phe Glu Ala Leu
      260      265      270
gct gca cat gat gcc ttt gtt gaa gct tct ggt gcc tta aat aca tta      864
Ala Ala His Asp Ala Phe Val Glu Ala Ser Gly Ala Leu Asn Thr Leu
      275      280      285      290
gct gta tct ctt ttc aag att gct aat gat att aga tac tta ggt tct      912
Ala Val Ser Leu Phe Lys Ile Ala Asn Asp Ile Arg Tyr Leu Gly Ser
      290      295      300

```

PF59083SeqList PF59083.txt

ggt	cca	aga	tgt	gga	tac	ggc	gaa	tta	tcc	ctt	cca	gaa	aat	gaa	cca	960
Gly	Pro	Arg	Cys	Gly	Tyr	Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	
305					310					315					320	
ggt	tcc	tcc	atc	atg	cca	ggt	aag	ggt	aac	cct	acc	caa	tgt	gaa	gct	1008
Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	
				325					330					335		
atg	acc	atg	ggt	tgt	gcg	caa	ggt	atg	ggt	aac	cat	act	act	atc	act	1056
Met	Thr	Met	Val	Cys	Ala	Gln	Val	Met	Gly	Asn	His	Thr	Thr	Ile	Thr	
				340					345					350		
ttt	tca	ggt	gca	tct	ggt	caa	ttt	gaa	tta	aat	ggt	ttc	aag	cct	gtc	1104
Phe	Ser	Gly	Ala	Ser	Gly	Gln	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	
		355					360					365				
atg	gcc	agc	aac	tta	ttg	tct	tcg	att	aga	tta	att	ggt	gat	gta	tgt	1152
Met	Ala	Ser	Asn	Leu	Leu	Ser	Ser	Ile	Arg	Leu	Ile	Gly	Asp	Val	Cys	
	370					375					380					
aag	tca	ttc	aga	atc	cac	tgt	ggt	gaa	ggt	att	ggt	gcc	aat	gaa	gaa	1200
Lys	Ser	Phe	Arg	Ile	His	Cys	Val	Glu	Gly	Ile	Val	Ala	Asn	Glu	Glu	
385					390					395					400	
aag	att	tca	aaa	gtc	ttg	aat	gag	tcc	tta	atg	ttg	gtc	aca	gcc	ttg	1248
Lys	Ile	Ser	Lys	Val	Leu	Asn	Glu	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	
				405					410					415		
aac	cca	aag	att	ggt	tac	gac	aat	gct	tcc	aag	gtc	gcc	aaa	aat	gcc	1296
Asn	Pro	Lys	Ile	Gly	Tyr	Asp	Asn	Ala	Ser	Lys	Val	Ala	Lys	Asn	Ala	
				420					425					430		
cac	aaa	aag	gga	ctc	acc	tta	aag	caa	tcc	tgt	tta	gat	tta	aac	atg	1344
His	Lys	Lys	Gly	Leu	Thr	Leu	Lys	Gln	Ser	Cys	Leu	Asp	Leu	Asn	Met	
		435					440					445				
ttg	tcc	gaa	gaa	gag	ttc	gac	caa	tggt	gtc	aga	cca	gaa	aat	atg	ctt	1392
Leu	Ser	Glu	Glu	Glu	Phe	Asp	Gln	Trp	Val	Arg	Pro	Glu	Asn	Met	Leu	
	450					455					460					
ggt	cca	aaa	taa													1404
Gly	Pro	Lys														
465																

<210> 9644

<211> 467

<212> PRT

<213> Debaryomyces hansenii CBS767

<400> 9644

Met	Ser	Gly	Asn	Lys	Ala	Asn	Glu	Arg	Val	Glu	Ser	Asp	Ala	Phe	Gly	
1				5					10					15		
Glu	Ile	Ser	Val	Pro	Asn	Asp	Lys	Tyr	Trp	Gly	Ala	Gln	Ser	Gln	Arg	
			20					25					30			
Ser	Leu	Gly	Asn	Phe	Asp	Ile	Gly	Asp	Ile	Arg	Met	Pro	Glu	Ser	Ile	
		35					40					45				
Val	Lys	Ser	Phe	Gly	Ile	Leu	Lys	Lys	Ala	Ala	Ala	Ile	Val	Asn	Glu	
	50					55					60					
Glu	Ile	Gly	Ala	Leu	Asp	Pro	Leu	Leu	Ala	Lys	Ala	Ile	Lys	Glu	Ala	
65					70					75					80	
Ala	Thr	Glu	Val	Ala	Glu	Gly	Lys	Leu	Thr	Glu	His	Phe	Pro	Leu	Val	
				85					90					95		
Val	Tyr	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	
			100					105					110			
Val	Ile	Ser	Asn	Arg	Ala	Ile	Glu	Ile	Leu	Gly	Gly	Glu	Met	Gly	Ser	
		115					120					125				
Lys	Ser	Pro	Val	His	Pro	Asn	Asp	His	Cys	Asn	Met	Ser	Gln	Ser	Ser	
	130					135					140					
Asn	Asp	Thr	Phe	Pro	Thr	Val	Met	His	Ile	Ala	Ala	Val	Thr	Glu	Ile	
145					150					155					160	
Ser	Asn	Lys	Leu	Ile	Pro	Ser	Leu	Thr	Gln	Leu	Arg	Asp	Ala	Phe	Asp	
			165						170					175		
Ala	Lys	Ala	Lys	Glu	Phe	Glu	Lys	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	
			180					185					190			
Leu	Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	
		195					200					205				
Val	Gln	Gln	Leu	Ser	Phe	Gly	Ile	Glu	Arg	Ile	Gln	Gln	Thr	Leu	Pro	
	210					215					220					
Arg	Leu	Ser	Tyr	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	

PF59083SeqList PF59083.txt

225 230 235 240
 Asn Thr Ser Lys Gly Phe Asp Val Lys Ile Ala Lys Glu Val Ser Asn
 Ile Thr Gly Leu Lys Phe Gln Thr Ala Pro Asn Lys Phe Glu Ala Leu
 Ala Ala His Asp Ala Phe Val Glu Ala Ser Gly Ala Leu Asn Thr Leu
 Ala Val Ser Leu Phe Lys Ile Ala Asn Asp Ile Arg Tyr Leu Gly Ser
 Gly Pro Arg Cys Gly Tyr Gly Glu Leu Ser Leu Pro Glu Asn Glu Pro
 Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala
 Met Thr Met Val Cys Ala Gln Val Met Gly Asn His Thr Thr Ile Thr
 Phe Ser Gly Ala Ser Gly Gln Phe Glu Leu Asn Val Phe Lys Pro Val
 Met Ala Ser Asn Leu Leu Ser Ser Ile Arg Leu Ile Gly Asp Val Cys
 Lys Ser Phe Arg Ile His Cys Val Glu Gly Ile Val Ala Asn Glu Glu
 Lys Ile Ser Lys Val Leu Asn Glu Ser Leu Met Leu Val Thr Ala Leu
 Asn Pro Lys Ile Gly Tyr Asp Asn Ala Ser Lys Val Ala Lys Asn Ala
 His Lys Lys Gly Leu Thr Leu Lys Gln Ser Cys Leu Asp Leu Asn Met
 Leu Ser Glu Glu Glu Phe Asp Gln Trp Val Arg Pro Glu Asn Met Leu
 Gly Pro Lys
 465

<210> 9645

<211> 1470

<212> DNA

<213> Yarrowia lipolytica CLIB122

<220>

<221> CDS

<222> (1)..(1470)

<400> 9645

atg ctc cga aca gtc cga cta gcc aag gtc tct cga cct ctc acc ctt	48
Met Leu Arg Thr Val Arg Leu Ala Lys Val Ser Arg Pro Leu Thr Leu	
1 5 10 15	
cga acc ttc tcc acc acc ccc gcc ttc ctc ggc aag cga gtc gag aag	96
Arg Thr Phe Ser Thr Thr Pro Ala Phe Leu Gly Lys Arg Val Glu Lys	
20 25 30	
gac gcc ttt gga gac att gat gtc gac gac tcc cac tac tgg ggc gcc	144
Asp Ala Phe Gly Asp Ile Asp Val Asp Asp Ser His Tyr Trp Gly Ala	
35 40 45	
cag acc cag cga tct ctg cag aac ttt gac att ggc gga gag aag gcc	192
Gln Thr Gln Arg Ser Leu Gln Asn Phe Asp Ile Gly Gly Glu Lys Ala	
50 55 60	
aag atg ccc gag ccc att gtc aag gcc ttt ggc atc ctc aag aag gcc	240
Lys Met Pro Glu Pro Ile Val Lys Ala Phe Gly Ile Leu Lys Lys Ala	
65 70 75 80	
gct gcc acc gtc aac atg aag tac ggt ctg gac ccc aag gtt ggc gag	288
Ala Ala Thr Val Asn Met Lys Tyr Gly Leu Asp Pro Lys Val Gly Glu	
85 90 95	
gcc atc cag aag gct gcc cag gag gtc att gac ggc aag ctt acc aag	336
Ala Ile Gln Lys Ala Ala Gln Glu Val Ile Asp Gly Lys Leu Thr Lys	
100 105 110	
gat ttc ccc ctg gtt gtc ttc cag acc ggt tcc ggt acc cag tcc aac	384
Asp Phe Pro Leu Val Val Phe Gln Thr Gly Ser Gly Thr Gln Ser Asn	
115 120 125	
atg aac tcc aac gag gtc atc tcc aac cga gcc att gag atg ctc ggc	432
Met Asn Ser Asn Glu Val Ile Ser Asn Arg Ala Ile Glu Met Leu Gly	
130 135 140	

PF59083SeqList PF59083.txt

gga	aag	ctc	ggc	tcc	aag	tcc	ccc	gtg	cac	ccc	aac	gac	cac	gtc	aac	480
Gly	Lys	Leu	Gly	Ser	Lys	Ser	Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	
145					150					155					160	
atg	tcc	cag	tct	tcc	aac	gac	acc	ttc	ccc	acc	gtc	atg	cac	att	gcc	528
Met	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val	Met	His	Ile	Ala	
				165				170						175		
gcc	gtc	atg	gag	atc	acc	aag	aac	ctg	atc	ccc	cag	ctg	cag	ctg	ctc	576
Ala	Val	Met	Glu	Ile	Thr	Lys	Asn	Leu	Ile	Pro	Gln	Leu	Gln	Leu	Leu	
			180					185					190			
gag	gag	tcc	ctc	gcc	aag	aag	tct	gca	gag	ttc	gac	aag	att	atc	aag	624
Glu	Glu	Ser	Leu	Ala	Lys	Lys	Ser	Ala	Glu	Phe	Asp	Lys	Ile	Ile	Lys	
		195					200					205				
att	ggc	cga	acc	cat	ctg	cag	gac	gct	acc	ccc	ctg	acc	ctc	ggc	cag	672
Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	
	210					215					220					
gag	ttc	tcc	ggc	tac	gtg	acc	cag	gtc	aag	tac	ggc	att	gag	cga	gtc	720
Glu	Phe	Ser	Gly	Tyr	Val	Thr	Gln	Val	Lys	Tyr	Gly	Ile	Glu	Arg	Val	
225				230				235							240	
aag	gac	gtt	ctt	ccc	cga	ctc	cga	cac	ctt	gcc	cag	gga	gga	acc	gcc	768
Lys	Asp	Val	Leu	Pro	Arg	Leu	Arg	His	Leu	Ala	Gln	Gly	Gly	Thr	Ala	
				245				250						255		
gtc	ggc	acc	ggc	ctt	aac	acc	aag	aag	ggc	ttc	gac	act	gcc	gtc	gcc	816
Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	Asp	Thr	Ala	Val	Ala	
			260					265					270			
gct	gag	gtc	tcc	aag	atc	acc	ggc	gag	gag	ttc	tcc	acc	gcc	ccc	aac	864
Ala	Glu	Val	Ser	Lys	Ile	Thr	Gly	Glu	Glu	Phe	Ser	Thr	Ala	Pro	Asn	
		275					280					285				
aag	ttt	gag	gct	ctt	gcc	gcc	cac	gac	gcc	att	gtc	gag	gcc	tcc	ggt	912
Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Ile	Val	Glu	Ala	Ser	Gly	
	290				295						300					
gcc	ctc	aac	acc	ggt	gcc	gtg	tct	ctg	ttc	aag	att	gcc	aac	gat	atc	960
Ala	Leu	Asn	Thr	Val	Ala	Val	Ser	Leu	Phe	Lys	Ile	Ala	Asn	Asp	Ile	
305				310					315						320	
cga	tac	ctc	ggc	tcc	ggc	ccc	cga	tgt	ggc	tac	ggc	gag	ctt	gct	ctc	1008
Arg	Tyr	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Tyr	Gly	Glu	Leu	Ala	Leu	
				325				330						335		
ccc	gag	aac	gag	ccc	ggc	tct	tcc	atc	atg	ccc	ggc	aag	gtc	aac	ccc	1056
Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	
			340					345					350			
acc	cag	aac	gag	gct	ctg	acc	atg	gtc	tgc	tgc	cag	ggt	ttc	gga	aac	1104
Thr	Gln	Asn	Glu	Ala	Leu	Thr	Met	Val	Cys	Cys	Gln	Val	Phe	Gly	Asn	
		355					360					365				
aac	tcc	act	atc	acc	tac	gcc	ggc	gcc	tcc	ggc	cag	ttc	gag	ctg	aac	1152
Asn	Ser	Thr	Ile	Thr	Tyr	Ala	Gly	Ala	Ser	Gly	Gln	Phe	Glu	Leu	Asn	
	370					375					380					
gtc	ttc	aag	ccc	gtc	atg	atc	gcc	aac	ctg	ctc	gag	tcc	atc	cga	ctc	1200
Val	Phe	Lys	Pro	Val	Met	Ile	Ala	Asn	Leu	Leu	Glu	Ser	Ile	Arg	Leu	
385				390					395						400	
att	gct	gat	gga	tct	cga	tct	ttc	cga	atc	cac	tgt	gtc	gac	ggc	att	1248
Ile	Ala	Asp	Gly	Ser	Arg	Ser	Phe	Arg	Ile	His	Cys	Val	Asp	Gly	Ile	
				405				410						415		
gtc	gcc	aac	gag	aag	cga	atc	tcc	cag	ctc	atg	aac	gag	tct	ctc	atg	1296
Val	Ala	Asn	Glu	Lys	Arg	Ile	Ser	Gln	Leu	Met	Asn	Glu	Ser	Leu	Met	
			420					425					430			
ctg	gtc	acc	gcc	ctc	aac	ccc	aag	att	ggc	tac	gac	atg	gcc	tcc	aag	1344
Leu	Val	Thr	Ala	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	Asp	Met	Ala	Ser	Lys	
		435				440						445				
gtc	gcc	aag	aac	gcc	cac	aag	aag	gga	atc	act	ctt	aag	gag	tct	gcc	1392
Val	Ala	Lys	Asn	Ala	His	Lys	Lys	Gly	Ile	Thr	Leu	Lys	Glu	Ser	Ala	
	450					455					460					
ctc	gag	ctc	ggc	gct	ctc	acc	tct	gag	gag	ttt	gac	cag	tgg	gtc	cga	1440
Leu	Glu	Leu	Gly	Ala	Leu	Thr	Ser	Glu	Glu	Phe	Asp	Gln	Trp	Val	Arg	
465				470						475					480	
ccc	gag	aag	atg	att	ggc	ccc	tct	gac	taa							1470
Pro	Glu	Lys	Met	Ile	Gly	Pro	Ser	Asp								
				485												

<210> 9646

<211> 489

PF59083SeqList PF59083.txt

<212> PRT

<213> Yarrowia lipolytica CLIB122

<400> 9646

```

Met Leu Arg Thr Val Arg Leu Ala Lys Val Ser Arg Pro Leu Thr Leu
1      5      10      15
Arg Thr Phe Ser Thr Thr Pro Ala Phe Leu Gly Lys Arg Val Glu Lys
      20      25      30
Asp Ala Phe Gly Asp Ile Asp Val Asp Asp Ser His Tyr Trp Gly Ala
      35      40      45
Gln Thr Gln Arg Ser Leu Gln Asn Phe Asp Ile Gly Glu Lys Ala
      50      55      60
Lys Met Pro Glu Pro Ile Val Lys Ala Phe Gly Ile Leu Lys Lys Ala
65      70      75      80
Ala Ala Thr Val Asn Met Lys Tyr Gly Leu Asp Pro Lys Val Gly Glu
      85      90      95
Ala Ile Gln Lys Ala Ala Gln Glu Val Ile Asp Gly Lys Leu Thr Lys
      100      105      110
Asp Phe Pro Leu Val Val Phe Gln Thr Gly Ser Gly Thr Gln Ser Asn
      115      120      125
Met Asn Ser Asn Glu Val Ile Ser Asn Arg Ala Ile Glu Met Leu Gly
130      135      140
Gly Lys Leu Gly Ser Lys Ser Pro Val His Pro Asn Asp His Val Asn
145      150      155      160
Met Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr Val Met His Ile Ala
      165      170      175
Ala Val Met Glu Ile Thr Lys Asn Leu Ile Pro Gln Leu Gln Leu Leu
      180      185      190
Glu Glu Ser Leu Ala Lys Lys Ser Ala Glu Phe Asp Lys Ile Ile Lys
195      200      205
Ile Gly Arg Thr His Leu Gln Asp Ala Thr Pro Leu Thr Leu Gly Gln
210      215      220
Glu Phe Ser Gly Tyr Val Thr Gln Val Lys Tyr Gly Ile Glu Arg Val
225      230      235      240
Lys Asp Val Leu Pro Arg Leu Arg His Leu Ala Gln Gly Gly Thr Ala
      245      250      255
Val Gly Thr Gly Leu Asn Thr Lys Lys Gly Phe Asp Thr Ala Val Ala
      260      265      270
Ala Glu Val Ser Lys Ile Thr Gly Glu Glu Phe Ser Thr Ala Pro Asn
275      280      285
Lys Phe Glu Ala Leu Ala Ala His Asp Ala Ile Val Glu Ala Ser Gly
290      295      300
Ala Leu Asn Thr Val Ala Val Ser Leu Phe Lys Ile Ala Asn Asp Ile
305      310      315      320
Arg Tyr Leu Gly Ser Gly Pro Arg Cys Gly Tyr Gly Glu Leu Ala Leu
      325      330      335
Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro
      340      345      350
Thr Gln Asn Glu Ala Leu Thr Met Val Cys Cys Gln Val Phe Gly Asn
355      360      365
Asn Ser Thr Ile Thr Tyr Ala Gly Ala Ser Gly Gln Phe Glu Leu Asn
370      375      380
Val Phe Lys Pro Val Met Ile Ala Asn Leu Leu Glu Ser Ile Arg Leu
385      390      395      400
Ile Ala Asp Gly Ser Arg Ser Phe Arg Ile His Cys Val Asp Gly Ile
      405      410      415
Val Ala Asn Glu Lys Arg Ile Ser Gln Leu Met Asn Glu Ser Leu Met
      420      425      430
Leu Val Thr Ala Leu Asn Pro Lys Ile Gly Tyr Asp Met Ala Ser Lys
435      440      445
Val Ala Lys Asn Ala His Lys Lys Gly Ile Thr Leu Lys Glu Ser Ala
450      455      460
Leu Glu Leu Gly Ala Leu Thr Ser Glu Glu Phe Asp Gln Trp Val Arg
465      470      475      480
Pro Glu Lys Met Ile Gly Pro Ser Asp
      485

```

<210> 9647

<211> 1635

PF59083SeqList PF59083.txt

<212> DNA

<213> Aspergillus nidulans FGSC A4

<220>

<221> CDS

<222> (1)..(1635)

<400> 9647

atg gct tcc aga acc gcg gtg cgc tcg atg agc tct ttg aca cat gct	48
Met Ala Ser Arg Thr Ala Val Arg Ser Met Ser Ser Leu Thr His Ala	
1 5 10 15	
act gcc aaa gcc tcc aac acc tcc gca ttg gcc cgg gcc gcg acg ttg	96
Thr Ala Lys Ala Ser Asn Thr Ser Ala Leu Ala Arg Ala Ala Thr Leu	
20 25 30	
gct gct cgc tcc ccc gcc tcg ttc act agc cga cgc gcg ttg agc tcc	144
Ala Ala Arg Ser Pro Ala Ser Phe Thr Ser Arg Arg Ala Leu Ser Ser	
35 40 45	
aat agc cga cca gtt aca cag ttc ccc cgc ctt cag tcc ttc cag tct	192
Asn Ser Arg Pro Val Thr Gln Phe Pro Arg Leu Gln Ser Phe Gln Ser	
50 55 60	
ttc tcc agc aaa aga tcc ttc agc tca acc gtc gca atg gct tcc gag	240
Phe Ser Ser Lys Arg Ser Phe Ser Ser Thr Val Ala Met Ala Ser Glu	
65 70 75 80	
act cgc act gaa agt gat gct ttt ggc gag atc cag gtc ccc gcc gac	288
Thr Arg Thr Glu Ser Asp Ala Phe Gly Glu Ile Gln Val Pro Ala Asp	
85 90 95	
aag tac tgg ggc gcg cag act cag cgt tca ctg ggc aat ttc gac atc	336
Lys Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Gly Asn Phe Asp Ile	
100 105 110	
aac cag ccc cag gac gcg atg ccc gat gct gtt gtc aag gct ttt ggt	384
Asn Gln Pro Gln Asp Arg Met Pro Asp Ala Val Val Lys Ala Phe Gly	
115 120 125	
att ctc aag ggt gct gct gct acc gtc aac atg aag ttt ggc ctt gat	432
Ile Leu Lys Gly Ala Ala Ala Thr Val Asn Met Lys Phe Gly Leu Asp	
130 135 140	
ccc aag att ggt gag gct atc aag cag gct gcc gct gag gtc gcc gag	480
Pro Lys Ile Gly Glu Ala Ile Lys Gln Ala Ala Ala Glu Val Ala Glu	
145 150 155 160	
ggc aag ctc ctt gac cac ttc cct ctc gtc tgg cag acc ggt tcc	528
Gly Lys Leu Leu Asp His Phe Pro Leu Val Trp Gln Thr Gly Ser	
165 170 175	
ggc act cag tcc aac atg aac tcc aac gag gtt atc tcc aac cgt gcc	576
Gly Thr Gln Ser Asn Met Asn Ser Asn Glu Val Ile Ser Asn Arg Ala	
180 185 190	
att gag att ctc gga ggc aag atg ggc tcc aag aag ccc gtc cac ccc	624
Ile Glu Ile Leu Gly Gly Lys Met Gly Ser Lys Lys Pro Val His Pro	
195 200 205 210	
aac gac cac gtt aac atg tcc gct tcc tcc aat gac tct ttc cca acc	672
Asn Asp His Val Asn Met Ser Ala Ser Ser Asn Asp Ser Phe Pro Thr	
215 220 225	
gcc atg cac att gcc gcc gtt cta gag ctg gag aac act ctg ctt cct	720
Ala Met His Ile Ala Ala Val Leu Glu Leu Glu Asn Thr Leu Leu Pro	
230 235 240	
gct ctt acg agc ctt cgt aat gcc ctt cag aag aag gtg gac agc ttc	768
Ala Leu Thr Ser Leu Arg Asn Ala Leu Gln Lys Lys Val Asp Ser Phe	
245 250 255	
cag aac atc att aag atc ggc cgt acc cat ttg cag gat gcc act cct	816
Gln Asn Ile Ile Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr Pro	
260 265 270	
ctt acc ctt ggc cag gag ttc tcc gga tac gtt gcc cag ctc gac gcg	864
Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Val Ala Gln Leu Asp Arg	
275 280 285	
aac atc gag cgc gtc caa gcc tct ctg ccc cac ctg cgc tac ctt gct	912
Asn Ile Glu Arg Val Gln Ala Ser Leu Pro His Leu Arg Tyr Leu Ala	
290 295 300 305	
cag ggt ggt act gcc gtt ggt act ggt ctt aac acc ttc aag ggt ttc	960
Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Phe Lys Gly Phe	
310 315 320	
gac gag gcg att gcc gct gag gtg tcc aag atg act ggc acc gag ttc	1008

PF59083SeqList PF59083.txt

Asp	Glu	Ala	Ile	Ala	Ala	Glu	Val	Ser	Lys	Met	Thr	Gly	Thr	Glu	Phe	
				325					330					335		
aag	acc	gct	ccc	aac	aag	ttc	gag	gtt	ctt	gct	gct	cat	gat	gca	atc	1056
Lys	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Val	Leu	Ala	Ala	His	Asp	Ala	Ile	
			340					345					350			
gtc	gag	gcc	tcc	ggc	tcg	ctt	aac	acc	ctt	gcc	ggc	tcc	ctg	ttt	aag	1104
Val	Glu	Ala	Ser	Gly	Ser	Leu	Asn	Thr	Leu	Ala	Gly	Ser	Leu	Phe	Lys	
		355					360					365				
atc	gcc	cag	gac	atc	cgt	tac	ctc	gga	tcc	ggc	ccc	cgc	tgc	ggc	ctt	1152
Ile	Ala	Gln	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	
	370					375					380					
ggc	gag	ctc	atc	ctt	cct	gag	aac	gaa	cct	ggc	tct	tcc	atc	atg	cct	1200
Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
	385				390				395						400	
ggc	aag	gtc	aac	cct	acc	cag	tgc	gag	tcc	ttg	acc	atg	gtc	tgc	tct	1248
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ser	Leu	Thr	Met	Val	Cys	Ser	
			405					410						415		
caa	gtc	atg	ggc	aac	cac	gtc	gct	gct	acc	att	ggc	ggc	atg	aac	ggc	1296
Gln	Val	Met	Gly	Asn	His	Val	Ala	Ala	Thr	Ile	Gly	Gly	Met	Asn	Gly	
			420				425						430			
cag	ttc	gag	ctc	aat	gta	ttc	aag	cca	ctc	atg	atc	cgc	aac	ctt	ctt	1344
Gln	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Leu	Met	Ile	Arg	Asn	Leu	Leu	
		435				440						445				
cac	agt	gtg	cgc	att	ctc	gcc	gat	ggc	atg	aag	agc	ttt	gag	aag	aac	1392
His	Ser	Val	Arg	Ile	Leu	Ala	Asp	Gly	Met	Lys	Ser	Phe	Glu	Lys	Asn	
	450					455					460					
ctc	gtt	gtt	ggc	ctt	gag	gcc	aac	gag	tcc	aga	atc	agc	act	ctc	ctc	1440
Leu	Val	Val	Gly	Leu	Glu	Ala	Asn	Glu	Ser	Arg	Ile	Ser	Thr	Leu	Leu	
	465				470				475						480	
cac	gag	agt	ctg	atg	ctc	gtt	acc	tgc	ctc	aac	ccc	gtc	atc	ggc	tac	1488
His	Glu	Ser	Leu	Met	Leu	Val	Thr	Cys	Leu	Asn	Pro	Val	Ile	Gly	Tyr	
			485					490						495		
gac	atg	gct	tcc	aag	gtc	gcc	aag	aac	gcc	cac	aag	aag	ggc	atc	acc	1536
Asp	Met	Ala	Ser	Lys	Val	Ala	Lys	Asn	Ala	His	Lys	Lys	Gly	Ile	Thr	
			500				505						510			
ctc	aaa	gag	agt	gcc	atg	gag	ctc	aag	gct	ctt	agc	gag	gag	gac	ttt	1584
Leu	Lys	Glu	Ser	Ala	Met	Glu	Leu	Lys	Ala	Leu	Ser	Glu	Glu	Asp	Phe	
		515				520						525				
gac	aag	tat	gtc	cga	cca	gag	ctg	atg	ctg	agc	cct	aag	gag	aag	aaa	1632
Asp	Lys	Tyr	Val	Arg	Pro	Glu	Leu	Met	Leu	Ser	Pro	Lys	Glu	Lys	Lys	
	530					535					540					
tag																1635

<210> 9648

<211> 544

<212> PRT

<213> Aspergillus nidulans FGSC A4

<400> 9648

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

PF59083SeqList PF59083.txt

Pro Lys Ile Gly Glu Ala Ile Lys Gln Ala Ala Ala Glu Val Ala Glu
145 150 155 160
Gly Lys Leu Leu Asp His Phe Pro Leu Val Val Trp Gln Thr Gly Ser
165 170 175
Gly Thr Gln Ser Asn Met Asn Ser Asn Glu Val Ile Ser Asn Arg Ala
180 185 190
Ile Glu Ile Leu Gly Gly Lys Met Gly Ser Lys Lys Pro Val His Pro
195 200 205
Asn Asp His Val Asn Met Ser Ala Ser Ser Asn Asp Ser Phe Pro Thr
210 215 220
Ala Met His Ile Ala Ala Val Leu Glu Leu Glu Asn Thr Leu Leu Pro
225 230 235 240
Ala Leu Thr Ser Leu Arg Asn Ala Leu Gln Lys Lys Val Asp Ser Phe
245 250 255
Gln Asn Ile Ile Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr Pro
260 265 270
Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Val Ala Gln Leu Asp Arg
275 280 285
Asn Ile Glu Arg Val Gln Ala Ser Leu Pro His Leu Arg Tyr Leu Ala
290 295 300
Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Phe Lys Gly Phe
305 310 315 320
Asp Glu Ala Ile Ala Ala Glu Val Ser Lys Met Thr Gly Thr Glu Phe
325 330 335
Lys Thr Ala Pro Asn Lys Phe Glu Val Leu Ala Ala His Asp Ala Ile
340 345 350
Val Glu Ala Ser Gly Ser Leu Asn Thr Leu Ala Gly Ser Leu Phe Lys
355 360 365
Ile Ala Gln Asp Ile Arg Tyr Leu Gly Ser Gly Pro Arg Cys Gly Leu
370 375 380
Gly Glu Leu Ile Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro
385 390 395 400
Gly Lys Val Asn Pro Thr Gln Cys Glu Ser Leu Thr Met Val Cys Ser
405 410 415
Gln Val Met Gly Asn His Val Ala Ala Thr Ile Gly Gly Met Asn Gly
420 425 430
Gln Phe Glu Leu Asn Val Phe Lys Pro Leu Met Ile Arg Asn Leu Leu
435 440 445
His Ser Val Arg Ile Leu Ala Asp Gly Met Lys Ser Phe Glu Lys Asn
450 455 460
Leu Val Val Gly Leu Glu Ala Asn Glu Ser Arg Ile Ser Thr Leu Leu
465 470 475 480
His Glu Ser Leu Met Leu Val Thr Cys Leu Asn Pro Val Ile Gly Tyr
485 490 495
Asp Met Ala Ser Lys Val Ala Lys Asn Ala His Lys Lys Gly Ile Thr
500 505 510
Leu Lys Glu Ser Ala Met Glu Leu Lys Ala Leu Ser Glu Glu Asp Phe
515 520 525
Asp Lys Tyr Val Arg Pro Glu Leu Met Leu Ser Pro Lys Glu Lys Lys
530 535 540

<210> 9649

<211> 1389

<212> DNA

<213> Candida albicans SC5314

<220>

<221> CDS

<222> (1)..(1389)

<223> transl_table=12

<400> 9649

atg tca cgt att gaa tct gac gct ttt ggt gaa atc tca gtg ccg gct	48
Met Ser Arg Ile Glu Ser Asp Ala Phe Gly Glu Ile Ser Val Pro Ala	
1 5 10 15	
gat aaa tat tgg ggt gct caa acc cag aga tct ttg ggt aac ttt gag	96
Asp Lys Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Gly Asn Phe Glu	
20 25 30	
atc ggc gat att aaa atg cca att cca ata att aaa gct ttc ggg act	144

PF59083SeqList PF59083.txt																
Ile	Gly	Asp	Ile	Lys	Met	Pro	Ile	Pro	Ile	Ile	Lys	Ala	Phe	Gly	Thr	
ttg	aaa	aaa	gcc	gca	gct	atc	ggt	aat	gaa	aaa	atg	ggt	tcc	tta	gac	192
Leu	Lys	Lys	Ala	Ala	Ala	Ile	Val	Asn	Glu	Lys	Met	Gly	Ser	Leu	Asp	
cct	aaa	tta	tca	tct	gct	att	caa	gaa	gct	gct	tcc	gag	gta	att	gag	240
Pro	Lys	Leu	Ser	Ser	Ala	Ile	Gln	Glu	Ala	Ala	Ser	Glu	Val	Ile	Glu	
65	gga	aaa	ttc	aat	gat	aat	ttc	cca	ttg	gtg	ggt	tat	caa	act	ggt	288
Gly	Lys	Phe	Asn	Asp	Asn	Phe	Pro	Leu	Val	Val	Tyr	Gln	Thr	Gly	Ser	
gga	acc	caa	tcg	aac	atg	aat	gcc	aat	gag	gta	atc	tcc	aac	cgt	gca	336
Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ser	Asn	Arg	Ala	
att	gaa	ata	ttg	ggt	gga	gaa	aaa	ggt	tcc	aaa	aaa	cca	ggt	cac	cca	384
Ile	Glu	Ile	Leu	Gly	Gly	Glu	Lys	Gly	Ser	Lys	Lys	Pro	Val	His	Pro	
aat	gac	cat	tgt	aat	atg	tct	caa	tct	tct	aat	gat	act	ttc	cca	act	432
Asn	Asp	His	Cys	Asn	Met	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	
gtc	atg	cac	att	gct	gct	ggt	agt	gaa	ggt	gaa	cag	tta	ttg	cca		480
Val	Met	His	Ile	Ala	Ala	Val	Ser	Glu	Val	Glu	Gln	Gln	Leu	Leu	Pro	
145	aaa	ttg	acc	gct	ttg	aga	gat	gcc	ttt	gaa	gct	aaa	tca	aaa	gaa	528
Lys	Leu	Thr	Ala	Leu	Arg	Asp	Ala	Phe	Glu	Ala	Lys	Ser	Lys	Glu	Phe	
agt	gac	atc	att	aaa	att	ggt	aga	act	cat	ttg	caa	gat	gct	act	cca	576
Ser	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	
ttg	aca	ttg	ggt	caa	gag	ttt	tct	ggt	tac	ggt	caa	caa	ttg	act	ttt	624
Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	Gln	Gln	Leu	Thr	Phe	
gga	atc	gaa	aga	att	aag	ctg	act	ttg	cca	aga	tta	tca	aat	tta	gca	672
Gly	Ile	Glu	Arg	Ile	Lys	Ser	Thr	Leu	Pro	Arg	Leu	Ser	Asn	Leu	Ala	
210	caa	ggt	ggt	act	gct	gta	aca	ggt	tta	aac	acc	aaa	aag	ggg	ttt	720
Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	
225	gat	ggt	aaa	att	gct	gaa	gaa	ata	tcc	aat	tta	acc	ggt	ttg	caa	768
Asp	Val	Lys	Ile	Ala	Glu	Glu	Ile	Ser	Asn	Leu	Thr	Gly	Leu	Gln	Phe	
cac	act	gct	cca	aac	aag	ttt	gaa	gca	ttg	gct	gca	cat	gat	gcc	atc	816
His	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Ile	
ggt	gaa	aca	tct	ggt	gct	ttg	aat	act	ttg	gct	ggt	tca	tta	tac	aaa	864
Val	Glu	Thr	Ser	Gly	Ala	Leu	Asn	Thr	Leu	Ala	Val	Ser	Leu	Tyr	Lys	
att	gcc	aat	gat	atc	aga	tac	ttg	ggg	tcc	ggt	cca	aga	tgt	ggt	tac	912
Ile	Ala	Asn	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Tyr	
ggt	gaa	tta	tct	tta	cct	gaa	aat	gaa	cca	gga	agt	ctg	atc	atg	cct	960
Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
305	gga	aaa	ggt	aat	cca	acc	caa	tgt	gaa	gcc	atg	act	atg	gtc	tgt	1008
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Met	Thr	Met	Met	Val	Cys	
caa	gta	atg	ggt	aat	aat	act	aca	atc	acc	ttt	tca	gga	gct	ctg	ggt	1056
Gln	Val	Met	Gly	Asn	Asn	Thr	Thr	Ile	Thr	Phe	Ser	Gly	Ala	Ser	Gly	
caa	ttt	gaa	ttg	aat	gta	ttc	aag	cct	gtg	atg	gca	tat	aac	tta	tta	1104
Gln	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Met	Ala	Tyr	Asn	Leu	Leu	
aat	tct	att	aga	ttg	tta	ggt	gat	gct	tgt	caa	tca	ttt	aga	ttg	cat	1152
Asn	Ser	Ile	Arg	Leu	Leu	Gly	Asp	Ala	Cys	Gln	Ser	Phe	Arg	Leu	His	
tgt	ggt	gaa	agt	att	aaa	gcc	aac	aag	gaa	aag	att	gat	aag	gtg	ttg	1200
Cys	Val	Glu	Ser	Ile	Lys	Ala	Asn	Lys	Glu	Lys	Ile	Asp	Lys	Val	Leu	
385	aat	gaa	tct	ttg	atg	tta	ggt	act	gct	ttg	aac	cca	aaa	att	gga	1248
aat	gaa	tct	ttg	atg	tta	ggt	act	gct	ttg	aac	cca	aaa	att	gga	tat	

PF59083SeqList PF59083.txt

Asn	Glu	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	
				405					410					415		
gat	aac	gct	tcg	aag	gct	gct	aag	aat	gcc	cat	aaa	aaa	ggc	att	acc	1296
Asp	Asn	Ala	Ser	Lys	Ala	Ala	Lys	Asn	Ala	His	Lys	Lys	Gly	Ile	Thr	
			420					425					430			
tta	aag	gaa	tcc	tgt	ttg	gag	ttg	gaa	tta	tta	act	tca	gaa	gag	ttt	1344
Leu	Lys	Glu	Ser	Cys	Leu	Glu	Leu	Glu	Leu	Leu	Thr	Ser	Glu	Glu	Phe	
		435				440						445				
gac	gaa	tgg	gtc	aga	cca	gaa	aaa	atg	att	ggc	cca	aag	gat	tag		1389
Asp	Glu	Trp	Val	Arg	Pro	Glu	Lys	Met	Ile	Gly	Pro	Lys	Asp			
	450					455					460					

<210> 9650

<211> 462

<212> PRT

<213> Candida albicans SC5314

<400> 9650

Met	Ser	Arg	Ile	Glu	Ser	Asp	Ala	Phe	Gly	Glu	Ile	Ser	Val	Pro	Ala	
1				5					10					15		
Asp	Lys	Tyr	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Gly	Asn	Phe	Glu	
			20					25					30			
Ile	Gly	Asp	Ile	Lys	Met	Pro	Ile	Pro	Ile	Ile	Lys	Ala	Phe	Gly	Thr	
		35					40					45				
Leu	Lys	Lys	Ala	Ala	Ala	Ile	Val	Asn	Glu	Lys	Met	Gly	Ser	Leu	Asp	
	50					55					60					
Pro	Lys	Leu	Ser	Ser	Ala	Ile	Gln	Glu	Ala	Ala	Ser	Glu	Val	Ile	Glu	
65					70				75						80	
Gly	Lys	Phe	Asn	Asp	Asn	Phe	Pro	Leu	Val	Val	Tyr	Gln	Thr	Gly	Ser	
			85					90						95		
Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ser	Asn	Arg	Ala	
			100					105					110			
Ile	Glu	Ile	Leu	Gly	Gly	Glu	Lys	Gly	Ser	Lys	Lys	Pro	Val	His	Pro	
		115					120					125				
Asn	Asp	His	Cys	Asn	Met	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	
	130					135					140					
Val	Met	His	Ile	Ala	Ala	Val	Ser	Glu	Val	Glu	Gln	Gln	Leu	Leu	Pro	
145					150				155						160	
Lys	Leu	Thr	Ala	Leu	Arg	Asp	Ala	Phe	Glu	Ala	Lys	Ser	Lys	Glu	Phe	
			165					170						175		
Ser	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	
		180						185					190			
Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	Gln	Gln	Leu	Thr	Phe	
		195					200					205				
Gly	Ile	Glu	Arg	Ile	Lys	Ser	Thr	Leu	Pro	Arg	Leu	Ser	Asn	Leu	Ala	
	210					215					220					
Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	
225					230				235						240	
Asp	Val	Lys	Ile	Ala	Glu	Glu	Ile	Ser	Asn	Leu	Thr	Gly	Leu	Gln	Phe	
			245						250					255		
His	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Ile	
		260						265					270			
Val	Glu	Thr	Ser	Gly	Ala	Leu	Asn	Thr	Leu	Ala	Val	Ser	Leu	Tyr	Lys	
		275					280					285				
Ile	Ala	Asn	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Tyr	
	290					295					300					
Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
305					310					315					320	
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Met	Thr	Met	Val	Cys	Ala	
			325						330					335		
Gln	Val	Met	Gly	Asn	Asn	Thr	Thr	Ile	Thr	Phe	Ser	Gly	Ala	Ser	Gly	
		340						345					350			
Gln	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Met	Ala	Tyr	Asn	Leu	Leu	
		355					360					365				
Asn	Ser	Ile	Arg	Leu	Leu	Gly	Asp	Ala	Cys	Gln	Ser	Phe	Arg	Leu	His	
	370					375					380					
Cys	Val	Glu	Ser	Ile	Lys	Ala	Asn	Lys	Glu	Lys	Ile	Asp	Lys	Val	Leu	
385					390					395					400	
Asn	Glu	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	

PF59083SeqList PF59083.txt

405
 Asp Asn Ala Ser Lys Ala Ala Lys Asn Ala His Lys Lys Gly Ile Thr
 420
 Leu Lys Glu Ser Cys Leu Glu Leu Glu Leu Leu Thr Ser Glu Glu Phe
 435
 Asp Glu Trp Val Arg Pro Glu Lys Met Ile Gly Pro Lys Asp
 450 455 460

<210> 9651

<211> 1419

<212> DNA

<213> Ustilago maydis 521

<220>

<221> CDS

<222> (1)..(1419)

<400> 9651

atg	tcg	cag	ggc	aag	ttc	cgt	tct	gaa	aag	gac	acg	ttt	ggt	ccc	ctc	48
Met	Ser	Gln	Gly	Lys	Phe	Arg	Ser	Glu	Lys	Asp	Thr	Phe	Gly	Pro	Leu	
1				5				10						15		
cag	gtg	ccc	gcc	gac	cgc	tac	tgg	ggc	gct	cag	acc	cag	cga	tcg	ctc	96
Gln	Val	Pro	Ala	Asp	Arg	Tyr	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	
		20						25					30			
caa	aac	ttt	gac	att	ggt	gga	cct	caa	gag	cgc	atg	ccc	gag	ccg	ctg	144
Gln	Asn	Phe	Asp	Ile	Gly	Gly	Pro	Gln	Glu	Arg	Met	Pro	Glu	Pro	Leu	
		35					40					45				
atc	gag	gcc	ttt	ggt	gtc	ctc	aag	aag	gcg	gct	gcc	acc	gtc	aac	aag	192
Ile	Glu	Ala	Phe	Gly	Val	Leu	Lys	Lys	Ala	Ala	Ala	Thr	Val	Asn	Lys	
		50				55					60					
tca	ttc	ggt	ctt	gac	ccc	aag	gtc	gcc	gat	gcg	att	tgc	cag	gct	gcc	240
Ser	Phe	Gly	Leu	Asp	Pro	Lys	Val	Ala	Asp	Ala	Ile	Cys	Gln	Ala	Ala	
65				70				75						80		
gac	gag	gtg	att	gcc	ggt	aag	ctc	cac	agc	cac	ttc	ccc	ctt	gtt	gtc	288
Asp	Glu	Val	Ile	Ala	Gly	Lys	Leu	His	Ser	His	Phe	Pro	Leu	Val	Val	
			85					90						95		
ttc	cag	acc	ggt	tca	ggt	acc	cag	acc	aac	atg	aac	gtc	aac	gag	gtc	336
Phe	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Thr	Asn	Met	Asn	Val	Asn	Glu	Val	
		100					105					110				
atc	agc	aac	cgt	gcc	atc	gag	atc	ctc	ggc	ggg	gag	ctc	ggc	agc	aag	384
Ile	Ser	Asn	Arg	Ala	Ile	Glu	Ile	Leu	Gly	Gly	Glu	Leu	Gly	Ser	Lys	
		115				120						125				
aaa	ccc	gtc	cac	cct	aac	gac	cac	gtc	aac	atg	agc	cag	tcg	tcc	aac	432
Lys	Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	Met	Ser	Gln	Ser	Ser	Asn	
		130				135					140					
gac	acc	ttc	ccc	acc	gcc	atg	cac	gtc	gcc	tcg	gtc	acc	cag	atc	acc	480
Asp	Thr	Phe	Pro	Thr	Ala	Met	His	Val	Ala	Ser	Val	Thr	Gln	Ile	Thr	
145				150				155						160		
aag	tcg	ctc	ctc	ccc	gct	ctt	gag	gag	ctt	cgc	gcc	gcg	ctc	gac	gcc	528
Lys	Ser	Leu	Leu	Pro	Ala	Leu	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Asp	Ala	
				165				170						175		
aag	cgc	gcc	gaa	ttt	gac	gat	atc	atc	aag	atc	gga	cgt	acg	cac	ttg	576
Lys	Arg	Ala	Glu	Phe	Asp	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	
		180					185					190				
cag	gac	gcg	acg	ccc	ttg	acg	ctc	ggc	cag	gag	ttc	tct	ggc	tac	gta	624
Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	
		195				200						205				
aag	cag	gtc	gag	aac	ggt	atc	gag	cgc	gtc	aag	gcg	ggt	att	cct	cgt	672
Lys	Gln	Val	Glu	Asn	Gly	Ile	Glu	Arg	Val	Lys	Ala	Val	Ile	Pro	Arg	
		210				215					220					
ctt	tcg	cag	ctc	gcc	cag	ggt	ggt	act	gct	gtc	gga	act	ggt	ctc	aac	720
Leu	Ser	Gln	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	
225				230				235						240		
acc	tac	atc	ggt	ttc	gac	aag	aaa	gtc	gct	gcc	gag	atc	tcc	aac	atc	768
Thr	Tyr	Ile	Gly	Phe	Asp	Lys	Lys	Val	Ala	Ala	Glu	Ile	Ser	Asn	Ile	
				245				250						255		
acc	ggc	ttg	cac	ttt	gag	acc	gca	gag	aac	aag	ttc	gaa	gcg	ctt	gca	816
Thr	Gly	Leu	His	Phe	Glu	Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	
			260				265						270			

PF59083SeqList PF59083.txt

gct	cac	gat	gcg	atc	gtg	gaa	gcc	agc	ggg	gct	ctc	aac	aca	gtg	gct	864
Ala	His	Asp	Ala	Ile	Val	Glu	Ala	Ser	Gly	Ala	Leu	Asn	Thr	Val	Ala	
		275					280					285				
gtg	tcg	ttg	atg	aaa	atc	gct	aac	gac	atc	cga	tac	ctc	ggc	tcg	gga	912
Val	Ser	Leu	Met	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	
	290					295					300					
cct	cgt	tgt	ggg	ctg	gga	gag	ctg	agc	ttg	ccc	gag	aac	gaa	ccg	ggt	960
Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	
305				310					315						320	
tcg	tcg	atc	atg	cca	ggc	aag	gtc	aac	ccc	acg	cag	tgc	gag	gcg	ctc	1008
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	
				325					330					335		
acc	atg	gtc	gct	gct	cag	gtc	atg	ggg	aac	aac	acc	acc	atc	tcg	gtc	1056
Thr	Met	Val	Ala	Ala	Gln	Val	Met	Gly	Asn	Asn	Thr	Thr	Ile	Ser	Val	
			340					345					350			
gcc	ggc	tcg	tac	ggg	cag	ttt	gag	ctc	aac	gtc	ttc	aag	ccg	gtc	ttg	1104
Ala	Gly	Ser	Tyr	Gly	Gln	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Leu	
		355					360					365				
gtc	aag	aac	ctg	ctc	cag	tcc	atc	cgt	ctg	ctc	gct	gat	ggc	gct	cg	1152
Val	Lys	Asn	Leu	Leu	Gln	Ser	Ile	Arg	Leu	Leu	Ala	Asp	Gly	Ala	Arg	
	370					375					380					
agc	ttc	acc	aag	aac	tgc	gtc	gtc	ggg	atc	gag	gct	aac	agg	gac	acg	1200
Ser	Phe	Thr	Lys	Asn	Cys	Val	Val	Gly	Ile	Glu	Ala	Asn	Arg	Asp	Thr	
385				390				395							400	
atc	aac	aag	att	ctc	aac	gaa	agt	ctc	atg	ctt	gct	acc	atc	ttg	aac	1248
Ile	Asn	Lys	Ile	Leu	Asn	Glu	Ser	Leu	Met	Leu	Ala	Thr	Ile	Leu	Asn	
				405				410						415		
tcg	cat	ctc	ggc	tac	gac	aat	gtc	gcc	gcg	gcc	gct	aag	aag	gct	cat	1296
Ser	His	Leu	Gly	Tyr	Asp	Asn	Val	Ala	Ala	Ala	Ala	Lys	Lys	Ala	His	
			420				425						430			
aag	gag	ggc	aca	aag	ttg	gtc	gac	gct	acc	gtc	gcg	ttg	ggg	ttc	atg	1344
Lys	Glu	Gly	Thr	Lys	Leu	Val	Asp	Ala	Thr	Val	Ala	Leu	Gly	Phe	Met	
		435				440					445					
acc	gag	gag	gag	ttc	aaa	aag	atc	gtc	agg	ccc	gag	ttc	atg	ctt	ggg	1392
Thr	Glu	Glu	Glu	Phe	Lys	Lys	Ile	Val	Arg	Pro	Glu	Phe	Met	Leu	Gly	
	450				455						460					
ccc	acc	gag	tac	aag	gcc	aag	aac	taa								1419
Pro	Thr	Glu	Tyr	Lys	Ala	Lys	Asn									
465					470											

<210> 9652

<211> 472

<212> PRT

<213> Ustilago maydis 521

<400> 9652

Met	Ser	Gln	Gly	Lys	Phe	Arg	Ser	Glu	Lys	Asp	Thr	Phe	Gly	Pro	Leu	
1				5					10					15		
Gln	Val	Pro	Ala	Asp	Arg	Tyr	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	
			20					25					30			
Gln	Asn	Phe	Asp	Ile	Gly	Gly	Pro	Gln	Glu	Arg	Met	Pro	Glu	Pro	Leu	
		35					40					45				
Ile	Glu	Ala	Phe	Gly	Val	Leu	Lys	Lys	Ala	Ala	Ala	Thr	Val	Asn	Lys	
	50					55					60					
Ser	Phe	Gly	Leu	Asp	Pro	Lys	Val	Ala	Asp	Ala	Ile	Cys	Gln	Ala	Ala	
65				70					75						80	
Asp	Glu	Val	Ile	Ala	Gly	Lys	Leu	His	Ser	His	Phe	Pro	Leu	Val	Val	
			85						90					95		
Phe	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Thr	Asn	Met	Asn	Val	Asn	Glu	Val	
		100					105						110			
Ile	Ser	Asn	Arg	Ala	Ile	Glu	Ile	Leu	Gly	Gly	Glu	Leu	Gly	Ser	Lys	
		115				120					125					
Lys	Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	Met	Ser	Gln	Ser	Ser	Asn	
	130				135						140					
Asp	Thr	Phe	Pro	Thr	Ala	Met	His	Val	Ala	Ser	Val	Thr	Gln	Ile	Thr	
145					150					155					160	
Lys	Ser	Leu	Leu	Pro	Ala	Leu	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Asp	Ala	
			165					170						175		
Lys	Arg	Ala	Glu	Phe	Asp	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	

PF59083SeqList PF59083.txt

180 185 190
 Gln Asp Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Val
 195 200 205
 Lys Gln Val Glu Asn Gly Ile Glu Arg Val Lys Ala Val Ile Pro Arg
 210 215 220
 Leu Ser Gln Leu Ala Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn
 225 230 235
 Thr Tyr Ile Gly Phe Asp Lys Lys Val Ala Ala Glu Ile Ser Asn Ile
 240 245 250
 Thr Gly Leu His Phe Glu Thr Ala Glu Asn Lys Phe Glu Ala Leu Ala
 255 260 265
 Ala His Asp Ala Ile Val Glu Ala Ser Gly Ala Leu Asn Thr Val Ala
 270 275 280
 Val Ser Leu Met Lys Ile Ala Asn Asp Ile Arg Tyr Leu Gly Ser Gly
 285 290 295
 Pro Arg Cys Gly Leu Gly Glu Leu Ser Leu Pro Glu Asn Glu Pro Gly
 300 305 310
 Ser Ser Ile Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu
 315 320 325
 Thr Met Val Ala Gln Val Met Gly Asn Asn Thr Thr Ile Ser Val
 330 335 340
 Ala Gly Ser Tyr Gly Gln Phe Glu Leu Asn Val Phe Lys Pro Val Leu
 345 350 355
 Val Lys Asn Leu Leu Gln Ser Ile Arg Leu Leu Ala Asp Gly Ala Arg
 360 365 370
 Ser Phe Thr Lys Asn Cys Val Val Gly Ile Glu Ala Asn Arg Asp Thr
 375 380 385
 Ile Asn Lys Ile Leu Asn Glu Ser Leu Met Leu Ala Thr Ile Leu Asn
 390 395 400
 Ser His Leu Gly Tyr Asp Asn Val Ala Ala Ala Lys Lys Ala His
 405 410 415
 Lys Glu Gly Thr Lys Leu Val Asp Ala Thr Val Ala Leu Gly Phe Met
 420 425 430
 Thr Glu Glu Glu Phe Lys Lys Ile Val Arg Pro Glu Phe Met Leu Gly
 435 440 445
 Pro Thr Glu Tyr Lys Ala Lys Asn
 450 455 460
 465 470

<210> 9653

<211> 1533

<212> DNA

<213> Cryptococcus neoformans var. neoformans B-3501A

<220>

<221> CDS

<222> (1)..(1533)

<400> 9653

atg	acg	act	ccc	aca	aag	aca	tcc	agt	ctc	aaa	acc	acc	cag	atg	ctc	48
Met	Thr	Thr	Pro	Thr	Lys	Thr	Ser	Ser	Leu	Lys	Thr	Thr	Gln	Met	Leu	
1				5					10					15		
gcc	cga	tca	ctc	aga	ctc	acc	cgt	act	ctt	ccc	cgt	gtc	tct	ctt	gct	96
Ala	Arg	Ser	Leu	Arg	Leu	Thr	Arg	Thr	Leu	Pro	Arg	Val	Ser	Leu	Ala	
			20					25					30			
tct	cgc	gga	ttc	tcc	tcc	act	tca	tac	atc	atg	gca	gag	caa	aag	ttc	144
Ser	Arg	Gly	Phe	Ser	Ser	Thr	Ser	Tyr	Ile	Met	Ala	Glu	Gln	Lys	Phe	
		35				40					45					
agg	aag	gag	aag	gac	act	ttt	ggg	gac	ctc	cag	gtc	ccc	gct	gac	agg	192
Arg	Lys	Glu	Lys	Asp	Thr	Phe	Gly	Asp	Leu	Gln	Val	Pro	Ala	Asp	Arg	
		50				55				60						
tac	tgg	ggg	gcc	cag	acg	cag	cga	agt	ttg	atg	aac	ttt	gac	atc	ggc	240
Tyr	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Met	Asn	Phe	Asp	Ile	Gly	
		65			70			75						80		
ggg	ccg	act	gag	cga	atg	cct	cct	ccc	ctc	atc	aag	gcc	ttt	ggc	gtc	288
Gly	Pro	Thr	Glu	Arg	Met	Pro	Pro	Pro	Leu	Ile	Lys	Ala	Phe	Gly	Val	
			85					90						95		
ctc	aag	aag	gcc	gcc	gct	gct	ggt	aac	cag	act	tat	ggc	ctc	cct	gcc	336
Leu	Lys	Lys	Ala	Ala	Ala	Ala	Val	Asn	Gln	Thr	Tyr	Gly	Leu	Pro	Ala	
			100					105					110			

PF59083SeqList PF59083.txt																
gag	gtt	gcc	gag	cac	atc	caa	aag	gct	gct	gac	gaa	gtc	att	tct	ggc	384
Glu	Val	Ala	Glu	His	Ile	Gln	Lys	Ala	Ala	Asp	Glu	Val	Ile	Ser	Gly	
		115					120					125				
aag	ctc	att	gac	gaa	ttc	ccc	ctc	gtc	gtc	ttc	caa	act	ggt	tcc	ggc	432
Lys	Leu	Ile	Asp	Glu	Phe	Pro	Leu	Val	Val	Phe	Gln	Thr	Gly	Ser	Gly	
		130				135					140					
acc	cag	acc	aac	atg	aat	gtg	aac	gag	gtc	att	tcc	aac	agg	gcc	att	480
Thr	Gln	Thr	Asn	Met	Asn	Val	Asn	Glu	Val	Ile	Ser	Asn	Arg	Ala	Ile	
145					150					155					160	
gaa	atg	atg	ggt	ggt	gag	ctt	ggc	agc	aag	aag	ccc	ggt	cac	ccc	aac	528
Glu	Met	Met	Gly	Gly	Glu	Leu	Gly	Ser	Lys	Lys	Pro	Val	His	Pro	Asn	
				165					170					175		
gac	cac	gtc	aac	atg	agc	cag	tct	tcc	aac	gac	act	ttc	ccc	acc	gct	576
Asp	His	Val	Asn	Met	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	
			180				185						190			
atg	cac	att	gct	gcc	gtt	gtt	gag	atc	aac	gag	cag	ctc	ctt	ccc	gcc	624
Met	His	Ile	Ala	Ala	Val	Val	Glu	Ile	Asn	Glu	Gln	Leu	Leu	Pro	Ala	
		195				200						205				
atg	aag	gag	ctc	cac	gct	gcc	ctc	aag	gcc	aag	cag	gac	gct	ttc	gag	672
Met	Lys	Glu	Leu	His	Ala	Ala	Leu	Lys	Ala	Lys	Gln	Asp	Ala	Phe	Glu	
		210				215					220					
aac	atc	atc	aag	atc	ggt	cga	act	cac	ttg	cag	gat	gct	acc	cct	ttg	720
Asn	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	Leu	
225					230					235					240	
act	ctc	ggt	cag	gag	ttc	tct	ggt	tac	gtc	acc	cag	ggt	gag	agg	ggt	768
Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	Thr	Gln	Val	Glu	Arg	Gly	
				245					250					255		
atc	ggc	cgt	gtc	gag	gcc	acc	ttg	aag	aat	ttg	agc	atg	ttg	gct	caa	816
Ile	Gly	Arg	Val	Glu	Ala	Thr	Leu	Lys	Asn	Leu	Ser	Met	Leu	Ala	Gln	
			260				265						270			
ggt	ggt	acc	gcc	gtt	ggt	act	ggt	ttg	aac	acc	agg	aag	ggc	ttt	gac	864
Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Arg	Lys	Gly	Phe	Asp	
		275					280					285				
gag	aag	gtt	gct	gcc	gag	atc	tca	aag	atc	acc	ggc	tac	gac	ttt	gtc	912
Glu	Lys	Val	Ala	Ala	Glu	Ile	Ser	Lys	Ile	Thr	Gly	Tyr	Asp	Phe	Val	
		290				295					300					
act	gct	ccc	aac	aag	ttt	gag	gcc	ctt	gcc	gct	cat	gac	gct	atc	gtc	960
Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Ile	Val	
305					310				315						320	
gag	gcc	tct	ggt	gcc	ctc	aac	gtc	gtc	gct	gtc	agc	ttc	atg	aag	atc	1008
Glu	Ala	Ser	Gly	Ala	Leu	Asn	Val	Val	Ala	Val	Ser	Phe	Met	Lys	Ile	
				325					330					335		
gcc	aac	gac	atc	agg	tac	ctc	gga	tct	ggt	cct	cga	tgc	ggt	ctc	ggt	1056
Ala	Asn	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	
			340				345						350			
gaa	ctc	gag	ttg	ccc	gag	aac	gag	cct	gga	tct	tcc	atc	atg	ccc	ggc	1104
Glu	Leu	Glu	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	
		355					360					365				
aag	gtc	aac	ccc	acc	cag	tgc	gag	gcc	ctc	acc	atg	ggt	gct	gcc	caa	1152
Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Ala	Ala	Gln	
		370				375					380					
gtc	atg	ggt	aac	aac	acc	acc	atc	tct	gtc	gcc	gga	tca	tac	ggc	cag	1200
Val	Met	Gly	Asn	Asn	Thr	Thr	Ile	Ser	Val	Ala	Gly	Ser	Tyr	Gly	Gln	
385					390					395					400	
ttc	gag	ctc	aac	gtc	ttc	aaa	ccc	gtt	ctc	atc	aag	aac	ctc	ttg	cag	1248
Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Leu	Ile	Lys	Asn	Leu	Leu	Gln	
				405					410					415		
tct	atc	cga	ctc	ttg	tct	gat	ggt	gcc	agg	agc	ttc	acc	aag	aac	tgt	1296
Ser	Ile	Arg	Leu	Leu	Ser	Asp	Gly	Ala	Arg	Ser	Phe	Thr	Lys	Asn	Cys	
			420				425						430			
gtc	gtc	ggt	atc	aag	gcg	aac	gag	gac	agg	atc	aag	aag	att	atg	aac	1344
Val	Val	Gly	Ile	Lys	Ala	Asn	Glu	Asp	Arg	Ile	Lys	Lys	Ile	Met	Asn	
		435					440					445				
gag	agt	ttg	atg	ttg	gct	acc	tgc	ttg	aac	agc	act	ttg	ggt	tac	gat	1392
Glu	Ser	Leu	Met	Leu	Ala	Thr	Cys	Leu	Asn	Ser	Thr	Leu	Gly	Tyr	Asp	
		450				455					460					
gac	gtc	gcc	gcc	atc	gcc	aaa	aag	gct	cac	aag	gag	ggt	ctc	acc	ctc	1440
Asp	Val	Ala	Ala	Ile	Ala	Lys	Lys	Ala	His	Lys	Glu	Gly	Leu	Thr	Leu	
465					470					475					480	

PF59083SeqList PF59083.txt

aag	gag	tct	acc	ctt	gct	ctc	ggc	aag	ctc	act	tct	gaa	caa	ttc	gac	1488
Lys	Glu	Ser	Thr	Leu	Ala	Leu	Gly	Lys	Leu	Thr	Ser	Glu	Gln	Phe	Asp	
				485					490					495		
gag	aag	gtc	agg	cct	gag	ctc	atg	ttg	gct	ccc	act	gac	gct	taa		1533
Glu	Lys	Val	Arg	Pro	Glu	Leu	Met	Leu	Ala	Pro	Thr	Asp	Ala			
			500					505					510			

<210> 9654

<211> 510

<212> PRT

<213> Cryptococcus neoformans var. neoformans B-3501A

<400> 9654

Met	Thr	Thr	Pro	Thr	Lys	Thr	Ser	Ser	Leu	Lys	Thr	Thr	Gln	Met	Leu	
1				5					10					15		
Ala	Arg	Ser	Leu	Arg	Leu	Thr	Arg	Thr	Leu	Pro	Arg	Val	Ser	Leu	Ala	
			20					25					30			
Ser	Arg	Gly	Phe	Ser	Ser	Thr	Ser	Tyr	Ile	Met	Ala	Glu	Gln	Lys	Phe	
		35					40					45				
Arg	Lys	Glu	Lys	Asp	Thr	Phe	Gly	Asp	Leu	Gln	Val	Pro	Ala	Asp	Arg	
	50					55					60					
Tyr	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Met	Asn	Phe	Asp	Ile	Gly	
65					70					75					80	
Gly	Pro	Thr	Glu	Arg	Met	Pro	Pro	Pro	Leu	Ile	Lys	Ala	Phe	Gly	Val	
				85					90					95		
Leu	Lys	Lys	Ala	Ala	Ala	Ala	Val	Asn	Gln	Thr	Tyr	Gly	Leu	Pro	Ala	
			100					105					110			
Glu	Val	Ala	Glu	His	Ile	Gln	Lys	Ala	Ala	Asp	Glu	Val	Ile	Ser	Gly	
		115				120					125					
Lys	Leu	Ile	Asp	Glu	Phe	Pro	Leu	Val	Val	Phe	Gln	Thr	Gly	Ser	Gly	
	130					135					140					
Thr	Gln	Thr	Asn	Met	Asn	Val	Asn	Glu	Val	Ile	Ser	Asn	Arg	Ala	Ile	
145					150					155					160	
Glu	Met	Met	Gly	Gly	Glu	Leu	Gly	Ser	Lys	Lys	Pro	Val	His	Pro	Asn	
			165						170					175		
Asp	His	Val	Asn	Met	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	
			180					185					190			
Met	His	Ile	Ala	Ala	Val	Val	Glu	Ile	Asn	Glu	Gln	Leu	Leu	Pro	Ala	
		195					200					205				
Met	Lys	Glu	Leu	His	Ala	Ala	Leu	Lys	Ala	Lys	Gln	Asp	Ala	Phe	Glu	
	210					215					220					
Asn	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	Leu	
225					230					235					240	
Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	Thr	Gln	Val	Glu	Arg	Gly	
			245						250					255		
Ile	Gly	Arg	Val	Glu	Ala	Thr	Leu	Lys	Asn	Leu	Ser	Met	Leu	Ala	Gln	
			260					265					270			
Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Arg	Lys	Gly	Phe	Asp	
		275					280					285				
Glu	Lys	Val	Ala	Ala	Glu	Ile	Ser	Lys	Ile	Thr	Gly	Tyr	Asp	Phe	Val	
	290					295					300					
Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Ile	Val	
305					310					315					320	
Glu	Ala	Ser	Gly	Ala	Leu	Asn	Val	Val	Ala	Val	Ser	Phe	Met	Lys	Ile	
			325						330					335		
Ala	Asn	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	
			340					345					350			
Glu	Leu	Glu	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	
		355					360					365				
Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Ala	Ala	Gln	
	370					375					380					
Val	Met	Gly	Asn	Asn	Thr	Thr	Ile	Ser	Val	Ala	Gly	Ser	Tyr	Gly	Gln	
385					390					395					400	
Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Leu	Ile	Lys	Asn	Leu	Leu	Gln	
			405						410					415		
Ser	Ile	Arg	Leu	Leu	Ser	Asp	Gly	Ala	Arg	Ser	Phe	Thr	Lys	Asn	Cys	
			420					425					430			
Val	Val	Gly	Ile	Lys	Ala	Asn	Glu	Asp	Arg	Ile	Lys	Lys	Ile	Met	Asn	
		435					440					445				

PF59083SeqList PF59083.txt

Glu Ser Leu Met Leu Ala Thr Cys Leu Asn Ser Thr Leu Gly Tyr Asp
 450 455 460
 Asp Val Ala Ala Ile Ala Lys Lys Ala His Lys Glu Gly Leu Thr Leu
 465 470 475 480
 Lys Glu Ser Thr Leu Ala Leu Gly Lys Leu Thr Ser Glu Gln Phe Asp
 485 490 495
 Glu Lys Val Arg Pro Glu Leu Met Leu Ala Pro Thr Asp Ala
 500 505 510

<210> 9655

<211> 1494

<212> DNA

<213> Tribolium castaneum

<220>

<221> CDS

<222> (1)..(1494)

<400> 9655

atg	gcg	tta	tca	agg	ctc	tac	agc	agt	cgc	gtg	act	ggg	agc	gca	aaa	48
Met	Ala	Leu	Ser	Arg	Leu	Tyr	Ser	Ser	Arg	Val	Thr	Gly	Ser	Ala	Lys	
1				5					10					15		
gcc	gcg	ttg	aat	ctc	tac	cgg	aaa	tct	ctc	cat	tct	caa	ata	gcc	cta	96
Ala	Ala	Leu	Asn	Leu	Tyr	Arg	Lys	Ser	Leu	His	Ser	Gln	Ile	Ala	Leu	
			20					25					30			
atg	tcg	gac	ttc	cgc	atc	gaa	aag	gac	act	ttc	ggc	gag	ctc	aaa	gtg	144
Met	Ser	Asp	Phe	Arg	Ile	Glu	Lys	Asp	Thr	Phe	Gly	Glu	Leu	Lys	Val	
		35					40					45				
ccc	tct	gac	aag	tac	tat	ggg	gcc	caa	acc	ctg	cga	tcc	gtc	atg	aac	192
Pro	Ser	Asp	Lys	Tyr	Tyr	Gly	Ala	Gln	Thr	Leu	Arg	Ser	Val	Met	Asn	
		50				55					60					
ttc	ccc	atc	ggg	ggc	gaa	ttc	gag	cgc	atg	ccg	tac	ccc	gtt	ata	acg	240
Phe	Pro	Ile	Gly	Gly	Glu	Phe	Glu	Arg	Met	Pro	Tyr	Pro	Val	Ile	Thr	
		65			70				75					80		
gcc	atg	ggg	gtc	ttg	aaa	gcc	gcc	gcc	acc	gtc	aac	aaa	gac	tac		288
Ala	Met	Gly	Val	Leu	Lys	Lys	Ala	Ala	Ala	Thr	Val	Asn	Lys	Asp	Tyr	
				85				90					95			
ggt	ctc	gac	ccc	aaa	atc	tcc	gac	gcg	att	tgc	aaa	gcc	gct	gac	gaa	336
Gly	Leu	Asp	Pro	Lys	Ile	Ser	Asp	Ala	Ile	Cys	Lys	Ala	Ala	Asp	Glu	
			100					105					110			
gtc	atc	tcc	ggc	aag	ctc	tac	tgc	gac	cat	ttc	ccc	ctc	gtc	att	tgg	384
Val	Ile	Ser	Gly	Lys	Leu	Tyr	Cys	Asp	His	Phe	Pro	Leu	Val	Ile	Trp	
		115					120					125				
caa	acg	ggc	tcc	ggc	acc	caa	acc	aac	atg	aac	acg	aac	gaa	gtg	atc	432
Gln	Thr	Gly	Ser	Gly	Thr	Gln	Thr	Asn	Met	Asn	Thr	Asn	Glu	Val	Ile	
		130				135					140					
agt	aat	cga	gct	att	gaa	ata	atg	ggc	gga	aaa	ctc	ggc	tcc	aag	gac	480
Ser	Asn	Arg	Ala	Ile	Glu	Ile	Met	Gly	Gly	Lys	Leu	Gly	Ser	Lys	Asp	
				150				155						160		
ccg	gtg	cac	ccc	aac	gac	cac	gtc	aac	aag	agc	cag	agc	agc	aac	gac	528
Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	Lys	Ser	Gln	Ser	Ser	Asn	Asp	
				165				170						175		
acc	ttc	ccc	aca	gcc	atg	cac	att	gcc	gtg	gcg	gtg	gaa	atc	caa	aac	576
Thr	Phe	Pro	Thr	Ala	Met	His	Ile	Ala	Val	Ala	Val	Glu	Ile	Gln	Asn	
			180					185					190			
acg	ctc	ctg	cct	ggc	ctc	aaa	atg	cta	aca	aat	agt	ctc	gat	aag	aaa	624
Thr	Leu	Leu	Pro	Gly	Leu	Lys	Met	Leu	Thr	Asn	Ser	Leu	Asp	Lys	Lys	
			195				200					205				
gcg	cag	gag	ttt	aag	gat	atc	atc	aaa	atc	ggg	cgc	acg	cac	acc	cag	672
Ala	Gln	Glu	Phe	Lys	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	
		210				215					220					
gac	gcc	gtc	ccc	ctg	act	ctg	ggg	cag	gaa	ttc	agc	ggc	tat	gtc	cag	720
Asp	Ala	Val	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	Gln	
				230						235				240		
cag	atg	aag	ttc	ggg	att	gat	cga	att	aac	gat	act	ttg	ccc	agg	ctg	768
Gln	Met	Lys	Phe	Gly	Ile	Asp	Arg	Ile	Asn	Asp	Thr	Leu	Pro	Arg	Leu	
				245				250						255		
tac	atg	ctg	gct	ttg	ggg	ggc	aca	gct	gtg	ggg	acg	ggg	ctc	aat	acc	816
Tyr	Met	Leu	Ala	Leu	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	

PF59083SeqList PF59083.txt

			260					265				270					
cgg	aaa	ggg	ttc	gcc	gag	aaa	tgt	gcc	gcc	gaa	att	tca	aaa	ctg	aca		864
Arg	Lys	Gly	Phe	Ala	Glu	Lys	Cys	Ala	Ala	Glu	Ile	Ser	Lys	Leu	Thr		
		275					280					285					
gga	ttg	ccc	ttc	act	tca	gca	ccg	aat	aag	ttt	gag	gct	ttg	gcc	gct		912
Gly	Leu	Pro	Phe	Thr	Ser	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala		
		290				295					300						
cat	gac	gcc	ctg	gtt	gag	gtc	tcg	ggg	gcg	ctc	aat	gtg	gtc	gct	tgc		960
His	Asp	Ala	Leu	Val	Glu	Val	Ser	Gly	Ala	Leu	Asn	Val	Val	Ala	Cys		
					310					315					320		
tcg	att	atg	aaa	att	gca	aac	gat	att	agg	ttt	ttg	gcg	tct	ggc	cct		1008
Ser	Ile	Met	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Ala	Ser	Gly	Pro		
				325					330					335			
cgc	tgc	ggc	ttg	ggc	gag	ctg	tcg	ctg	cct	gag	aac	gaa	ccc	ggc	agc		1056
Arg	Cys	Gly	Leu	Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser		
			340					345					350				
tcc	atc	atg	ccg	ggc	aaa	gtg	aac	cca	acc	cag	tgc	gaa	gcc	atc	acc		1104
Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Ile	Thr		
			355								365						
atg	gtg	gcc	gcc	cag	gtg	atg	ggt	aac	cac	gtg	gct	gtg	acc	att	ggt		1152
Met	Val	Ala	Ala	Gln	Val	Met	Gly	Asn	His	Val	Ala	Val	Thr	Ile	Gly		
					375						380						
ggt	tcg	aac	ggt	cat	ttc	gaa	ttg	aac	ggt	ttt	aag	ccc	atg	atg	gta		1200
Gly	Ser	Asn	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Met	Met	Val		
				390						395					400		
gcc	aat	ggt	tta	cga	tca	atc	cgt	ttg	ttg	gga	gat	tcc	agc	aaa	gct		1248
Ala	Asn	Val	Leu	Arg	Ser	Ile	Arg	Leu	Leu	Gly	Asp	Ser	Ser	Lys	Ala		
				405				410						415			
ttc	aca	acc	aat	tgt	gta	gat	ggc	att	gta	gcc	aac	aaa	gac	cga	atc		1296
Phe	Thr	Thr	Asn	Cys	Val	Asp	Gly	Ile	Val	Ala	Asn	Lys	Asp	Arg	Ile		
			420					425					430				
gat	aag	ctt	ttg	cac	gag	agt	ttg	atg	ttg	gtc	acg	gct	ctt	aac	cca		1344
Asp	Lys	Leu	Leu	His	Glu	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro		
			435				440					445					
cac	att	ggc	tac	gac	aag	gcg	gcc	caa	att	gcc	aaa	acg	gcg	cac	aag		1392
His	Ile	Gly	Tyr	Asp	Lys	Ala	Ala	Gln	Ile	Ala	Lys	Thr	Ala	His	Lys		
					455						460						

```
<210> 9656
<211> 497
<212> PRT
<213> Tribolium castaneum
```

<400>	9656														
Met	Ala	Leu	Ser	Arg ₅	Leu	Tyr	Ser	Ser	Arg ₁₀	Val	Thr	Gly	Ser	Ala ₁₅	Lys
Ala	Ala	Leu	Asn ₂₀	Leu	Tyr	Arg	Lys	Ser ₂₅	Leu	His	Ser	Gln	Ile ₃₀	Ala	Leu
Met	Ser	Asp ₃₅	Phe	Arg	Ile	Glu	Lys ₄₀	Asp	Thr	Phe	Gly	Glu ₄₅	Leu	Lys	Val
Pro	Ser ₅₀	Asp	Lys	Tyr	Tyr	Gly ₅₅	Ala	Gln	Thr	Leu	Arg ₆₀	Ser	Val	Met	Asn
Phe ₆₅	Pro	Ile	Gly	Gly	Glu ₇₀	Phe	Glu	Arg	Met ₇₅	Pro	Tyr	Pro	Val	Ile ₈₀	Thr
Ala	Met	Gly	Val	Leu ₈₅	Lys	Lys	Ala	Ala	Ala ₉₀	Thr	Val	Asn	Lys	Asp ₉₅	Tyr
Gly	Leu	Asp	Pro ₁₀₀	Lys	Ile	Ser	Asp	Ala ₁₀₅	Ile	Cys	Lys	Ala	Ala ₁₁₀	Asp	Glu
val	Ile	Ser ₁₁₅	Gly	Lys	Leu	Tyr	Cys ₁₂₀	Asp	His	Phe	Pro	Leu ₁₂₅	Val	Ile	Trp

PF59083SeqList PF59083.txt

Gln	Thr	Gly	Ser	Gly	Thr	Gln	Thr	Asn	Met	Asn	Thr	Asn	Glu	Val	Ile
130						135					140				
Ser	Asn	Arg	Ala	Ile	Glu	Ile	Met	Gly	Gly	Lys	Leu	Gly	Ser	Lys	Asp
145					150					155					160
Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	Lys	Ser	Gln	Ser	Ser	Asn	Asp
				165					170					175	
Thr	Phe	Pro	Thr	Ala	Met	His	Ile	Ala	Val	Ala	Val	Glu	Ile	Gln	Asn
				180				185					190		
Thr	Leu	Leu	Pro	Gly	Leu	Lys	Met	Leu	Thr	Asn	Ser	Leu	Asp	Lys	Lys
		195				200						205			
Ala	Gln	Glu	Phe	Lys	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln
210						215					220				
Asp	Ala	Val	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	Gln
225					230					235					240
Gln	Met	Lys	Phe	Gly	Ile	Asp	Arg	Ile	Asn	Asp	Thr	Leu	Pro	Arg	Leu
				245					250					255	
Tyr	Met	Leu	Ala	Leu	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr
			260					265					270		
Arg	Lys	Gly	Phe	Ala	Glu	Lys	Cys	Ala	Ala	Glu	Ile	Ser	Lys	Leu	Thr
		275					280					285			
Gly	Leu	Pro	Phe	Thr	Ser	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala
290						295					300				
His	Asp	Ala	Leu	Val	Glu	Val	Ser	Gly	Ala	Leu	Asn	Val	Val	Ala	Cys
305					310					315					320
Ser	Ile	Met	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Ala	Ser	Gly	Pro
				325					330					335	
Arg	Cys	Gly	Leu	Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser
			340					345					350		
Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Ile	Thr
		355					360					365			
Met	Val	Ala	Ala	Gln	Val	Met	Gly	Asn	His	Val	Ala	Val	Thr	Ile	Gly
		370				375					380				
Gly	Ser	Asn	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Met	Met	Val
385					390					395					400
Ala	Asn	Val	Leu	Arg	Ser	Ile	Arg	Leu	Leu	Gly	Asp	Ser	Ser	Lys	Ala
				405					410					415	
Phe	Thr	Thr	Asn	Cys	Val	Asp	Gly	Ile	Val	Ala	Asn	Lys	Asp	Arg	Ile
			420					425					430		
Asp	Lys	Leu	Leu	His	Glu	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro
		435					440					445			
His	Ile	Gly	Tyr	Asp	Lys	Ala	Ala	Gln	Ile	Ala	Lys	Thr	Ala	His	Lys
		450				455					460				
Glu	Asn	Ser	Thr	Leu	Lys	Glu	Thr	Ala	Ile	Lys	Leu	Gly	Ile	Leu	Thr
465					470					475					480
Glu	Glu	Gln	Phe	Lys	Glu	Trp	Val	Lys	Pro	Glu	Glu	Met	Leu	Gly	Pro
				485					490					495	

Lys

<210> 9657
 <211> 1401
 <212> DNA
 <213> Herminiimonas arsenicoxydans

<220>
 <221> CDS
 <222> (1)..(1401)
 <223> transl_table=11

<400> 9657	
atg cgt caa gaa cgc gac ttc ctc ggc atc aaa gcc atc cct cca cca	48
Met Arg Gln Glu Arg Asp Phe Leu Gly Ile Lys Ala Ile Pro Pro Pro	
1 5 10 15	
gcc tat tgg ggt gta cac acg gcc cgc gca gtg gag aat ttt ccc atc	96
Ala Tyr Trp Gly Val His Thr Ala Arg Ala Val Glu Asn Phe Pro Ile	
20 25 30	
acc gga caa acc gtt gcg caa atg ccg gag ctc att cgt gct ttt gca	144
Thr Gly Gln Thr Val Ala Gln Met Pro Glu Leu Ile Arg Ala Phe Ala	
35 40 45	

PF59083SeqList PF59083.txt

ttc	gta	aag	aaa	gct	gcc	gct	cat	gcc	aac	ctg	caa	atg	ggc	gta	ctc	192
Phe	Val	Lys	Lys	Ala	Ala	Ala	His	Ala	Asn	Leu	Gln	Met	Gly	Val	Leu	
	50					55					60					
aac	acc	agc	cag	gcc	gac	gcg	atc	tca	aaa	gca	tgt	gac	gat	ctg	atc	240
Asn	Thr	Ser	Gln	Ala	Asp	Ala	Ile	Ser	Lys	Ala	Cys	Asp	Asp	Leu	Ile	
	65				70					75					80	
gcc	gga	caa	ctg	cac	gac	caa	ttc	gtc	gtc	gat	gtc	ata	caa	ggg	ggc	288
Ala	Gly	Gln	Leu	His	Asp	Gln	Phe	Val	Val	Asp	Val	Ile	Gln	Gly	Gly	
				85				90						95		
gca	ggc	aca	tca	acc	aat	atg	aat	gcc	aac	gag	gta	atc	gcc	aat	cgt	336
Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	
			100					105					110			
gcg	ctt	gag	cac	ctc	ggg	ttg	gac	aag	ggg	cg	tac	gac	gtc	att	cac	384
Ala	Leu	Glu	His	Leu	Gly	Leu	Asp	Lys	Gly	Arg	Tyr	Asp	Val	Ile	His	
		115					120					125				
ccg	aat	gat	cac	gtc	aat	gca	tcc	cag	agt	acc	aac	gac	gcc	tat	cca	432
Pro	Asn	Asp	His	Val	Asn	Ala	Ser	Gln	Ser	Thr	Asn	Asp	Ala	Tyr	Pro	
	130					135					140					
aca	gca	ctg	aaa	att	gcg	atc	tgg	ttc	gac	ctt	cat	cag	ctg	ctg	cag	480
Thr	Ala	Leu	Lys	Ile	Ala	Ile	Trp	Phe	Asp	Leu	His	Gln	Leu	Leu	Gln	
	145				150				155						160	
gcc	ctc	gct	aat	ctg	cg	ggc	gcc	ttt	gaa	gcc	aag	gcc	acc	gaa	ttc	528
Ala	Leu	Ala	Asn	Leu	Arg	Gly	Ala	Phe	Glu	Ala	Lys	Ala	Thr	Glu	Phe	
				165				170						175		
gtt	tcc	att	ctg	aag	ata	gga	cgt	acc	cag	tta	caa	gac	gcc	gtg	ccg	576
Val	Ser	Ile	Leu	Lys	Ile	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	
			180				185						190			
atg	acg	ctg	ggg	cag	gaa	ttt	gca	gca	ttt	gcc	agc	atg	att	gcc	gac	624
Met	Thr	Leu	Gly	Gln	Glu	Phe	Ala	Ala	Phe	Ala	Ser	Met	Ile	Ala	Asp	
		195					200					205				
gac	gag	aag	cg	ctg	cg	gaa	acc	gcc	atc	ctg	atg	acc	gaa	gtg	aac	672
Asp	Glu	Lys	Arg	Leu	Arg	Glu	Thr	Ala	Ile	Leu	Met	Thr	Glu	Val	Asn	
	210					215					220					
ctg	ggc	ggc	acc	gcc	atc	ggg	acc	ggc	atc	aac	gcg	ccg	gtg	ggg	tat	720
Leu	Gly	Gly	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Ala	Pro	Val	Gly	Tyr	
	225				230				235						240	
gtc	gat	gtc	gtc	att	ccc	aaa	ctc	gcc	gaa	ctg	tcg	ggc	gtc	cct	gta	768
Val	Asp	Val	Val	Ile	Pro	Lys	Leu	Ala	Glu	Leu	Ser	Gly	Val	Pro	Val	
				245				250						255		
acc	aag	gca	cg	gac	atg	att	gcc	gcg	acc	tcg	gat	acc	agc	ggc	ttc	816
Thr	Lys	Ala	Arg	Asp	Met	Ile	Ala	Ala	Thr	Ser	Asp	Thr	Ser	Gly	Phe	
			260				265						270			
gtc	gat	gtc	tcg	ggc	ata	ctc	aag	cg	atc	gcc	acc	aag	ctt	tcc	aag	864
Val	Asp	Val	Ser	Gly	Ile	Leu	Lys	Arg	Ile	Ala	Thr	Lys	Leu	Ser	Lys	
			275				280					285				
atc	agc	aac	gat	ctg	cgt	ctg	ctc	tcc	tcc	ggc	ccc	cag	gcc	ggg	atc	912
Ile	Ser	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Gln	Ala	Gly	Ile	
	290				295						300					
ggc	gac	atc	cag	ttg	ccg	gcg	cg	cag	gca	ggg	tcg	tcg	atc	atg	ccg	960
Gly	Asp	Ile	Gln	Leu	Pro	Ala	Arg	Gln	Ala	Gly	Ser	Ser	Ile	Met	Pro	
	305				310					315					320	
ggc	aag	gtc	aat	ccc	gtg	atc	ccc	gag	gtg	atg	aac	cag	gtg	gcc	ttt	1008
Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Met	Asn	Gln	Val	Ala	Phe	
				325				330						335		
gaa	gtc	atc	ggg	aac	gac	gtt	gcc	atc	acc	atg	gca	tcg	gaa	ggc	ggg	1056
Glu	Val	Ile	Gly	Asn	Asp	Val	Ala	Ile	Thr	Met	Ala	Ser	Glu	Gly	Gly	
			340				345						350			
caa	ctg	caa	ctc	aac	gcc	ttt	gaa	ccc	ttg	atc	ggc	tgg	gca	ctg	cac	1104
Gln	Leu	Gln	Leu	Asn	Ala	Phe	Glu	Pro	Leu	Ile	Gly	Trp	Ala	Leu	His	
		355					360					365				
aag	agt	gtg	ata	cac	ctt	gcc	aag	gct	tgc	cac	acg	ctt	cag	gtg	aac	1152
Lys	Ser	Val	Ile	His	Leu	Ala	Lys	Ala	Cys	His	Thr	Leu	Gln	Val	Asn	
	370				375						380					
tgc	gta	gaa	ggc	atc	aag	agc	aat	cag	gat	tta	ctg	gcg	cag	cgt	atc	1200
Cys	Val	Glu	Gly	Ile	Lys	Ser	Asn	Gln	Asp	Leu	Leu	Ala	Gln	Arg	Ile	
	385				390					395					400	
gca	gag	tcc	gtc	acc	ttg	gtc	acg	gca	ctg	aat	ccg	ctg	atc	ggg	tat	1248
Ala	Glu	Ser	Val	Thr	Leu	Val	Thr	Ala	Leu	Asn	Pro	Leu	Ile	Gly	Tyr	
				405				410						415		

PF59083SeqList PF59083.txt

gaa	aag	gcg	gcg	gcg	att	gca	aaa	gcc	gcc	atc	gca	agc	ggc	aag	ccg	1296
Glu	Lys	Ala	Ala	Ala	Ile	Ala	Lys	Ala	Ala	Ile	Ala	Ser	Gly	Lys	Pro	
			420					425					430			
att	gcc	gtg	gtg	gca	gaa	gag	ctg	ggc	atc	atg	agt	cag	gct	gac	atg	1344
Ile	Ala	Val	Val	Ala	Glu	Glu	Leu	Gly	Ile	Met	Ser	Gln	Ala	Asp	Met	
		435					440					445				
cag	aaa	ttc	ttg	cga	cct	gaa	aac	ctg	act	cag	gca	ggc	gcc	ttg	att	1392
Gln	Lys	Phe	Leu	Arg	Pro	Glu	Asn	Leu	Thr	Gln	Ala	Gly	Ala	Leu	Ile	
	450					455					460					
tca	ggc	taa														1401
Ser	Gly															
465																

<210> 9658

<211> 466

<212> PRT

<213> Herminiimonas arsenicoxydans

<400> 9658

Met	Arg	Gln	Glu	Arg	Asp	Phe	Leu	Gly	Ile	Lys	Ala	Ile	Pro	Pro	Pro	
1				5					10					15		
Ala	Tyr	Trp	Gly	Val	His	Thr	Ala	Arg	Ala	Val	Glu	Asn	Phe	Pro	Ile	
			20					25					30			
Thr	Gly	Gln	Thr	Val	Ala	Gln	Met	Pro	Glu	Leu	Ile	Arg	Ala	Phe	Ala	
		35					40					45				
Phe	Val	Lys	Lys	Ala	Ala	Ala	His	Ala	Asn	Leu	Gln	Met	Gly	Val	Leu	
	50					55					60					
Asn	Thr	Ser	Gln	Ala	Asp	Ala	Ile	Ser	Lys	Ala	Cys	Asp	Asp	Leu	Ile	
65					70				75						80	
Ala	Gly	Gln	Leu	His	Asp	Gln	Phe	Val	Val	Asp	Val	Ile	Gln	Gly	Gly	
				85				90					95			
Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	
			100					105					110			
Ala	Leu	Glu	His	Leu	Gly	Leu	Asp	Lys	Gly	Arg	Tyr	Asp	Val	Ile	His	
		115					120					125				
Pro	Asn	Asp	His	Val	Asn	Ala	Ser	Gln	Ser	Thr	Asn	Asp	Ala	Tyr	Pro	
	130					135					140					
Thr	Ala	Leu	Lys	Ile	Ala	Ile	Trp	Phe	Asp	Leu	His	Gln	Leu	Leu	Gln	
145					150				155					160		
Ala	Leu	Ala	Asn	Leu	Arg	Gly	Ala	Phe	Glu	Ala	Lys	Ala	Thr	Glu	Phe	
				165				170					175			
Val	Ser	Ile	Leu	Lys	Ile	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	
			180				185					190				
Met	Thr	Leu	Gly	Gln	Glu	Phe	Ala	Phe	Ala	Ser	Met	Ile	Ala	Asp		
		195					200				205					
Asp	Glu	Lys	Arg	Leu	Arg	Glu	Thr	Ala	Ile	Leu	Met	Thr	Glu	Val	Asn	
	210					215					220					
Leu	Gly	Gly	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Ala	Pro	Val	Gly	Tyr	
225					230				235						240	
Val	Asp	Val	Val	Ile	Pro	Lys	Leu	Ala	Glu	Leu	Ser	Gly	Val	Pro	Val	
				245					250					255		
Thr	Lys	Ala	Arg	Asp	Met	Ile	Ala	Ala	Thr	Ser	Asp	Thr	Ser	Gly	Phe	
			260					265					270			
Val	Asp	Val	Ser	Gly	Ile	Leu	Lys	Arg	Ile	Ala	Thr	Lys	Leu	Ser	Lys	
			275				280					285				
Ile	Ser	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Gln	Ala	Gly	Ile	
	290					295					300					
Gly	Asp	Ile	Gln	Leu	Pro	Ala	Arg	Gln	Ala	Gly	Ser	Ser	Ile	Met	Pro	
305					310					315					320	
Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Met	Asn	Gln	Val	Ala	Phe	
				325					330					335		
Glu	Val	Ile	Gly	Asn	Asp	Val	Ala	Ile	Thr	Met	Ala	Ser	Glu	Gly	Gly	
			340					345					350			
Gln	Leu	Gln	Leu	Asn	Ala	Phe	Glu	Pro	Leu	Ile	Gly	Trp	Ala	Leu	His	
		355					360					365				
Lys	Ser	Val	Ile	His	Leu	Ala	Lys	Ala	Cys	His	Thr	Leu	Gln	Val	Asn	
	370					375					380					
Cys	Val	Glu	Gly	Ile	Lys	Ser	Asn	Gln	Asp	Leu	Ala	Gln	Arg	Ile		
385					390				395					400		

PF59083SeqList PF59083.txt

Ala Glu Ser Val Thr Leu Val Thr Ala Leu Asn Pro Leu Ile Gly Tyr
 405 410 415
 Glu Lys Ala Ala Ala Ile Ala Lys Ala Ala Ile Ala Ser Gly Lys Pro
 420 425 430
 Ile Ala Val Val Ala Glu Glu Leu Gly Ile Met Ser Gln Ala Asp Met
 435 440 445
 Gln Lys Phe Leu Arg Pro Glu Asn Leu Thr Gln Ala Gly Ala Leu Ile
 450 455 460
 Ser Gly
 465

<210> 9659

<211> 1407

<212> DNA

<213> Burkholderia vietnamiensis G4

<220>

<221> CDS

<222> (1)..(1407)

<223> transl_table=11

<400> 9659

atg	acg	gaa	cgc	ggc	ttt	cgc	gtc	gaa	gcg	gat	cta	tta	ggg	cag	cga	48
Met	Thr	Glu	Arg	Gly	Phe	Arg	Val	Glu	Ala	Asp	Leu	Leu	Gly	Gln	Arg	
1				5					10					15		
aac	gtg	ccc	gac	tcg	gcg	tac	tac	ggc	gtc	cat	acg	ctg	cgc	gcg	cag	96
Asn	Val	Pro	Asp	Ser	Ala	Tyr	Tyr	Gly	Val	His	Thr	Leu	Arg	Ala	Gln	
			20					25					30			
gag	aac	ttc	gac	atc	tcc	ggg	cgc	acg	atc	gcg	tcg	ctg	ccg	tac	ctc	144
Glu	Asn	Phe	Asp	Ile	Ser	Gly	Arg	Thr	Ile	Ala	Ser	Leu	Pro	Tyr	Leu	
			35				40					45				
gtc	gtc	gcg	ctg	gcg	gcg	gtc	aag	gaa	gcg	gcc	gcc	gac	gcg	aac	tgc	192
Val	Val	Ala	Leu	Ala	Ala	Val	Lys	Glu	Ala	Ala	Ala	Asp	Ala	Asn	Cys	
	50					55				60						
gag	ctc	ggg	ctg	ctg	ccg	cgt	gcg	tat	cgc	gac	gcg	atc	gcc	gcc	gcc	240
Glu	Leu	Gly	Leu	Leu	Pro	Arg	Ala	Tyr	Arg	Asp	Ala	Ile	Ala	Ala	Ala	
	65				70				75						80	
tgc	gcc	gaa	atc	cgc	gac	ggc	cgc	ctg	cac	gac	cag	ttc	gtg	gtc	gac	288
Cys	Ala	Glu	Ile	Arg	Asp	Gly	Arg	Leu	His	Asp	Gln	Phe	Val	Val	Asp	
				85					90				95			
gtc	atc	cag	ggc	ggg	gcg	ggc	acg	tcg	acc	aac	atg	aac	gcg	aac	gag	336
Val	Ile	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	
			100				105					110				
gtg	atc	tgc	aac	cgc	gcg	ctc	gaa	atc	atg	ggg	cat	gca	cgc	ggc	cag	384
Val	Ile	Cys	Asn	Arg	Ala	Leu	Glu	Ile	Met	Gly	His	Ala	Arg	Gly	Gln	
			115				120					125				
tac	gaa	cat	ctg	cat	ccg	aac	gag	cac	gtc	aac	ctc	gca	cag	agc	acc	432
Tyr	Glu	His	Leu	His	Pro	Asn	Glu	His	Val	Asn	Leu	Ala	Gln	Ser	Thr	
	130				135					140						
aac	gac	gtc	tac	ccg	acc	gcg	atc	cgc	atc	gcg	acc	tgc	ttc	gcg	gtc	480
Asn	Asp	Val	Tyr	Pro	Thr	Ala	Ile	Arg	Ile	Ala	Thr	Cys	Phe	Ala	Val	
	145				150					155					160	
gag	caa	ctg	ctc	gag	gcg	atg	gcg	cac	ctg	cgc	gac	gcg	ttc	gcg	cag	528
Glu	Gln	Leu	Leu	Glu	Ala	Met	Ala	His	Leu	Arg	Asp	Ala	Phe	Ala	Gln	
				165					170				175			
aag	gcc	gac	gca	ttc	gcc	gat	ctg	ctc	aag	ctc	ggc	cgc	acg	cag	ttg	576
Lys	Ala	Asp	Ala	Phe	Ala	Asp	Leu	Leu	Lys	Leu	Gly	Arg	Thr	Gln	Leu	
			180				185					190				
cag	gac	gcg	gtg	ccg	atg	acg	ctc	ggc	cag	gag	ttc	tcg	acc	tat	gcg	624
Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Thr	Tyr	Ala	
		195				200						205				
gtg	atg	gtg	agc	gaa	gac	atc	gcg	cgc	ctg	cag	gag	gcc	ggc	tggt	ctg	672
Val	Met	Val	Ser	Glu	Asp	Ile	Ala	Arg	Leu	Gln	Glu	Ala	Gly	Trp	Leu	
	210				215					220						
atg	cgc	gag	atc	aac	ctc	ggc	acc	gcg	atc	ggc	acc	ggc	atc	acc		720
Met	Arg	Glu	Ile	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Thr	
	225				230				235						240	
gcg	cat	ccc	gac	tat	gcg	gcg	aag	gcg	ctg	gcc	gcg	ctg	cgg	cgc	atc	768
Ala	His	Pro	Asp	Tyr	Ala	Ala	Lys	Ala	Leu	Ala	Leu	Arg	Arg	Arg	Ile	

PF59083SeqList PF59083.txt

245																250																255																816
acc Thr	ggc Gly	ctc Leu	gac Asp 260	ctg Leu	agc Ser	acc Thr	gcg Ala	ccg Pro 265	aac Asn	ctg Leu	atc Ile	gag Glu	gcg Ala 270	acg Thr	cag Gln																																	
275																280																285																864
gat Asp	tgc Cys	ggc Gly	gcg Ala	ttc Phe	gtg Val	cag Gln	atg Met	tcg Ser	ggc Gly	gtg Val	ctg Leu	aag Lys 285	cgg Arg	atc Ile	gcc Ala																																	
290																295																300																912
gtc Val	aag Lys	ctg Leu	tcg Ser	aag Lys	atc Ile	tgc Cys	aac Asn	gac Asp	ctg Leu	cgg Arg	ctg Leu	ctg Leu	tcg Ser	agc Ser	ggc Gly																																	
305																310																315																960
ccg Pro	cgc Arg	gcc Ala	ggc Gly	ttc Phe	ggc Gly	gag Glu	atc Ile	aac Asn	ctg Leu	ccg Pro	ccg Pro	gtg Val	cag Gln	gcc Ala	ggt Gly 320																																	
325																330																335																1008
tcg Ser	tcg Ser	atc Ile	atg Met	ccg Pro	ggc Gly	aag Lys	gtg Val	aac Asn	ccg Pro	gtg Val	att Ile	ccg Pro	gaa Glu	gtc Val 335	gtg Val																																	
340																345																350																1056
aac Asn	cag Gln	gtc Val	gcg Ala	ttc Phe	gag Glu	gtg Val	ttc Phe	ggc Gly	aac Asn	gac Asp	ctg Leu	acc Thr	gtg Val 350	acg Thr	ttc Phe																																	
355																360																365																1104
gcc Ala	gcc Ala	gag Glu	gcc Ala	ggc Gly	cag Gln	ctg Leu	cag Gln	ctc Leu	aac Asn	gcg Ala	ttc Phe	gag Glu	ccg Pro	gtg Val	atc Ile																																	
370																375																380																1152
gcc Ala	agc Ser	gcg Ala	ctg Leu	ttc Phe	cgc Arg	agc Ser	ttc Phe	ggc Gly	cat His	ctg Leu	agc Ser	gcg Ala	gcc Ala	tgc Cys	acg Thr																																	
385																390																395																1200
acg Thr	ctc Leu	gcc Ala	gat Asp	cgc Arg	tgc Cys	gtg Val	agc Ser	ggc Gly	atc Ile	acc Thr	gcg Ala	aac Asn	ccc Pro	gag Glu	cgg Arg 400																																	
405																410																415																1248
ctg Leu	cgc Arg	gac Asp	acg Thr	atg Met	gag Glu	cgc Arg	tcg Ser	gtc Val	gcg Ala	ctc Leu	gcc Ala	acc Thr	gcg Ala	ctg Leu	aac Asn																																	
420																425																430																1296
ccg Pro	tac Tyr	atc Ile	ggc Gly	tac Tyr	aag Lys	cgc Arg	gcc Ala	acc Thr	gcc Ala	gtc Val	gcc Ala	aag Lys	gag Glu	gcg Ala	cac His																																	
435																440																445																1344
gag Glu	agc Ser	ggc Gly	aag Lys	tcg Ser	att Ile	cgc Arg	gag Glu	gtc Val	gtg Val	ctg Leu	gaa Glu	cac His	cgg Arg	ctg Leu	atg Met																																	
450																455																460																1392
acc Thr	gat Asp	gcg Ala	caa Gln	ctc Leu	gac Asp	gac Asp	gcg Ala	ctg Leu	caa Gln	ccc Pro	gaa Glu	gcg Ala	ctg Leu	atc Ile	cgc Arg																																	
465																																																1407
ccg Pro	cgc Arg	gct Ala	tac Tyr	tga																																												

<210> 9660

<211> 468

<212> PRT

<213> Burkholderia vietnamiensis G4

<400> 9660

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

Seite 10128

PF59083SeqList PF59083.txt

145 150 155 160
Glu Gln Leu Leu Glu Ala Met Ala His Leu Arg Asp Ala Phe Ala Gln
165 170 175
Lys Ala Asp Ala Phe Ala Asp Leu Leu Lys Leu Gly Arg Thr Gln Leu
180 185
Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Ser Thr Tyr Ala
195 200 205
Val Met Val Ser Glu Asp Ile Ala Arg Leu Gln Glu Ala Gly Trp Leu
210 215 220
Met Arg Glu Ile Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Ile Thr
225 230 235
Ala His Pro Asp Tyr Ala Ala Lys Ala Leu Ala Ala Leu Arg Arg Ile
245 250 255
Thr Gly Leu Asp Leu Ser Thr Ala Pro Asn Leu Ile Glu Ala Thr Gln
260 265 270
Asp Cys Gly Ala Phe Val Gln Met Ser Gly Val Leu Lys Arg Ile Ala
275 280 285
Val Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly
290 295 300
Pro Arg Ala Gly Phe Gly Glu Ile Asn Leu Pro Pro Val Gln Ala Gly
305 310 315
Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Val
325 330 335
Asn Gln Val Ala Phe Glu Val Phe Gly Asn Asp Leu Thr Val Thr Phe
340 345 350
Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Ala Phe Glu Pro Val Ile
355 360 365
Ala Ser Ala Leu Phe Arg Ser Phe Gly His Leu Ser Ala Ala Cys Thr
370 375 380
Thr Leu Ala Asp Arg Cys Val Ser Gly Ile Thr Ala Asn Pro Glu Arg
385 390 395
Leu Arg Asp Thr Met Glu Arg Ser Val Ala Leu Ala Thr Ala Leu Asn
405 410 415
Pro Tyr Ile Gly Tyr Lys Arg Ala Thr Ala Val Ala Lys Glu Ala His
420 425 430
Glu Ser Gly Lys Ser Ile Arg Glu Val Val Leu Glu His Arg Leu Met
435 440 445
Thr Asp Ala Gln Leu Asp Asp Ala Leu Gln Pro Glu Ala Leu Ile Arg
450 455 460
Pro Arg Ala Tyr
465

<210> 9661
<211> 1392
<212> DNA
<213> Candidatus Protochlamydia amoebophila UWE25

<220>
<221> CDS
<222> (1)..(1392)
<223> transl_table=11

<400> 9661
atg gac tat cga aca gaa aaa gac acc tta gga gaa gtt aga gtt tct 48
Met Asp Tyr Arg Thr Glu Lys Asp Thr Leu Gly Glu Val Arg Val Ser
1 5 10 15
gca gac tgt tat tat gga gct caa acg aag cgt tcc tac gat aat ttt 96
Ala Asp Cys Tyr Tyr Gly Ala Gln Thr Lys Arg Ser Tyr Asp Asn Phe
20 25 30
tcg att gga ata gaa aaa atg cct aag gaa gta att cat gcg ctt gct 144
Ser Ile Gly Ile Glu Lys Met Pro Lys Glu Val Ile His Ala Leu Ala
35 40 45
cta atc aag aaa gcg gcc gcc tta act aac gaa cag ctt ggt tta tta 192
Leu Ile Lys Lys Ala Ala Ala Leu Thr Asn Glu Gln Leu Gly Leu Leu
50 55 60
cca aaa aat aaa caa ctc gtg att tgt gaa gtt tgc gac gaa att tta 240
Pro Lys Asn Lys Gln Leu Val Ile Cys Glu Val Cys Asp Glu Ile Leu
65 70 75 80
tct ggc tgc tta gat gat caa ttt ccg tta tct gtt tgg cag aca ggg 288
Seite 10129

PF59083SeqList PF59083.txt

Ser	Gly	Cys	Leu	Asp	Asp	Gln	Phe	Pro	Leu	Ser	Val	Trp	Gln	Thr	Gly	
tct	gga	acg	caa	aca	aac	atg	aac	ctc	aat	gaa	gtg	att	agt	aat	agg	336
Ser	Gly	Thr	Gln	Thr	Asn	Met	Asn	Leu	Asn	Glu	Val	Ile	Ser	Asn	Arg	
			100					105					110			
gcc	att	gaa	aag	ctg	ggt	ggg	gtg	ctt	ggt	tct	aaa	tat	ccg	atc	cat	384
Ala	Ile	Glu	Lys	Leu	Gly	Gly	Val	Leu	Gly	Ser	Lys	Tyr	Pro	Ile	His	
			115				120					125				
ccc	aat	gat	gat	gtc	aac	tta	tct	caa	tcg	tct	aat	gat	gtg	ttt	cct	432
Pro	Asn	Asp	Asp	Val	Asn	Leu	Ser	Gln	Ser	Ser	Asn	Asp	Val	Phe	Pro	
						135						140				
tca	gcc	atg	cat	att	gcg	gtg	atg	ttt	gat	ata	tct	aag	aag	ttg	tta	480
Ser	Ala	Met	His	Ile	Ala	Val	Met	Phe	Asp	Ile	Ser	Lys	Lys	Leu	Leu	
145					150					155					160	
cca	agt	tta	aga	gaa	cta	aaa	gaa	act	tta	gaa	gcg	aaa	ggt	gaa	gct	528
Pro	Ser	Leu	Arg	Glu	Leu	Lys	Glu	Thr	Leu	Glu	Ala	Lys	Val	Glu	Ala	
				165					170					175		
ttt	aaa	gat	att	gta	aaa	att	ggg	cgt	acg	cat	tta	atg	gat	gcg	acc	576
Phe	Lys	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Thr	
			180					185					190			
cct	tta	aca	ctt	gga	caa	gaa	ttt	tcg	ggg	tat	gtc	agc	caa	ata	gag	624
Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	Ser	Gln	Ile	Glu	
			195				200					205				
cat	gga	ata	caa	gct	cta	aaa	aat	acg	ttt	gcg	cat	ctt	tct	gaa	ttg	672
His	Gly	Ile	Gln	Ala	Leu	Lys	Asn	Thr	Phe	Ala	His	Leu	Ser	Glu	Leu	
			210			215				220						
gcc	ttg	gga	gca	act	gct	gtg	gga	acg	gga	atg	aat	acg	cat	ccc	aac	720
Ala	Leu	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Met	Asn	Thr	His	Pro	Asn	
225					230				235						240	
tac	gca	aaa	tta	gtg	gct	gaa	aaa	att	agt	gag	ttg	tcc	gga	ttt	aat	768
Tyr	Ala	Lys	Leu	Val	Ala	Glu	Lys	Ile	Ser	Glu	Leu	Ser	Gly	Phe	Asn	
				245					250					255		
ttt	gtt	tct	gcc	agg	aat	aaa	ttt	gag	tcg	ctc	gcg	act	aat	gac	gct	816
Phe	Val	Ser	Ala	Arg	Asn	Lys	Phe	Glu	Ser	Leu	Ala	Thr	Asn	Asp	Ala	
			260					265					270			
ctt	gta	gaa	gtt	agc	ggg	gct	tta	aaa	agg	gtg	gcc	gtt	tca	gtg	ttt	864
Leu	Val	Glu	Val	Ser	Gly	Ala	Leu	Lys	Arg	Val	Ala	Val	Ser	Val	Phe	
			275				280					285				
aaa	att	gcc	aat	gat	att	cgg	tgg	ctt	tct	tca	ggc	cct	aga	tgt	gcc	912
Lys	Ile	Ala	Asn	Asp	Ile	Arg	Trp	Leu	Ser	Ser	Gly	Pro	Arg	Cys	Ala	
			290			295					300					
ata	gga	gaa	atc	gtt	att	cct	gct	aat	gaa	cca	ggc	tca	tcg	att	atg	960
Ile	Gly	Glu	Ile	Val	Ile	Pro	Ala	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	
305					310				315						320	
cca	gga	aaa	gtt	aat	cct	aca	caa	agt	gaa	gcc	tta	atg	atg	att	gcc	1008
Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Ser	Glu	Ala	Leu	Met	Met	Ile	Ala	
				325					330					335		
att	caa	gta	atg	ggg	aat	gat	ggg	atc	att	ggt	ttt	gca	ggt	tcg	caa	1056
Ile	Gln	Val	Met	Gly	Asn	Asp	Gly	Ile	Ile	Gly	Phe	Ala	Gly	Ser	Gln	
			340					345					350			
ggc	aat	cta	gaa	ttg	aat	gtt	ttt	cgc	cct	ctt	att	att	tat	aac	tta	1104
Gly	Asn	Leu	Glu	Leu	Asn	Val	Phe	Arg	Pro	Leu	Ile	Ile	Tyr	Asn	Leu	
			355				360					365				
att	caa	tct	att	cga	tta	ttg	agc	gat	gct	att	tct	aat	ttt	aac	caa	1152
Ile	Gln	Ser	Ile	Arg	Leu	Leu	Ser	Asp	Ala	Ile	Ser	Asn	Phe	Asn	Gln	
			370			375						380				
aaa	tgt	gtt	gtc	gga	ata	gag	gct	aac	caa	aca	aga	att	gca	gaa	cat	1200
Lys	Cys	Val	Val	Gly	Ile	Glu	Ala	Asn	Gln	Thr	Arg	Ile	Ala	Glu	His	
385					390				395					400		
ctg	aat	cgt	tcc	tta	atg	tta	gca	act	gct	ctt	aat	cat	gca	att	ggt	1248
Leu	Asn	Arg	Ser	Leu	Met	Leu	Ala	Thr	Ala	Leu	Asn	His	Ala	Ile	Gly	
				405				410						415		
tat	gat	cgt	gca	agt	caa	att	gta	aaa	aaa	gca	tac	tta	gaa	aat	ata	1296
Tyr	Asp	Arg	Ala	Ser	Gln	Ile	Val	Lys	Lys	Ala	Tyr	Leu	Glu	Asn	Ile	
			420				425						430			
aca	tta	aaa	gaa	gct	gca	cta	gct	tta	gcc	ttt	tta	acc	gaa	gat	gaa	1344
Thr	Leu	Lys	Glu	Ala	Ala	Leu	Ala	Leu	Ala	Phe	Leu	Thr	Glu	Asp	Glu	
			435				440					445				
ttt	gat	cag	att	atg	gat	cct	aaa	aaa	atg	att	ggg	cca	atg	act		1389

PF59083SeqList PF59083.txt

Phe Asp Gln Ile Met Asp Pro Lys Lys Met Ile Gly Pro Met Thr
 450 455 460
 taa

1392

<210> 9662
 <211> 463
 <212> PRT
 <213> Candidatus Protochlamydia amoebophila UWE25

<400> 9662
 Met Asp Tyr Arg Thr Glu Lys Asp Thr Leu Gly Glu Val Arg Val Ser
 1 5 10 15
 Ala Asp Cys Tyr Gly Ala Gln Thr Lys Arg Ser Tyr Asp Asn Phe
 20 25 30
 Ser Ile Gly Ile Glu Lys Met Pro Lys Glu Val Ile His Ala Leu Ala
 35 40 45
 Leu Ile Lys Lys Ala Ala Ala Leu Thr Asn Glu Gln Leu Gly Leu Leu
 50 55 60
 Pro Lys Asn Lys Gln Leu Val Ile Cys Glu Val Cys Asp Glu Ile Leu
 65 70 75 80
 Ser Gly Cys Leu Asp Asp Gln Phe Pro Leu Ser Val Trp Gln Thr Gly
 85 90 95
 Ser Gly Thr Gln Thr Asn Met Asn Leu Asn Glu Val Ile Ser Asn Arg
 100 105 110
 Ala Ile Glu Lys Leu Gly Gly Val Leu Gly Ser Lys Tyr Pro Ile His
 115 120 125
 Pro Asn Asp Asp Val Asn Leu Ser Gln Ser Ser Asn Asp Val Phe Pro
 130 135 140
 Ser Ala Met His Ile Ala Val Met Phe Asp Ile Ser Lys Lys Leu Leu
 145 150 155 160
 Pro Ser Leu Arg Glu Leu Lys Glu Thr Leu Glu Ala Lys Val Glu Ala
 165 170 175
 Phe Lys Asp Ile Val Lys Ile Gly Arg Thr His Leu Met Asp Ala Thr
 180 185 190
 Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Val Ser Gln Ile Glu
 195 200 205
 His Gly Ile Gln Ala Leu Lys Asn Thr Phe Ala His Leu Ser Glu Leu
 210 215 220
 Ala Leu Gly Ala Thr Ala Val Gly Thr Gly Met Asn Thr His Pro Asn
 225 230 235 240
 Tyr Ala Lys Leu Val Ala Glu Lys Ile Ser Glu Leu Ser Gly Phe Asn
 245 250 255
 Phe Val Ser Ala Arg Asn Lys Phe Glu Ser Leu Ala Thr Asn Asp Ala
 260 265 270
 Leu Val Glu Val Ser Gly Ala Leu Lys Arg Val Ala Val Ser Val Phe
 275 280 285
 Lys Ile Ala Asn Asp Ile Arg Trp Leu Ser Ser Gly Pro Arg Cys Ala
 290 295 300
 Ile Gly Glu Ile Val Ile Pro Ala Asn Glu Pro Gly Ser Ser Ile Met
 305 310 315 320
 Pro Gly Lys Val Asn Pro Thr Gln Ser Glu Ala Leu Met Met Ile Ala
 325 330 335
 Ile Gln Val Met Gly Asn Asp Gly Ile Ile Gly Phe Ala Gly Ser Gln
 340 345 350
 Gly Asn Leu Glu Leu Asn Val Phe Arg Pro Leu Ile Ile Tyr Asn Leu
 355 360 365
 Ile Gln Ser Ile Arg Leu Leu Ser Asp Ala Ile Ser Asn Phe Asn Gln
 370 375 380
 Lys Cys Val Val Gly Ile Glu Ala Asn Gln Thr Arg Ile Ala Glu His
 385 390 395 400
 Leu Asn Arg Ser Leu Met Leu Ala Thr Ala Leu Asn His Ala Ile Gly
 405 410 415
 Tyr Asp Arg Ala Ser Gln Ile Val Lys Lys Ala Tyr Leu Glu Asn Ile
 420 425 430
 Thr Leu Lys Glu Ala Ala Leu Ala Leu Ala Phe Leu Thr Glu Asp Glu
 435 440 445
 Phe Asp Gln Ile Met Asp Pro Lys Lys Met Ile Gly Pro Met Thr

450

<210> 9663
<211> 1434
<212> DNA
<213> Bacillus thuringiensis serovar konkukian str. 97-27

<220>
<221> CDS
<222> (1)..(1434)
<223> transl_table=11

```

<400> 9663
atg ata gca acg aag gat ata cgt ata gaa aaa gac ttt tta ggt gaa      48
Met Ile Ala Thr Lys Asp Ile Arg Ile Glu Lys Asp Phe Leu Gly Glu
1      5      10      15
aag gaa gta cca agt ata gct tat tac ggt gta caa aca tta cgc gct      96
Lys Glu Val Pro Ser Ile Ala Tyr Tyr Gly Val Gln Thr Leu Arg Ala
20      25      30
gta gaa aac ttc ccg att aca gga tat cgc att cat ccg tca ctc att      144
Val Glu Asn Phe Pro Ile Thr Gly Tyr Arg Ile His Pro Ser Leu Ile
35      40      45
acg gca atg gca att gtg aaa aaa gcg gcg gca ctt gca aat atg gat      192
Thr Ala Met Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met Asp
50      55      60
act gga tac tta gcg aaa gat att gga cat gaa att gcg gag gca gcg      240
Thr Gly Tyr Leu Ala Lys Asp Ile Gly His Glu Ile Ala Glu Ala Ala
65      70      75      80
caa gag att gtt gat gga aag ttc cat gat caa ttt att gtg gat cca      288
Gln Glu Ile Val Asp Gly Lys Phe His Asp Gln Phe Ile Val Asp Pro
85      90      95
atc caa ggc ggt gct gga act tct att aat atg aat aca aac gaa gta      336
Ile Gln Gly Gly Ala Gly Thr Ser Ile Asn Met Asn Thr Asn Glu Val
100      105      110
atc gct aat cga gcg tta gaa cgt atg gga tat gaa aaa ggc gag tat      384
Ile Ala Asn Arg Ala Leu Glu Arg Met Gly Tyr Glu Lys Gly Glu Tyr
115      120      125
gca aaa att agc cca aat acg cat gta aac atg gct caa tca acg aat      432
Ala Lys Ile Ser Pro Asn Thr His Val Asn Met Ala Gln Ser Thr Asn
130      135      140
gat gcg ttt cca acg ggg att cat att gca act ctt atg atg tta gaa      480
Asp Ala Phe Pro Thr Gly Ile His Ile Ala Thr Leu Met Met Leu Glu
145      150      155      160
gaa ctt ctt att aca atg gaa gaa ctt cat gct gct ttt cgt gca aaa      528
Glu Leu Leu Ile Thr Met Glu Glu Leu His Ala Ala Phe Arg Ala Lys
165      170      175
gca aaa gag ttc gat cac gtc att aaa atg gga cgt aca cat tta caa      576
Ala Lys Glu Phe Asp His Val Ile Lys Met Gly Arg Thr His Leu Gln
180      185      190
gat gct gtg ccg att cgt ctt ggt caa gaa ttt gaa gcg tat agc cga      624
Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser Arg
195      200      205
gtg ctt gcg cgt gat ata aaa aga att aaa cag tct cgc caa cat tta      672
Val Leu Ala Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His Leu
210      215      220
tat gaa gtg aat atg ggg gcg aca gct gtt ggt acg gga tta aat gca      720
Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn Ala
225      230      235      240
aac cct acg tac att gaa caa gtg gtt aaa cac ttg cga aca ttt agc      768
Asn Pro Thr Tyr Ile Glu Gln Val Val Lys His Leu Arg Thr Phe Ser
245      250      255
gga ttc cca ctt gtt ggt gca gag cat ttg gtt gat gca acg caa aat      816
Gly Phe Pro Leu Val Gly Ala Glu His Leu Val Asp Ala Thr Gln Asn
260      265      270
aca gat gca tac aca gaa gta tct gca gca tta aaa gta tgt atg atg      864
Thr Asp Ala Tyr Thr Glu Val Ser Ala Ala Leu Lys Val Cys Met Met
275      280      285
aat atg tct aaa att gcg aat gac ctt cgt att atg gca tct ggt cca      912
Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Ile Met Ala Ser Gly Pro

```

PF59083SeqList PF59083.txt

290	295	300	
cgt gtt gga ttg gcg gaa att caa tta cca gct cgc caa cca ggt tca			960
Arg Val Gly Leu Ala Glu Ile Gln Leu Pro Ala Arg Gln Pro Gly Ser			
305	310	315	320
tct att atg ccg ggt aaa gta aat cct gtt atg gca gaa gta att aat			1008
Ser Ile Met Pro Gly Lys Val Asn Pro Met Ala Glu Val Ile Asn			
	325	330	335
caa gtg gct ttc caa gta att ggt aat gat cat aca att tgc tta gcg			1056
Gln Val Ala Phe Gln Val Ile Gly Asn Asp His Thr Ile Cys Leu Ala			
	340	345	350
tca gaa gcc gga caa ttg gag ctc aac gta atg gag ccg gtg ctt gta			1104
Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu Val			
	355	360	365
ttt aat tta att caa tct att agt att atg aat aac gga ttc cgt gta			1152
Phe Asn Leu Ile Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg Val			
	370	375	380
ttc cgt gaa tat tgt att aaa gga att aca gca aat gaa gaa ttg ctg			1200
Phe Arg Glu Tyr Cys Ile Lys Gly Ile Thr Ala Asn Glu Glu Leu Leu			
	385	390	400
aag caa tat gtt gag aaa agt gtt gga att att aca gca gtt aac cct			1248
Lys Gln Tyr Val Glu Lys Ser Val Gly Ile Thr Ala Val Asn Pro			
	405	410	415
cat att ggt tat gaa gca gca tct cgc att gca cgt gaa gcg att gaa			1296
His Ile Gly Tyr Glu Ala Ala Ser Arg Ile Ala Arg Glu Ala Ile Glu			
	420	425	430
aca gga aaa tct gtt agg gag tta tgt tta gaa cat ggt gta ctg aca			1344
Thr Gly Lys Ser Val Arg Glu Leu Cys Leu Glu His Gly Val Leu Thr			
	435	440	445
gaa gaa gaa ttg gat att att tta gat cca ttc gaa atg acg cat cct			1392
Glu Glu Glu Leu Asp Ile Ile Leu Asp Pro Phe Glu Met Thr His Pro			
	450	455	460
gaa att gct ggg gct tct tta tta aag gat aag aag atg taa			1434
Glu Ile Ala Gly Ala Ser Leu Leu Lys Asp Lys Lys Met			
	465	470	475

<210> 9664

<211> 477

<212> PRT

<213> Bacillus thuringiensis serovar konkukian str. 97-27

<400> 9664

Met Ile Ala Thr Lys Asp Ile Arg Ile Glu Lys Asp Phe Leu Gly Glu	
1	5
Lys Glu Val Pro Ser Ile Ala Tyr Tyr Gly Val Gln Thr Leu Arg Ala	
	10
Val Glu Asn Phe Pro Ile Thr Gly Tyr Arg Ile His Pro Ser Leu Ile	
	15
Thr Ala Met Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met Asp	
	20
Thr Gly Tyr Leu Ala Lys Asp Ile Gly His Glu Ile Ala Glu Ala Ala	
	25
Gln Glu Ile Val Asp Gly Lys Phe His Asp Gln Phe Ile Val Asp Pro	
	30
Ile Gln Gly Gly Ala Gly Thr Ser Ile Asn Met Asn Thr Asn Glu Val	
	35
Ile Ala Asn Arg Ala Leu Glu Arg Met Gly Tyr Glu Lys Gly Glu Tyr	
	40
Ala Lys Ile Ser Pro Asn Thr His Val Asn Met Ala Gln Ser Thr Asn	
	45
Asp Ala Phe Pro Thr Gly Ile His Ile Ala Thr Leu Met Met Leu Glu	
	50
Glu Leu Leu Ile Thr Met Glu Glu Leu His Ala Ala Phe Arg Ala Lys	
	55
Ala Lys Glu Phe Asp His Val Ile Lys Met Gly Arg Thr His Leu Gln	
	60
Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser Arg	
	65
Val Leu Ala Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His Leu	
	70
	75
	80
	85
	90
	95
	100
	105
	110
	115
	120
	125
	130
	135
	140
	145
	150
	155
	160
	165
	170
	175
	180
	185
	190
	195
	200
	205
	210
	215
	220

PF59083SeqList PF59083.txt

Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn Ala
 225 230 235 240
 Asn Pro Thr Tyr Ile Glu Gln Val Val Lys His Leu Arg Thr Phe Ser
 245 250 255
 Gly Phe Pro Leu Val Gly Ala Glu His Leu Val Asp Ala Thr Gln Asn
 260 265 270
 Thr Asp Ala Tyr Thr Glu Val Ser Ala Ala Leu Lys Val Cys Met Met
 275 280 285
 Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Ile Met Ala Ser Gly Pro
 290 295 300
 Arg Val Gly Leu Ala Glu Ile Gln Leu Pro Ala Arg Gln Pro Gly Ser
 305 310 315 320
 Ser Ile Met Pro Gly Lys Val Asn Pro Val Met Ala Glu Val Ile Asn
 325 330 335
 Gln Val Ala Phe Gln Val Ile Gly Asn Asp His Thr Ile Cys Leu Ala
 340 345 350
 Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu Val
 355 360 365
 Phe Asn Leu Ile Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg Val
 370 375 380
 Phe Arg Glu Tyr Cys Ile Lys Gly Ile Thr Ala Asn Glu Glu Leu Leu
 385 390 395 400
 Lys Gln Tyr Val Glu Lys Ser Val Gly Ile Ile Thr Ala Val Asn Pro
 405 410 415
 His Ile Gly Tyr Glu Ala Ala Ser Arg Ile Ala Arg Glu Ala Ile Glu
 420 425 430
 Thr Gly Lys Ser Val Arg Glu Leu Cys Leu Glu His Gly Val Leu Thr
 435 440 445
 Glu Glu Glu Leu Asp Ile Ile Leu Asp Pro Phe Glu Met Thr His Pro
 450 455 460
 Glu Ile Ala Gly Ala Ser Leu Leu Lys Asp Lys Lys Met
 465 470 475

<210> 9665

<211> 1419

<212> DNA

<213> Acinetobacter sp. ADP1

<220>

<221> CDS

<222> (1)..(1419)

<223> transl_table=11

<400> 9665

atg aac gct gaa att caa act cgt aca gaa aag gat tta ctg ggt cta	48
Met Asn Ala Glu Ile Gln Thr Arg Thr Glu Lys Asp Leu Leu Gly Leu	
1 5 10 15	
cgt gaa gta cca aat caa ttt tac ttc ggt atc caa act tta cga gca	96
Arg Glu Val Pro Asn Gln Phe Tyr Phe Gly Ile Gln Thr Leu Arg Ala	
20 25 30	
att gaa aac ttc aat cta agc tct aat aaa atc aat caa tat cca aat	144
Ile Glu Asn Phe Asn Leu Ser Ser Asn Lys Ile Asn Gln Tyr Pro Asn	
35 40 45	
ttg atc aaa tca tta gcg atg gtg aag cat gca tgt gca gaa gca aac	192
Leu Ile Lys Ser Leu Ala Met Val Lys His Ala Cys Ala Glu Ala Asn	
50 55 60	
cat act ttg ggt aaa tta agt gat tta aaa ttt aat gca atc aaa tat	240
His Thr Leu Gly Lys Leu Ser Asp Leu Lys Phe Asn Ala Ile Lys Tyr	
65 70 75 80	
agc tgt gat cag tta att caa ggt ttt tac cac gaa cag ttc ccc att	288
Ser Cys Asp Gln Leu Ile Gln Gly Phe Tyr His Glu Gln Phe Pro Ile	
85 90 95	
gac ctc att cag ggt ggt gcg ggt acc tct acc aac atg aat gcc aat	336
Asp Leu Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn	
100 105 110	
gaa gta att gca aat att gca tta gag cat ttg ggt cat aaa aaa ggt	384
Glu Val Ile Ala Asn Ile Ala Leu Glu His Leu Gly His Lys Lys Gly	
115 120 125	
gaa tac aac ttt tta cat cca aac aat gat gtg aat atg tct caa tcg	432

PF59083SeqList PF59083.txt

Glu	Tyr	Asn	Phe	Leu	His	Pro	Asn	Asn	Asp	Val	Asn	Met	Ser	Gln	Ser	
130						135					140					
acc	aat	gac	ggt	tat	cca	act	gca	att	cgc	tta	ggt	tta	tta	ttc	agc	480
Thr	Asn	Asp	Val	Tyr	Pro	Thr	Ala	Ile	Arg	Leu	Gly	Leu	Leu	Phe	Ser	
145					150					155					160	
tta	gat	gat	tta	aat	acg	cct	ttt	gaa	aat	ttg	att	gct	agc	cta	cgc	528
Leu	Asp	Asp	Leu	Asn	Thr	Pro	Phe	Glu	Asn	Leu	Ile	Ala	Ser	Leu	Arg	
				165				170						175		
cgt	aag	ggt	gat	gaa	ttt	gca	cat	att	ttg	aaa	atg	ggc	cgt	act	cag	576
Arg	Lys	Gly	Asp	Glu	Phe	Ala	His	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	
				180				185					190			
ctt	caa	gac	gcc	ggt	cca	atg	act	ttg	ggt	caa	gaa	ttt	aat	gct	ttt	624
Leu	Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Asn	Ala	Phe	
		195				200						205				
gct	tct	aca	ctt	gaa	aaa	gat	ttg	atc	aag	att	aga	gaa	atc	gcg	cct	672
Ala	Ser	Thr	Leu	Glu	Lys	Asp	Leu	Ile	Lys	Ile	Arg	Glu	Ile	Ala	Pro	
		210				215					220					
caa	act	cta	aat	tat	atg	aat	ctt	ggc	ggt	act	gcg	att	ggt	aca	gga	720
Gln	Thr	Leu	Asn	Tyr	Met	Asn	Leu	Gly	Gly	Thr	Ala	Ile	Gly	Thr	Gly	
225					230					235					240	
atc	aat	aca	gaa	caa	aaa	tat	acc	caa	ctt	gcc	att	gat	gca	ctt	gcg	768
Ile	Asn	Thr	Glu	Gln	Lys	Tyr	Thr	Gln	Leu	Ala	Ile	Asp	Ala	Leu	Ala	
				245				250						255		
aca	att	agc	cag	aaa	gat	atc	aag	tct	gct	ccc	gat	tta	atc	gaa	gcg	816
Thr	Ile	Ser	Gln	Lys	Asp	Ile	Lys	Ser	Ala	Pro	Asp	Leu	Ile	Glu	Ala	
			260					265					270			
act	tca	gat	atg	ggt	gat	ttt	gta	ttg	ttg	tca	gga	tta	ctt	aaa	cgt	864
Thr	Ser	Asp	Met	Gly	Asp	Phe	Val	Leu	Leu	Ser	Gly	Leu	Leu	Lys	Arg	
		275				280						285				
aca	gca	act	aaa	ctc	tca	aaa	atc	gcc	aat	gat	cta	cgt	tta	ctt	tca	912
Thr	Ala	Thr	Lys	Leu	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Leu	Leu	Ser	
		290				295					300					
agt	ggt	cca	cgt	act	ggg	atc	aat	gaa	att	aat	cta	gag	ccg	cgc	caa	960
Ser	Gly	Pro	Arg	Thr	Gly	Ile	Asn	Glu	Ile	Asn	Leu	Glu	Pro	Arg	Gln	
305					310					315					320	
cct	ggc	agc	tca	atc	atg	cca	ggt	aaa	gta	aac	cca	ggt	att	cca	gag	1008
Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	
				325					330					335		
gca	atg	aat	ctt	gta	tgt	ttc	cag	att	att	gcg	aat	gat	ttg	gct	gta	1056
Ala	Met	Asn	Leu	Val	Cys	Phe	Gln	Ile	Ile	Ala	Asn	Asp	Leu	Ala	Val	
				340				345					350			
act	tta	tct	gct	gaa	gcg	ggt	caa	tta	caa	tta	aat	gca	atg	gaa	ccc	1104
Thr	Leu	Ser	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Ala	Met	Glu	Pro	
		355				360						365				
ctg	att	gca	ttc	aaa	ctg	ttt	gaa	tca	att	gag	tta	ctt	ggt	aat	gcg	1152
Leu	Ile	Ala	Phe	Lys	Leu	Phe	Glu	Ser	Ile	Glu	Leu	Leu	Gly	Asn	Ala	
		370				375					380					
ctc	gtc	atg	ttc	caa	acc	aag	tgt	atc	gat	acc	gtg	act	gca	aac	gaa	1200
Leu	Val	Met	Phe	Gln	Thr	Lys	Cys	Ile	Asp	Thr	Val	Thr	Ala	Asn	Glu	
				385		390				395					400	
caa	cat	tgt	aaa	gca	ctt	gtc	gat	aat	tcc	att	gga	att	gtg	act	gct	1248
Gln	His	Cys	Lys	Ala	Leu	Val	Asp	Asn	Ser	Ile	Gly	Ile	Val	Thr	Ala	
				405				410					415			
ctg	aat	cct	tat	ctt	gga	tat	gaa	acc	aca	aca	cgt	att	gct	aaa	act	1296
Leu	Asn	Pro	Tyr	Leu	Gly	Tyr	Glu	Thr	Thr	Thr	Arg	Ile	Ala	Lys	Thr	
			420				425						430			
gca	aat	gaa	agt	ggt	tta	agc	gta	ttg	agt	ctg	atc	aaa	tct	gaa	aac	1344
Ala	Asn	Glu	Ser	Gly	Leu	Ser	Val	Leu	Ser	Leu	Ile	Lys	Ser	Glu	Asn	
		435				440						445				
ctg	ttg	tct	gat	gat	caa	ctt	tca	gaa	att	tta	gcg	ggt	gac	aat	atg	1392
Leu	Leu	Ser	Asp	Asp	Gln	Leu	Ser	Glu	Ile	Leu	Ala	Val	Asp	Asn	Met	
		450				455					460					
gtg	caa	ccg	aaa	gct	gaa	atg	ggt	taa								1419
Val	Gln	Pro	Lys	Ala	Glu	Met	Val									
465					470											

<210> 9666

<211> 472

<212> PRT

<213> Acinetobacter sp. ADP1

<400> 9666

```

Met Asn Ala Glu Ile Gln Thr Arg Thr Glu Lys Asp Leu Leu Gly Leu
1      5      10      15
Arg Glu Val Pro Asn Gln Phe Tyr Phe Gly Ile Gln Thr Leu Arg Ala
      20      25      30
Ile Glu Asn Phe Asn Leu Ser Ser Asn Lys Ile Asn Gln Tyr Pro Asn
      35      40      45
Leu Ile Lys Ser Leu Ala Met Val Lys His Ala Cys Ala Glu Ala Asn
      50      55      60
His Thr Leu Gly Lys Leu Ser Asp Leu Lys Phe Asn Ala Ile Lys Tyr
65      70      75      80
Ser Cys Asp Gln Leu Ile Gln Gly Phe Tyr His Glu Gln Phe Pro Ile
      85      90      95
Asp Leu Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn
      100      105      110
Glu Val Ile Ala Asn Ile Ala Leu Glu His Leu Gly His Lys Lys Gly
      115      120      125
Glu Tyr Asn Phe Leu His Pro Asn Asn Asp Val Asn Met Ser Gln Ser
130      135      140
Thr Asn Asp Val Tyr Pro Thr Ala Ile Arg Leu Gly Leu Leu Phe Ser
145      150      155      160
Leu Asp Asp Leu Asn Thr Pro Phe Glu Asn Leu Ile Ala Ser Leu Arg
      165      170      175
Arg Lys Gly Asp Glu Phe Ala His Ile Leu Lys Met Gly Arg Thr Gln
      180      185      190
Leu Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Asn Ala Phe
      195      200      205
Ala Ser Thr Leu Glu Lys Asp Leu Ile Lys Ile Arg Glu Ile Ala Pro
210      215      220
Gln Thr Leu Asn Tyr Met Asn Leu Gly Gly Thr Ala Ile Gly Thr Gly
225      230      235      240
Ile Asn Thr Glu Gln Lys Tyr Thr Gln Leu Ala Ile Asp Ala Leu Ala
      245      250      255
Thr Ile Ser Gln Lys Asp Ile Lys Ser Ala Pro Asp Leu Ile Glu Ala
      260      265      270
Thr Ser Asp Met Gly Asp Phe Val Leu Leu Ser Gly Leu Leu Lys Arg
      275      280      285
Thr Ala Thr Lys Leu Ser Lys Ile Ala Asn Asp Leu Arg Leu Leu Ser
290      295      300
Ser Gly Pro Arg Thr Gly Ile Asn Glu Ile Asn Leu Glu Pro Arg Gln
305      310      315      320
Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu
      325      330      335
Ala Met Asn Leu Val Cys Phe Gln Ile Ile Ala Asn Asp Leu Ala Val
      340      345      350
Thr Leu Ser Ala Glu Ala Gly Gln Leu Gln Leu Asn Ala Met Glu Pro
      355      360      365
Leu Ile Ala Phe Lys Leu Phe Glu Ser Ile Glu Leu Leu Gly Asn Ala
      370      375      380
Leu Val Met Phe Gln Thr Lys Cys Ile Asp Thr Val Thr Ala Asn Glu
385      390      395      400
Gln His Cys Lys Ala Leu Val Asp Asn Ser Ile Gly Ile Val Thr Ala
      405      410      415
Leu Asn Pro Tyr Leu Gly Tyr Glu Thr Thr Thr Arg Ile Ala Lys Thr
      420      425      430
Ala Asn Glu Ser Gly Leu Ser Val Leu Ser Leu Ile Lys Ser Glu Asn
      435      440      445
Leu Leu Ser Asp Asp Gln Leu Ser Glu Ile Leu Ala Val Asp Asn Met
450      455      460
Val Gln Pro Lys Ala Glu Met Val
465      470

```

<210> 9667

<211> 1440

<212> DNA

<213> Erwinia carotovora subsp. atroseptica SCRI1043

PF59083SeqList PF59083.txt

<220>
<221> CDS
<222> (1)..(1440)
<223> transl_table=11

<400> 9667

atg tca acg aat atc cgt att gaa gaa gac ctg tta ggc act cgt gaa	48
Met Ser Thr Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Thr Arg Glu	
1 5 10 15	
gtc ccc gct gac gcg tat tat ggt atc cat acg ctg cgt gcg att gag	96
Val Pro Ala Asp Ala Tyr Tyr Gly Ile His Thr Leu Arg Ala Ile Glu	
20 25 30	
aac ttt tat atc agc aat agc act att agc gat att cca gaa ttt gtt	144
Asn Phe Tyr Ile Ser Asn Ser Thr Ile Ser Asp Ile Pro Glu Phe Val	
35 40 45	
cgt gcc atg gtg atg gta aaa aaa gca gcc gca ctg gcg aat aaa gaa	192
Arg Ala Met Val Met Val Lys Lys Ala Ala Ala Leu Ala Asn Lys Glu	
50 55 60	
ctg caa acc atc ccg cgt aaa att gcc gac act att ctg caa gcc tgt	240
Leu Gln Thr Ile Pro Arg Lys Ile Ala Asp Thr Ile Leu Gln Ala Cys	
65 70 75 80	
gat gaa gtg ctg aat aac ggt aaa tgt ctg gat cag ttc cct gtc gat	288
Asp Glu Val Leu Asn Asn Gly Lys Cys Leu Asp Gln Phe Pro Val Asp	
85 90 95	
gtg tat cag ggt ggt gcg ggt acg tca gtc aac atg aac acc aac gaa	336
Val Tyr Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu	
100 105 110	
gtg ctg gcg aat atc ggt ctg gaa ctg atg ggt cat cag aaa ggt gaa	384
Val Leu Ala Asn Ile Gly Leu Glu Leu Met Gly His Gln Lys Gly Glu	
115 120 125	
tac cag tac ctg aac ccg aac gac cac ctg aac aaa tgc cag tcc acc	432
Tyr Gln Tyr Leu Asn Pro Asn Asp His Leu Asn Lys Cys Gln Ser Thr	
130 135 140	
aac gat gct tac ccg acg ggg ttc cgt att gcg gta tac acc tca atc	480
Asn Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Thr Ser Ile	
145 150 155 160	
ctg aag ctg gta gaa gcc att act cag ttg agc gat ggc ttt gag cgt	528
Leu Lys Leu Val Glu Ala Ile Thr Gln Leu Ser Asp Gly Phe Glu Arg	
165 170 175	
aaa gca aaa gag ttc gaa aac atc ctg aaa atg ggt cgt acc cag ttg	576
Lys Ala Lys Glu Phe Glu Asn Ile Leu Lys Met Gly Arg Thr Gln Leu	
180 185 190	
cag gac gcc gtg ccg atg acc ctc ggc caa gaa ttc cac gcg ttc aac	624
Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe His Ala Phe Asn	
195 200 205	
gta ctg ctg aaa gaa gaa aac cgt aac ctg ctg cgt acc gca gag ctg	672
Val Leu Leu Lys Glu Glu Asn Arg Asn Leu Leu Arg Thr Ala Glu Leu	
210 215 220	
ctg ctg gaa gta aac ctt ggc gca acc gcc atc ggt acc cgt ctg aac	720
Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Arg Leu Asn	
225 230 235 240	
acg ccg gat gag tac cag aag ctt gct gtt cag cac ttg gca aaa atc	768
Thr Pro Asp Glu Tyr Gln Lys Leu Ala Val Gln His Leu Ala Lys Ile	
245 250 255	
agc ggc ctg cct tgc gta ccg gct gaa gac ctg atc gag gcg acc tcc	816
Ser Gly Leu Pro Cys Val Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser	
260 265 270	
gac tgc ggt gct tac gtg atg atg cac agc gcc ctg aaa cgc gta gcg	864
Asp Cys Gly Ala Tyr Val Met Met His Ser Ala Leu Lys Arg Val Ala	
275 280 285	
gtt aaa atg tcg aag atc tgt aac gac ttg cgc ctg ctg tct tcc ggc	912
Val Lys Met Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly	
290 295 300	
cca cgt act ggt ctg aac gaa atc aac ctg cca gaa ttg cag gcg gga	960
Pro Arg Thr Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly	
305 310 315 320	
tca tcc atc atg cca gcc aaa gtt aac cct gta gta ccg gaa gtg gtg	1008
Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val	
325 330 335	

PF59083SeqList PF59083.txt

aat	cag	gtg	tgc	ttc	aag	gtc	atc	ggc	aac	gat	acc	tgc	gtg	acc	atg	1056
Asn	Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Cys	Val	Thr	Met	
		340						345				350				
gcg	gca	gaa	gca	ggc	cag	ttg	cag	ttg	aac	gtg	atg	gaa	ccg	gtt	atc	1104
Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile	
		355					360					365				
gga	caa	gcc	atg	ttc	gaa	tct	atc	cag	att	ctg	tct	aac	gcc	tgc	tac	1152
Gly	Gln	Ala	Met	Phe	Glu	Ser	Ile	Gln	Ile	Leu	Ser	Asn	Ala	Cys	Tyr	
	370					375					380					
aac	ctg	ctg	gaa	aaa	tgt	gtc	aac	ggc	atc	acc	gcc	aac	aaa	gaa	gtg	1200
Asn	Leu	Leu	Glu	Lys	Cys	Val	Asn	Gly	Ile	Thr	Ala	Asn	Lys	Glu	Val	
385					390					395					400	
tgt	gaa	gct	tat	gtc	ttc	aac	tct	atc	ggg	atc	gtg	acc	tac	ctg	aac	1248
Cys	Glu	Ala	Tyr	Val	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	
				405					410					415		
ccg	ttc	atc	ggg	cac	aac	ggc	gat	atc	gtt	ggg	aaa	atc	tgt	gcc		1296
Pro	Phe	Ile	Gly	His	His	Asn	Gly	Asp	Ile	Val	Gly	Lys	Ile	Cys	Ala	
			420					425					430			
gaa	acc	ggc	aaa	agc	gtg	cgt	gaa	gtc	gtg	ctg	gag	cgc	ggc	ctg	ctg	1344
Glu	Thr	Gly	Lys	Ser	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gly	Leu	Leu	
		435					440					445				
acc	gaa	gaa	cag	ctg	gac	gac	att	ttc	tcc	atc	cag	aac	ctg	atg	cac	1392
Thr	Glu	Glu	Gln	Leu	Asp	Asp	Ile	Phe	Ser	Ile	Gln	Asn	Leu	Met	His	
	450					455					460					
cca	gcc	tac	aaa	gcc	aaa	cgc	tac	acc	gac	gaa	aac	gaa	gcc	gtt		1437
Pro	Ala	Tyr	Lys	Ala	Lys	Arg	Tyr	Thr	Asp	Glu	Asn	Glu	Ala	Val		
465					470					475						
taa																1440

<210> 9668

<211> 479

<212> PRT

<213> *Erwinia carotovora* subsp. *atroseptica* SCRI1043

<400> 9668

Met	Ser	Thr	Asn	Ile	Arg	Ile	Glu	Glu	Asp	Leu	Leu	Gly	Thr	Arg	Glu	
1				5					10					15		
Val	Pro	Ala	Asp	Ala	Tyr	Tyr	Gly	Ile	His	Thr	Leu	Arg	Ala	Ile	Glu	
			20					25					30			
Asn	Phe	Tyr	Ile	Ser	Asn	Ser	Thr	Ile	Ser	Asp	Ile	Pro	Glu	Phe	Val	
		35					40					45				
Arg	Ala	Met	Val	Met	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Lys	Glu	
		50				55					60					
Leu	Gln	Thr	Ile	Pro	Arg	Lys	Ile	Ala	Asp	Thr	Ile	Leu	Gln	Ala	Cys	
65					70				75						80	
Asp	Glu	Val	Leu	Asn	Asn	Gly	Lys	Cys	Leu	Asp	Gln	Phe	Pro	Val	Asp	
				85					90					95		
Val	Tyr	Gln	Gly	Ala	Gly	Thr	Ser	Val	Asn	Met	Asn	Thr	Asn	Glu		
		100					105						110			
Val	Leu	Ala	Asn	Ile	Gly	Leu	Glu	Leu	Met	Gly	His	Gln	Lys	Gly	Glu	
		115					120					125				
Tyr	Gln	Tyr	Leu	Asn	Pro	Asn	Asp	His	Leu	Asn	Lys	Cys	Gln	Ser	Thr	
		130				135					140					
Asn	Asp	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Ile	Ala	Val	Tyr	Thr	Ser	Ile	
145					150					155					160	
Leu	Lys	Leu	Val	Glu	Ala	Ile	Thr	Gln	Leu	Ser	Asp	Gly	Phe	Glu	Arg	
				165					170					175		
Lys	Ala	Lys	Glu	Phe	Glu	Asn	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	
		180						185					190			
Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	His	Ala	Phe	Asn	
		195					200					205				
Val	Leu	Leu	Lys	Glu	Glu	Asn	Arg	Asn	Leu	Leu	Arg	Thr	Ala	Glu	Leu	
		210				215					220					
Leu	Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Arg	Leu	Asn	
225					230					235					240	
Thr	Pro	Asp	Glu	Tyr	Gln	Lys	Leu	Ala	Val	Gln	His	Leu	Ala	Lys	Ile	
				245					250					255		

PF59083SeqList PF59083.txt

Ser Gly Leu Pro Cys Val Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser
 260 265 270
 Asp Cys Gly Ala Tyr Val Met Met His Ser Ala Leu Lys Arg Val Ala
 275 280 285
 Val Lys Met Ser Lys Ile Cys Asn Asp Leu Arg Leu Ser Ser Gly
 290 295 300
 Pro Arg Thr Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly
 305 310 315 320
 Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val
 325 330 335
 Asn Gln Val Cys Phe Lys Val Ile Gly Asn Asp Thr Cys Val Thr Met
 340 345 350
 Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile
 355 360 365
 Gly Gln Ala Met Phe Glu Ser Ile Gln Ile Leu Ser Asn Ala Cys Tyr
 370 375 380
 Asn Leu Leu Glu Lys Cys Val Asn Gly Ile Thr Ala Asn Lys Glu Val
 385 390 395 400
 Cys Glu Ala Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn
 405 410 415
 Pro Phe Ile Gly His His Asn Gly Asp Ile Val Gly Lys Ile Cys Ala
 420 425 430
 Glu Thr Gly Lys Ser Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu
 435 440 445
 Thr Glu Glu Gln Leu Asp Asp Ile Phe Ser Ile Gln Asn Leu Met His
 450 455 460
 Pro Ala Tyr Lys Ala Lys Arg Tyr Thr Asp Glu Asn Glu Ala Val
 465 470 475

<210> 9669

<211> 1440

<212> DNA

<213> Erwinia carotovora subsp. atroseptica SCRI1043

<220>

<221> CDS

<222> (1)..(1440)

<223> transl_table=11

<400> 9669

atg tca gaa aac atc cgt att gaa gaa gac ctg tta ggc acc cga gaa	48
Met Ser Glu Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Thr Arg Glu	
1 5 10 15	
gtt ccc gca gac gcg tat tat ggc gtt cat acg ctg cgc gcc gtc gaa	96
Val Pro Ala Asp Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Val Glu	
20 25 30	
aac ttc tat atc agt aac aat aaa atc agt gac att ccc gag ttc gta	144
Asn Phe Tyr Ile Ser Asn Asn Lys Ile Ser Asp Ile Pro Glu Phe Val	
35 40 45	
cgc ggc atg gtc atg gtg aag aaa gcc gcc gcg ctg gcg aac aaa gag	192
Arg Gly Met Val Met Val Lys Lys Ala Ala Ala Leu Ala Asn Lys Glu	
50 55 60	
cta caa act atc ccg aaa aaa atc gcc gac gtc atc atc cgc gcc tgt	240
Leu Gln Thr Ile Pro Lys Lys Ile Ala Asp Val Ile Ile Arg Ala Cys	
65 70 75 80	
gat gaa gtt ctg aat aac ggc aaa tgc atg gac cag ttc cca gta gat	288
Asp Glu Val Leu Asn Asn Gly Lys Cys Met Asp Gln Phe Pro Val Asp	
85 90 95	
gtg tat cag ggg gga gca ggt acg tcg gtc aac atg aat acc aac gaa	336
Val Tyr Gln Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu	
100 105 110	
gta tta gcc aat att ggt ctg gag ctg atg ggc cac cag aaa ggc gaa	384
Val Leu Ala Asn Ile Gly Leu Glu Leu Met Gly His Gln Lys Gly Glu	
115 120 125	
tac cag tat ctg aac ccc aac gat cat ctg aat aaa tgc caa tcc acc	432
Tyr Gln Tyr Leu Asn Pro Asn Asp His Leu Asn Lys Cys Gln Ser Thr	
130 135 140	
aat gat gcc tac ccc acc gga ttt cgt atc gcg gtc tac gcg gcc ata	480
Asn Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Ala Ala Ile	

PF59083SeqList PF59083.txt

145	ctg	aaa	ttg	acg	gat	gcg	ata	gcg	aag	ttg	agc	gat	ggc	ttc	gag	cac	528
	Leu	Lys	Leu	Thr	Asp	Ala	Ile	Ala	Lys	Leu	Ser	Asp	Gly	Phe	Glu	His	
					165					170					175		
	aaa	gcc	aaa	gaa	ttt	gaa	gac	ggt	ctg	aag	atg	ggg	cgg	acc	cag	ttg	576
	Lys	Ala	Lys	Glu	Phe	Glu	Asp	Val	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	
				180					185					190			
	cag	gac	gcc	gtg	cca	atg	acg	ctc	ggt	cag	gaa	ttt	cat	gcg	ttt	aac	624
	Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	His	Ala	Phe	Asn	
			195					200					205				
	gtg	ctg	ttg	caa	gag	gaa	atc	aaa	aac	ctg	ctg	cgc	acg	gcg	gaa	ctg	672
	Val	Leu	Leu	Gln	Glu	Glu	Ile	Lys	Asn	Leu	Leu	Arg	Thr	Ala	Glu	Leu	
		210				215						220					
	cta	ctt	gaa	gtc	aat	ctg	ggg	gcc	acc	gcg	atc	ggt	aca	cgc	ctg	aac	720
	Leu	Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Arg	Leu	Asn	
	225				230					235					240		
	aca	cca	gac	ggc	tac	cag	caa	ctg	gcg	gta	cag	cgt	ttg	gcg	gaa	gtc	768
	Thr	Pro	Asp	Gly	Tyr	Gln	Gln	Leu	Ala	Val	Gln	Arg	Leu	Ala	Glu	Val	
				245				250						255			
	agc	ggc	ctg	ccg	tgt	gtg	cca	gca	gaa	gac	ttg	atc	gaa	gcc	acg	tca	816
	Ser	Gly	Leu	Pro	Cys	Val	Pro	Ala	Glu	Asp	Leu	Ile	Glu	Ala	Thr	Ser	
				260				265					270				
	gac	tgt	ggt	gcc	tat	gta	atg	gta	cac	agt	tcg	ctg	aag	cgt	ctg	gct	864
	Asp	Cys	Gly	Ala	Tyr	Val	Met	Val	His	Ser	Ser	Leu	Lys	Arg	Leu	Ala	
			275				280						285				
	gtg	aag	ctg	tcg	aag	att	tgt	aat	gac	ctg	cgt	ttg	ctc	tct	tcc	ggc	912
	Val	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	
		290				295						300					
	cct	cgc	gct	ggc	ctg	aat	gaa	atc	aac	ctg	cca	gag	ttg	cag	gcg	ggt	960
	Pro	Arg	Ala	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	Ala	Gly	
	305				310					315					320		
	tcc	tcc	atc	atg	cct	gcc	aaa	ggt	aac	ccc	gtg	gtg	ccg	gaa	gtc	gtc	1008
	Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Val	Pro	Glu	Val	Val	
				325				330						335			
	aat	caa	gtg	tgc	ttc	aag	gtc	atc	ggt	aac	gac	acc	tgc	gtc	act	atg	1056
	Asn	Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Cys	Val	Thr	Met	
				340				345					350				
	gcg	tcg	gag	gcc	ggg	caa	tta	cag	tta	aac	gtg	atg	gag	ccg	gtt	atc	1104
	Ala	Ser	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile	
			355					360					365				
	ggt	cag	gca	atg	ttt	gaa	tca	acc	cac	att	ctg	act	aac	gcc	tgc	tac	1152
	Gly	Gln	Ala	Met	Phe	Glu	Ser	Thr	His	Ile	Leu	Thr	Asn	Ala	Cys	Tyr	
		370			375					380							
	aac	ctg	ctg	gag	aaa	tgc	gtc	agc	ggt	atc	acc	gct	aat	aag	ggc	gtc	1200
	Asn	Leu	Leu	Glu	Lys	Cys	Val	Ser	Gly	Ile	Thr	Ala	Asn	Lys	Gly	Val	
	385				390					395					400		
	tgc	gaa	gcc	tat	gtt	ttc	aac	tcc	atc	gga	att	gtg	acg	tac	ctg	aac	1248
	Cys	Glu	Ala	Tyr	Val	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	
				405				410						415			
	ccg	ttc	atc	ggc	cac	aat	ggc	gac	att	gtc	ggc	aga	atc	tgt	gcg		1296
	Pro	Phe	Ile	Gly	His	Asn	Gly	Asp	Ile	Val	Gly	Arg	Ile	Cys	Ala		
				420			425					430					
	gaa	aca	gga	aag	agc	gtg	cgt	gaa	gtc	gta	ctg	gag	cgc	ggt	ctg	ctg	1344
	Glu	Thr	Gly	Lys	Ser	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gly	Leu	Leu	
			435				440					445					
	aca	gaa	gct	gag	ctg	gat	gac	att	ttc	tcc	atc	cag	aac	ctg	atg	cac	1392
	Thr	Glu	Ala	Glu	Leu	Asp	Asp	Ile	Phe	Ser	Ile	Gln	Asn	Leu	Met	His	
		450			455			460									
	cca	gcg	tac	aaa	gcc	aaa	cgc	tac	act	gat	gaa	aac	gag	ctt	cct		1437
	Pro	Ala	Tyr	Lys	Ala	Lys	Arg	Tyr	Thr	Asp	Glu	Asn	Glu	Leu	Pro		
	465				470					475							
	taa																1440

<210> 9670

<211> 479

<212> PRT

<213> Erwinia carotovora subsp. atroseptica SCRI1043

Seite 10140

PF59083SeqList PF59083.txt

<400> 9670

```

Met Ser Glu Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Thr Arg Glu
1      5      10      15
Val Pro Ala Asp Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Val Glu
20      25      30
Asn Phe Tyr Ile Ser Asn Asn Lys Ile Ser Asp Ile Pro Glu Phe Val
35      40      45
Arg Gly Met Val Met Val Lys Lys Ala Ala Ala Leu Ala Asn Lys Glu
50      55      60
Leu Gln Thr Ile Pro Lys Lys Ile Ala Asp Val Ile Ile Arg Ala Cys
65      70      75      80
Asp Glu Val Leu Asn Asn Gly Lys Cys Met Asp Gln Phe Pro Val Asp
85      90      95
Val Tyr Gln Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu
100      105      110
Val Leu Ala Asn Ile Gly Leu Glu Leu Met Gly His Gln Lys Gly Glu
115      120      125
Tyr Gln Tyr Leu Asn Pro Asn Asp His Leu Asn Lys Cys Gln Ser Thr
130      135      140
Asn Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Ala Ala Ile
145      150      155      160
Leu Lys Leu Thr Asp Ala Ile Ala Lys Leu Ser Asp Gly Phe Glu His
165      170      175
Lys Ala Lys Glu Phe Glu Asp Val Leu Lys Met Gly Arg Thr Gln Leu
180      185      190
Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe His Ala Phe Asn
195      200      205
Val Leu Leu Gln Glu Glu Ile Lys Asn Leu Leu Arg Thr Ala Glu Leu
210      215      220
Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Arg Leu Asn
225      230      235      240
Thr Pro Asp Gly Tyr Gln Gln Leu Ala Val Gln Arg Leu Ala Glu Val
245      250      255
Ser Gly Leu Pro Cys Val Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser
260      265      270
Asp Cys Gly Ala Tyr Val Met Val His Ser Ser Leu Lys Arg Leu Ala
275      280      285
Val Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly
290      295      300
Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly
305      310      315      320
Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val
325      330      335
Asn Gln Val Cys Phe Lys Val Ile Gly Asn Asp Thr Cys Val Thr Met
340      345      350
Ala Ser Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile
355      360      365
Gly Gln Ala Met Phe Glu Ser Thr His Ile Leu Thr Asn Ala Cys Tyr
370      375      380
Asn Leu Leu Glu Lys Cys Val Ser Gly Ile Thr Ala Asn Lys Gly Val
385      390      395      400
Cys Glu Ala Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn
405      410      415
Pro Phe Ile Gly His His Asn Gly Asp Ile Val Gly Arg Ile Cys Ala
420      425      430
Glu Thr Gly Lys Ser Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu
435      440      445
Thr Glu Ala Glu Leu Asp Asp Ile Phe Ser Ile Gln Asn Leu Met His
450      455      460
Pro Ala Tyr Lys Ala Lys Arg Tyr Thr Asp Glu Asn Glu Leu Pro
465      470      475

```

<210> 9671

<211> 1473

<212> DNA

<213> Propionibacterium acnes KPA171202

<220>

PF59083SeqList PF59083.txt

<221> CDS
<222> (1)..(1473)
<223> transl_table=11

<400> 9671

ttg act gag atc cgg atc gaa gaa gat ctt ctt ggg aaa cgg gaa atc	48
Met Thr Glu Ile Arg Ile Glu Glu Asp Leu Leu Gly Lys Arg Glu Ile	
1 5 10 15	
tcg aat gag cac tac tat gga att cat act ttg cgg gct tta gag aac	96
Ser Asn Glu His Tyr Tyr Gly Ile His Thr Leu Arg Ala Leu Glu Asn	
20 25 30	
ttc caa ata tca cgc gga tgt atg aat gac gag cct gac ttc att cgt	144
Phe Gln Ile Ser Arg Gly Cys Met Asn Asp Glu Pro Asp Phe Ile Arg	
35 40 45	
gga atg gtt cag gta aag aag gca aca gct ctg acg aat aag cag ttg	192
Gly Met Val Gln Val Lys Lys Ala Thr Ala Leu Thr Asn Lys Gln Leu	
50 55 60	
aag gtt ctc ccg agt gat gtc gct gac gcc att gtc gct gca tgc gat	240
Lys Val Leu Pro Ser Asp Val Ala Asp Ala Ile Val Ala Ala Cys Asp	
65 70 75 80	
gcg atc ttg gat gat ggg cgc tgt atg gac caa ttc ccg act gat tcc	288
Ala Ile Leu Asp Asp Gly Arg Cys Met Asp Gln Phe Pro Thr Asp Ser	
85 90 95	
ttc caa gga gga ggc gga acc tcg atc aac atg aac acc aat gag gtt	336
Phe Gln Gly Gly Ala Gly Thr Ser Ile Asn Met Asn Thr Asn Glu Val	
100 105 110	
gtc gcc aat ttg gcc ctc gaa atg ttg gga tac ccg aaa ggc acc tat	384
Val Ala Asn Leu Ala Leu Glu Met Leu Gly Tyr Pro Lys Gly Thr Tyr	
115 120 125	
gac gtc atc cac ccc aac gat gat gtc aat aag tcc cag tcg act aac	432
Asp Val Ile His Pro Asn Asp Asp Val Asn Lys Ser Gln Ser Thr Asn	
130 135 140	
gac gct tac ccc acc ggg ttc cgg ctc ggg gtg tac gct ttg cta gag	480
Asp Ala Tyr Pro Thr Gly Phe Arg Leu Gly Val Tyr Ala Leu Leu Glu	
145 150 155 160	
ggg ctg aag cga gcc gtc gcc gac ctc gca gac agt ttc gat gcc aag	528
Gly Leu Lys Arg Ala Val Ala Asp Leu Ala Asp Ser Phe Asp Ala Lys	
165 170 175	
gct gag gaa ttt gcc gat gta ctg aag atg ggg cgt acc caa ttg cag	576
Ala Glu Glu Phe Ala Asp Val Leu Lys Met Gly Arg Thr Gln Leu Gln	
180 185 190	
gat gcc gtc ccc atg act ttg ggt gag gag ttt gac ggg tac gca cac	624
Asp Ala Val Pro Met Thr Leu Gly Glu Glu Phe Asp Gly Tyr Ala His	
195 200 205	
aac atc cgt gct gaa ctg gac cgg ctt gat att gga agc gat ctt ctc	672
Asn Ile Arg Ala Glu Leu Asp Arg Leu Asp Ile Gly Ser Asp Leu Leu	
210 215 220	
gta gag gtc aac ctg ggc ggc acc gcc atc gga act cgg atc aac acc	720
Val Glu Val Asn Leu Gly Gly Thr Ala Ile Gly Thr Arg Ile Asn Thr	
225 230 235 240	
cca gac gga tat gct gaa ctt gct gct gag aaa ctg gcc gag gtg acc	768
Pro Asp Gly Tyr Ala Glu Leu Ala Ala Glu Lys Leu Ala Glu Val Thr	
245 250 255	
gga tac ccg att cgt ccc tcc acc aac ctc atg gaa tcg tct tac gac	816
Gly Tyr Pro Ile Arg Pro Ser Thr Asn Leu Met Glu Ser Ser Tyr Asp	
260 265 270	
aac ggc gcc tac att gct gtc cat tct att atc aaa cgc cta gca gcg	864
Asn Gly Ala Tyr Ile Ala Val His Ser Ile Ile Lys Arg Leu Ala Ala	
275 280 285 290	
aag atc tcc aag atc tgc aac gat tta cga ttg ctt tca tct gga ccg	912
Lys Ile Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro	
295 300 305	
agg gct ggg ctc aag gaa atc aac ctt cca gag atg cag gcg gga tcg	960
Arg Ala Gly Leu Lys Glu Ile Asn Leu Pro Glu Met Gln Ala Gly Ser	
310 315 320	
tcc atc atg ccg gcg aag gtg aat ccg gtc att ccc gag gtc gtc aat	1008
Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn	
325 330 335	
cag atc tgc ttc aaa gta ttt gga aac gat gtc acc gtc tgt ttc gct	1056

PF59083SeqList PF59083.txt

Gln	Ile	Cys	Phe	Lys	Val	Phe	Gly	Asn	Asp	Val	Thr	Val	Cys	Phe	Ala		
			340					345					350				
gcc	gag	gcc	ggt	cag	cta	gaa	ctt	aat	gtg	atg	gaa	ccg	gcg	ctg	tcg		1104
Ala	Glu	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Ala	Leu	Ser		
		355					360					365					
caa	gca	atg	ttc	gag	tcc	atc	cac	ctg	ctg	acc	aat	gcc	tgc	gac	acg		1152
Gln	Ala	Met	Phe	Glu	Ser	Ile	His	Leu	Leu	Thr	Asn	Ala	Cys	Asp	Thr		
	370					375					380						
ttg	cgt	agc	aag	tgc	att	gac	ggg	atc	acc	gca	aat	gtg	gag	cgg	tgc		1200
Leu	Arg	Ser	Lys	Cys	Ile	Asp	Gly	Ile	Thr	Ala	Asn	Val	Glu	Arg	Cys		
	385				390					395					400		
cgg	gag	tat	gtc	acc	aat	tcc	atc	ggg	atc	gtg	acc	tac	ttg	aat	gat		1248
Arg	Glu	Tyr	Val	Thr	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	Asp		
			405				410							415			
gtg	att	gga	cac	cat	caa	ggc	gat	ctc	att	ggc	gag	gaa	gct	gcc	cgt		1296
Val	Ile	Gly	His	His	Gln	Gly	Asp	Leu	Ile	Gly	Glu	Glu	Ala	Ala	Arg		
			420				425						430				
acc	gga	aag	tca	ggt	cgt	gag	gtc	gtc	ctc	gaa	cac	gac	ctc	atc	ccg		1344
Thr	Gly	Lys	Ser	Val	Arg	Glu	Val	Val	Leu	Glu	His	Asp	Leu	Ile	Pro		
		435				440						445					
gag	gaa	agg	ctg	gac	gag	atc	atg	tcg	acc	cag	aac	ttc	ctg	cac	ccc		1392
Glu	Glu	Arg	Leu	Asp	Glu	Ile	Met	Ser	Thr	Gln	Asn	Phe	Leu	His	Pro		
	450				455					460							
cgg	tat	tcc	gga	cgt	acc	tac	gag	ccg	agt	gac	cgc	ggg	ctc	ccg	gag		1440
Arg	Tyr	Ser	Gly	Arg	Thr	Tyr	Glu	Pro	Ser	Asp	Arg	Gly	Leu	Pro	Glu		
	465				470					475					480		
gat	ccc	agg	aca	ttc	gtg	tcc	gag	cgt	tgc	tga							1473
Asp	Pro	Arg	Thr	Phe	Val	Ser	Glu	Arg	Cys								
				485					490								

<210> 9672

<211> 490

<212> PRT

<213> Propionibacterium acnes KPA171202

<400> 9672

Met	Thr	Glu	Ile	Arg	Ile	Glu	Glu	Asp	Leu	Leu	Gly	Lys	Arg	Glu	Ile		
1			5					10						15			
Ser	Asn	Glu	His	Tyr	Tyr	Gly	Ile	His	Thr	Leu	Arg	Ala	Leu	Glu	Asn		
			20					25					30				
Phe	Gln	Ile	Ser	Arg	Gly	Cys	Met	Asn	Asp	Glu	Pro	Asp	Phe	Ile	Arg		
		35				40						45					
Gly	Met	Val	Gln	Val	Lys	Lys	Ala	Thr	Ala	Leu	Thr	Asn	Lys	Gln	Leu		
	50					55				60							
Lys	Val	Leu	Pro	Ser	Asp	Val	Ala	Asp	Ala	Ile	Val	Ala	Ala	Cys	Asp		
	65				70				75					80			
Ala	Ile	Leu	Asp	Asp	Gly	Arg	Cys	Met	Asp	Gln	Phe	Pro	Thr	Asp	Ser		
			85					90						95			
Phe	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Ile	Asn	Met	Asn	Thr	Asn	Glu	Val		
		100					105						110				
Val	Ala	Asn	Leu	Ala	Leu	Glu	Met	Leu	Gly	Tyr	Pro	Lys	Gly	Thr	Tyr		
		115				120						125					
Asp	Val	Ile	His	Pro	Asn	Asp	Asp	Val	Asn	Lys	Ser	Gln	Ser	Thr	Asn		
	130				135						140						
Asp	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Leu	Gly	Val	Tyr	Ala	Leu	Leu	Glu		
	145				150				155					160			
Gly	Leu	Lys	Arg	Ala	Val	Ala	Asp	Leu	Ala	Asp	Ser	Phe	Asp	Ala	Lys		
			165					170						175			
Ala	Glu	Glu	Phe	Ala	Asp	Val	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln		
		180					185						190				
Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Glu	Glu	Phe	Asp	Gly	Tyr	Ala	His		
		195				200						205					
Asn	Ile	Arg	Ala	Glu	Leu	Asp	Arg	Leu	Asp	Ile	Gly	Ser	Asp	Leu	Leu		
	210				215						220						
Val	Glu	Val	Asn	Leu	Gly	Thr	Ala	Ile	Gly	Thr	Arg	Ile	Asn	Thr			
	225				230				235					240			
Pro	Asp	Gly	Tyr	Ala	Glu	Leu	Ala	Ala	Glu	Lys	Leu	Ala	Glu	Val	Thr		
			245					250						255			
Gly	Tyr	Pro	Ile	Arg	Pro	Ser	Thr	Asn	Leu	Met	Glu	Ser	Ser	Tyr	Asp		

PF59083SeqList PF59083.txt

```

      260      265      270
Asn Gly Ala Tyr Ile Ala Val His Ser Ile Ile Lys Arg Leu Ala Ala
      275      280      285
Lys Ile Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro
      290      295      300
Arg Ala Gly Leu Lys Glu Ile Asn Leu Pro Glu Met Gln Ala Gly Ser
      305      310      315
Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn
      320      325      330
Gln Ile Cys Phe Lys Val Phe Gly Asn Asp Val Thr Val Cys Phe Ala
      335      340      345
Ala Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Ala Leu Ser
      350      355      360
Gln Ala Met Phe Glu Ser Ile His Leu Leu Thr Asn Ala Cys Asp Thr
      365      370      375
Leu Arg Ser Lys Cys Ile Asp Gly Ile Thr Ala Asn Val Glu Arg Cys
      380      385      390
Arg Glu Tyr Val Thr Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Asp
      395      400      405
Val Ile Gly His Gln Gly Asp Leu Ile Gly Glu Glu Ala Ala Arg
      410      415      420
Thr Gly Lys Ser Val Arg Glu Val Val Leu Glu His Asp Leu Ile Pro
      425      430      435
Glu Glu Arg Leu Asp Glu Ile Met Ser Thr Gln Asn Phe Leu His Pro
      440      445      450
Arg Tyr Ser Gly Arg Thr Tyr Glu Pro Ser Asp Arg Gly Leu Pro Glu
      455      460      465
Asp Pro Arg Thr Phe Val Ser Glu Arg Cys
      470      475      480
      485      490

```

<210> 9673

<211> 1425

<212> DNA

<213> Leifsonia xyli subsp. xyli str. CTCB07

<220>

<221> CDS

<222> (1)..(1425)

<223> transl_table=11

<400> 9673

```

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

```


PF59083SeqList PF59083.txt

Thr 145	Ala	Ile	Lys	Ile	Gly 150	Leu	Thr	Phe	Ala	Leu 155	Gly	His	Leu	Leu	Asp 160	
gag	ctg	gcg	ctg	ctc	cg	gac	tca	ttc	gcg	agc	aaa	ggt	gcg	gag	ttc	528
Glu	Leu	Ala	Leu	Leu	Arg	Asp	Ser	Phe	Ala	Ser	Lys	Gly	Ala	Glu	Phe	
				165					170					175		
cg	cac	att	ctc	aag	gtc	ggc	cg	acg	cag	ctc	cag	gat	gcc	gtg	ccg	576
Arg	His	Ile	Leu	Lys	Val	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	
			180					185					190			
atg	gcg	ctc	ggc	cag	gag	ttc	agc	ggt	ttc	gcc	acc	acg	ctc	acc	gag	624
Met	Ala	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Phe	Ala	Thr	Thr	Leu	Thr	Glu	
			195				200					205				
gac	cac	gcc	cg	ctc	aca	gag	acg	aag	tcc	ctc	ctc	gcc	gag	atc	aac	672
Asp	His	Ala	Arg	Leu	Thr	Glu	Thr	Lys	Ser	Leu	Leu	Ala	Glu	Ile	Asn	
						215					220					
ctt	ggc	gcc	aca	gcg	atc	ggc	acc	ggg	atc	acc	gcg	gac	gcc	ggc	tat	720
Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Thr	Ala	Asp	Ala	Gly	Tyr	
225				230					235						240	
gcc	gct	gcg	gcg	gtc	aaa	cac	ctc	aac	ctc	atc	acc	ggc	ctc	agc	ctc	768
Ala	Ala	Ala	Ala	Val	Lys	His	Leu	Asn	Leu	Ile	Thr	Gly	Leu	Ser	Leu	
				245					250					255		
gag	acc	gcc	ccc	gac	ctc	atc	gaa	tcg	acc	agc	gac	gcg	ggc	gct	ttc	816
Glu	Thr	Ala	Pro	Asp	Leu	Ile	Glu	Ser	Thr	Ser	Asp	Ala	Gly	Ala	Phe	
			260					265					270			
atg	tcg	ttc	tcc	gga	tcg	ctg	aag	cg	agc	gcg	atc	aaa	ctc	tcg	aag	864
Met	Ser	Phe	Ser	Gly	Ser	Leu	Lys	Arg	Ser	Ala	Ile	Lys	Leu	Ser	Lys	
			275				280					285				
atc	tgc	aac	gac	ctg	cg	ctg	ctc	tcc	tcc	gga	ccg	cag	gcc	gga	ctc	912
Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Gln	Ala	Gly	Leu	
	290				295						300					
ggc	gag	atc	aac	ctc	ccg	ccg	cg	cag	gcc	ggt	tcg	agc	atc	atg	ccg	960
Gly	Glu	Ile	Asn	Leu	Pro	Pro	Arg	Gln	Ala	Gly	Ser	Ser	Ile	Met	Pro	
305				310						315					320	
ggc	aaa	gtc	aac	ccc	gtc	atc	ccc	gag	gtc	gtc	aac	cag	gtc	gcc	ttc	1008
Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln	Val	Ala	Phe	
				325				330						335		
tcg	gtg	gcc	ggg	gct	gac	gtc	acc	gtc	acg	atg	gcg	gcg	gag	ggc	ggc	1056
Ser	Val	Ala	Gly	Ala	Asp	Val	Thr	Val	Thr	Met	Ala	Ala	Glu	Gly	Gly	
			340					345					350			
cag	ctc	cag	ctg	aac	gcc	ttc	gag	ccg	gtg	atc	gcc	cat	tcg	ctg	ctc	1104
Gln	Leu	Gln	Leu	Asn	Ala	Phe	Glu	Pro	Val	Ile	Ala	His	Ser	Leu	Leu	
			355				360					365				
cag	agc	atc	acc	tgg	atg	gct	cag	gcg	ttc	cac	act	ctc	cg	gtc	aac	1152
Gln	Ser	Ile	Thr	Trp	Met	Ala	Gln	Ala	Phe	His	Thr	Leu	Arg	Val	Asn	
					375						380					
tgc	gtg	gac	ggc	atc	act	gcc	aat	gag	gag	cga	ctc	ggc	ggg	atg	gtc	1200
Cys	Val	Asp	Gly	Ile	Thr	Ala	Asn	Glu	Glu	Arg	Leu	Gly	Gly	Met	Val	
385				390					395						400	
ggt	tcc	tcg	gtc	ggc	gtc	atc	acc	gcg	ctc	act	ccg	cac	atc	ggc	tac	1248
Gly	Ser	Ser	Val	Gly	Val	Ile	Thr	Ala	Leu	Thr	Pro	His	Ile	Gly	Tyr	
			405					410						415		
gcg	gcc	gcg	gcc	gcg	ctc	gcg	aaa	tcg	gcg	ctg	ctg	acc	ggc	cg	aac	1296
Ala	Ala	Ala	Ala	Ala	Leu	Ala	Lys	Ser	Ala	Leu	Leu	Thr	Gly	Arg	Asn	
			420					425					430			
gtg	gcc	gac	ctc	gtg	gtc	gag	gcg	aac	ctc	atg	agc	cgt	gtg	gag	gtc	1344
Val	Ala	Asp	Leu	Val	Val	Glu	Ala	Asn	Leu	Met	Ser	Arg	Val	Glu	Val	
			435				440					445				
atg	cg	ctg	ctg	tcc	ccg	gcg	cg	ctg	tcg	ggg	ctg	gaa	gcg	atc	acg	1392
Met	Arg	Leu	Leu	Ser	Pro	Ala	Arg	Leu	Ser	Gly	Leu	Glu	Ala	Ile	Thr	
					455						460					
aca	gcc	atc	ccg	gtg	atc	gac	cag	cag	gcg	tga						1425
Thr	Ala	Ile	Pro	Val	Ile	Asp	Gln	Gln	Ala							
465					470											

<210> 9674

<211> 474

<212> PRT

<213> Leifsonia xyli subsp. xyli str. CTCB07

<400> 9674

PF59083SeqList PF59083.txt

```

Met Arg Val Glu Thr Asp Ser Leu Gly Ala Arg Asp Ile Pro Ala Asp
1      5      10      15
Ala Tyr Trp Gly Val His Thr Ser Arg Ala Leu Glu Asn Phe Pro Ile
      20      25      30
Ala Lys Arg Pro Ile Ser Val Tyr Pro Asp Leu Ile Val Ala Leu Ala
      35      40      45
Ser Val Lys Gln Ala Ala Ala Arg Ala Asn Leu Glu Ile Gly Val Leu
      50      55      60
Asp Ala His Lys Ala Gly Leu Ile Asp Arg Ala Cys Gln Leu Ile Ile
65      70      75      80
Asp Gly Arg Phe His Asp Gln Phe Val Val Gly Val Met Gln Gly Gly
      85      90      95
Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu Val Ile Ala Asn Ile
      100      105      110
Ala Leu Glu Leu Asp Gly His Ala Lys Ala Glu Tyr Gln Arg Leu Ser
      115      120      125
Pro Ile Asp Asp Val Asn Arg Ser Gln Ser Thr Asn Asp Thr Tyr Pro
      130      135      140
Thr Ala Ile Lys Ile Gly Leu Thr Phe Ala Leu Gly His Leu Leu Asp
145      150      155      160
Glu Leu Ala Leu Leu Arg Asp Ser Phe Ala Ser Lys Gly Ala Glu Phe
      165      170      175
Arg His Ile Leu Lys Val Gly Arg Thr Gln Leu Gln Asp Ala Val Pro
      180      185      190
Met Ala Leu Gly Gln Glu Phe Ser Gly Phe Ala Thr Thr Leu Thr Glu
      195      200      205
Asp His Ala Arg Leu Thr Glu Thr Lys Ser Leu Leu Ala Glu Ile Asn
      210      215      220
Leu Gly Ala Thr Ala Ile Gly Thr Gly Ile Thr Ala Asp Ala Gly Tyr
225      230      235      240
Ala Ala Ala Ala Val Lys His Leu Asn Leu Ile Thr Gly Leu Ser Leu
      245      250      255
Glu Thr Ala Pro Asp Leu Ile Glu Ser Thr Ser Asp Ala Gly Ala Phe
      260      265      270
Met Ser Phe Ser Gly Ser Leu Lys Arg Ser Ala Ile Lys Leu Ser Lys
      275      280      285
Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Gln Ala Gly Leu
      290      295      300
Gly Glu Ile Asn Leu Pro Pro Arg Gln Ala Gly Ser Ser Ile Met Pro
305      310      315      320
Gly Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Val Ala Phe
      325      330      335
Ser Val Ala Gly Ala Asp Val Thr Val Thr Met Ala Ala Glu Gly Gly
      340      345      350
Gln Leu Gln Leu Asn Ala Phe Glu Pro Val Ile Ala His Ser Leu Leu
      355      360      365
Gln Ser Ile Thr Trp Met Ala Gln Ala Phe His Thr Leu Arg Val Asn
      370      375      380
Cys Val Asp Gly Ile Thr Ala Asn Glu Glu Arg Leu Gly Gly Met Val
385      390      395      400
Gly Ser Ser Val Gly Val Ile Thr Ala Leu Thr Pro His Ile Gly Tyr
      405      410      415
Ala Ala Ala Ala Ala Leu Ala Lys Ser Ala Leu Leu Thr Gly Arg Asn
      420      425      430
Val Ala Asp Leu Val Val Glu Ala Asn Leu Met Ser Arg Val Glu Val
      435      440      445
Met Arg Leu Leu Ser Pro Ala Arg Leu Ser Gly Leu Glu Ala Ile Thr
      450      455      460
Thr Ala Ile Pro Val Ile Asp Gln Gln Ala
465      470

```

<210> 9675

<211> 1884

<212> DNA

<213> Desulfotalea psychrophila Lsv54

<220>

<221> CDS

<222> (1)..(1884)

<223> transl_table=11

<400> 9675

ttg	gag	gat	att	atg	aag	tta	gat	gaa	aat	act	ctt	aag	cag	gca	gcg	48
Met	Glu	Asp	Ile	Met	Lys	Leu	Asp	Glu	Asn	Thr	Leu	Lys	Gln	Ala	Ala	
1				5					10					15		
ctg	acg	gcg	gga	att	gaa	gag	gta	gat	tta	cag	aca	ttt	ttt	gct	cag	96
Leu	Thr	Ala	Gly	Ile	Glu	Glu	Val	Asp	Leu	Gln	Thr	Phe	Phe	Ala	Gln	
			20					25					30			
ggt	gag	cgt	ata	gag	tat	gca	gcc	ggt	gat	tgg	ctc	ttt	cag	gaa	tca	144
Gly	Glu	Arg	Ile	Glu	Tyr	Ala	Ala	Gly	Asp	Trp	Leu	Phe	Gln	Glu	Ser	
		35					40					45				
act	cct	aga	aac	tgg	gca	gga	att	att	ctt	gcc	gga	gag	att	cag	ctt	192
Thr	Pro	Arg	Asn	Trp	Ala	Gly	Ile	Ile	Leu	Ala	Gly	Glu	Ile	Gln	Leu	
	50					55				60						
gtt	cgt	ggc	ctg	cat	ggt	agc	tct	cac	cgt	gtt	ggt	acc	gtt	tct	gcg	240
Val	Arg	Gly	Leu	His	Gly	Ser	Ser	His	Arg	Val	Gly	Thr	Val	Ser	Ala	
65				70					75						80	
gga	gga	ttg	ata	tcc	gag	ggt	gtc	ttt	att	gat	cag	gat	tcc	cat	gcc	288
Gly	Gly	Leu	Ile	Ser	Glu	Gly	Val	Phe	Ile	Asp	Gln	Asp	Ser	His	Ala	
				85					90					95		
aat	gga	ggt	tat	acc	cgt	tta	ggg	gcg	gtg	gtc	tgg	cag	gtt	tcc	cgg	336
Asn	Gly	Gly	Tyr	Thr	Arg	Leu	Gly	Ala	Val	Val	Trp	Gln	Val	Ser	Arg	
			100				105						110			
gaa	aag	att	gat	gtt	ttc	aga	aag	gag	caa	ccg	gag	ata	ttt	tat	cga	384
Glu	Lys	Ile	Asp	Val	Phe	Arg	Lys	Glu	Gln	Pro	Glu	Ile	Phe	Tyr	Arg	
		115					120					125				
ttg	gtt	tcc	cgg	gtc	gcg	gtg	gcc	atc	aat	agg	cgt	atg	cgc	aca	ctt	432
Leu	Val	Ser	Arg	Val	Ala	Val	Ala	Ile	Asn	Arg	Arg	Met	Arg	Thr	Leu	
	130					135					140					
tcc	gag	cag	ctt	tat	ggt	gaa	acc	tgt	aaa	aga	cgg	acg	atg	agc	ggt	480
Ser	Glu	Gln	Leu	Tyr	Gly	Glu	Thr	Cys	Lys	Arg	Arg	Thr	Met	Ser	Gly	
145				150					155						160	
ttt	cgc	ctg	gaa	cat	gat	tcc	ctg	gga	cat	agg	gag	att	ccc	ggt	gat	528
Phe	Arg	Leu	Glu	His	Asp	Ser	Leu	Gly	His	Arg	Glu	Ile	Pro	Gly	Asp	
				165					170					175		
gcc	tat	tat	ggg	gtg	caa	act	cag	aga	gct	ata	gag	aat	ttt	ccg	atc	576
Ala	Tyr	Tyr	Gly	Val	Gln	Thr	Gln	Arg	Ala	Ile	Glu	Asn	Phe	Pro	Ile	
			180				185						190			
tcc	ggg	gtg	ccg	gta	agt	aat	ttt	agt	cat	ctc	atc	gaa	gga	ttt	gcc	624
Ser	Gly	Val	Pro	Val	Ser	Asn	Phe	Ser	His	Leu	Ile	Glu	Gly	Phe	Ala	
		195				200						205				
ttt	att	aag	att	gct	gct	gct	cgc	gct	aac	ttt	gag	ctt	ggg	gtg	atg	672
Phe	Ile	Lys	Ile	Ala	Ala	Ala	Arg	Ala	Asn	Phe	Glu	Leu	Gly	Val	Met	
	210					215					220					
gat	ggg	gag	aag	atg	gag	gct	ctc	tgt	gga	gct	tgt	gtt	gag	ctc	tta	720
Asp	Gly	Glu	Lys	Met	Glu	Ala	Leu	Cys	Gly	Ala	Cys	Val	Glu	Leu	Leu	
225				230					235					240		
gag	ggt	aaa	ttg	cat	gag	cat	ttt	gca	gtg	gat	atg	ttc	cag	ggc	ggg	768
Glu	Gly	Lys	Leu	His	Glu	His	Phe	Ala	Val	Asp	Met	Phe	Gln	Gly	Gly	
				245					250					255		
gcg	ggc	acc	tcc	acc	aat	atg	aat	gcc	aac	gag	gtc	ata	acc	aac	cgt	816
Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Thr	Asn	Arg	
			260				265						270			
ggt	ctg	gag	ctt	atg	ggg	cat	gag	aag	gga	gag	tat	cag	tac	ctg	cat	864
Gly	Leu	Glu	Leu	Met	Gly	His	Glu	Lys	Gly	Glu	Tyr	Gln	Tyr	Leu	His	
		275				280						285				
ccc	aac	gat	cat	gcc	aac	tgt	tct	cag	tcg	acc	aac	gat	acc	tat	ccc	912
Pro	Asn	Asp	His	Ala	Asn	Cys	Ser	Gln	Ser	Thr	Asn	Asp	Thr	Tyr	Pro	
	290					295					300					
acg	gcg	gtc	aaa	ctt	gcc	gta	ctg	ctc	tcg	cat	cgt	aac	ctg	gcc	cga	960
Thr	Ala	Val	Lys	Leu	Ala	Val	Leu	Leu	Ser	His	Arg	Asn	Leu	Ala	Arg	
305				310					315					320		
ggg	atg	gag	gat	ctg	aaa	aat	gcc	ctt	ctg	caa	aaa	tcc	gtt	gag	ttt	1008
Gly	Met	Glu	Asp	Leu	Lys	Asn	Ala	Leu	Leu	Gln	Lys	Ser	Val	Glu	Phe	
				325				330						335		
aag	gat	gtt	ttg	aag	atg	gga	cga	acg	gaa	aat	cag	gat	gcg	gtg	ccc	1056
Lys	Asp	Val	Leu	Lys	Met	Gly	Arg	Thr	Glu	Asn	Gln	Asp	Ala	Val	Pro	
			340					345					350			

PF59083SeqList PF59083.txt

atg	act	ctt	ggc	cag	gaa	ttt	agt	gcc	tat	gct	gta	atg	gtg	gga	agt	1104
Met	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Ala	Tyr	Ala	Val	Met	Val	Gly	Ser	
		355					360					365				
gcc	atg	cgt	ggc	ata	gag	ggt	gca	tcc	gaa	gag	ttt	atg	cat	att	aat	1152
Ala	Met	Arg	Ala	Ile	Glu	Gly	Ala	Ser	Glu	Glu	Phe	Met	His	Ile	Asn	
		370				375					380					
atg	ggg	gct	act	ggc	att	ggc	acc	ggc	att	aac	tgt	cct	cta	ggc	tat	1200
Met	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Cys	Pro	Leu	Gly	Tyr	
		385			390					395					400	
gcc	gat	ctg	gta	act	gaa	aag	ctt	gtt	gag	gtg	agt	ggc	ttt	ccc	ctg	1248
Ala	Asp	Leu	Val	Thr	Glu	Lys	Leu	Val	Glu	Val	Ser	Gly	Phe	Pro	Leu	
				405					410					415		
aaa	aga	gca	gga	aat	ctt	gtt	gag	gcc	acc	caa	aat	gcg	ggg	acc	ttt	1296
Lys	Arg	Ala	Gly	Asn	Leu	Val	Glu	Ala	Thr	Gln	Asn	Ala	Gly	Thr	Phe	
			420					425					430			
gtc	cag	atg	tct	gcg	acc	atg	aaa	cgg	gct	gcg	gtg	caa	att	tca	aag	1344
Val	Gln	Met	Ser	Ala	Thr	Met	Lys	Arg	Ala	Ala	Val	Gln	Ile	Ser	Lys	
		435					440					445				
ata	tgt	aat	gat	ctg	cgc	tgg	ctc	tcc	tcc	ggg	ccc	cgt	tgt	ggg	ctc	1392
Ile	Cys	Asn	Asp	Leu	Arg	Trp	Leu	Ser	Ser	Gly	Pro	Arg	Cys	Gly	Leu	
		450				455					460					
aat	gag	ata	aac	ctg	cca	ccc	atg	cag	cca	ggc	tct	tcc	atc	atg	ccg	1440
Asn	Glu	Ile	Asn	Leu	Pro	Pro	Met	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	
		465			470					475					480	
ggc	aag	gtt	aat	cct	gtt	att	cct	gag	gtg	gtc	aat	cag	atc	tgc	tat	1488
Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln	Ile	Cys	Tyr	
				485					490					495		
cag	gtt	att	ggc	tac	gat	act	gtg	gtt	tcc	atg	gcc	gcc	gag	tcc	agt	1536
Gln	Val	Ile	Gly	Tyr	Asp	Thr	Val	Val	Ser	Met	Ala	Ala	Glu	Ser	Ser	
			500					505					510			
gag	ttg	gag	ctc	tgt	atg	gcg	gag	cca	att	att	gcc	tac	gac	ctg	ctc	1584
Glu	Leu	Glu	Leu	Cys	Met	Ala	Glu	Pro	Ile	Ile	Ala	Tyr	Asp	Leu	Leu	
		515					520					525				
cac	ggg	atg	atg	att	ctt	aaa	aat	gcc	tgc	gtc	acc	ttg	gcc	tct	cgt	1632
His	Gly	Met	Met	Ile	Leu	Lys	Asn	Ala	Cys	Val	Thr	Leu	Ala	Ser	Arg	
		530				535					540					
tgc	atc	gtc	ggg	att	gag	gcg	aat	cgt	gac	gtc	tgt	cgt	tcc	tat	gtg	1680
Cys	Ile	Val	Gly	Ile	Glu	Ala	Asn	Arg	Asp	Val	Cys	Arg	Ser	Tyr	Val	
		545			550					555					560	
gaa	aat	agc	att	ggg	ctt	gtt	acc	gct	ttg	gtc	ccg	gtt	atc	ggg	tat	1728
Glu	Asn	Ser	Ile	Gly	Leu	Val	Thr	Ala	Leu	Val	Pro	Val	Ile	Gly	Tyr	
				565					570					575		
gag	ccg	tct	gct	gcc	att	gcc	aag	gag	gcc	ctg	aag	aca	ggg	ggc	agc	1776
Glu	Pro	Ser	Ala	Ala	Ile	Ala	Lys	Glu	Ala	Leu	Lys	Thr	Gly	Gly	Ser	
			580					585					590			
gtt	tat	aat	ctt	gtc	ctg	gag	aag	ggg	ctg	ctt	acc	aag	aag	gag	ctg	1824
Val	Tyr	Asn	Leu	Val	Leu	Glu	Lys	Gly	Leu	Leu	Thr	Lys	Lys	Glu	Leu	
		595				600					605					
gat	gat	atg	ctc	tcg	cct	gaa	aag	atg	acc	gat	cca	cgg	gat	att	cct	1872
Asp	Asp	Met	Leu	Ser	Pro	Glu	Lys	Met	Thr	Asp	Pro	Arg	Asp	Ile	Pro	
		610				615					620					
cag	cac	ctc	tag													1884
Gln	His	Leu														
625																

<210> 9676

<211> 627

<212> PRT

<213> Desulfotalea psychrophila Lsv54

<400> 9676

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

PF59083SeqList PF59083.txt

Val 65	Arg	Gly	Leu	His	Gly 70	Ser	Ser	His	Arg	Val 75	Gly	Thr	Val	Ser	Ala 80
Gly	Gly	Leu	Ile	Ser 85	Glu	Gly	Val	Phe	Ile 90	Asp	Gln	Asp	Ser	His 95	Ala
Asn	Gly	Gly	Tyr 100	Thr	Arg	Leu	Gly	Ala 105	Val	Val	Trp	Gln	Val 110	Ser	Arg
Glu	Lys	Ile 115	Asp	Val	Phe	Arg	Lys 120	Glu	Gln	Pro	Glu	Ile 125	Phe	Tyr	Arg
Leu 130	Val	Ser	Arg	Val	Ala 135	Val	Ala	Ile	Asn	Arg	Arg 140	Met	Arg	Thr	Leu
Ser 145	Glu	Gln	Leu	Tyr	Gly 150	Glu	Thr	Cys	Lys	Arg 155	Arg	Thr	Met	Ser	Gly 160
Phe	Arg	Leu	Glu	His 165	Asp	Ser	Leu	Gly	His 170	Arg	Glu	Ile	Pro	Gly 175	Asp
Ala	Tyr	Tyr	Gly 180	Val	Gln	Thr	Gln	Arg 185	Ala	Ile	Glu	Asn	Phe 190	Pro	Ile
Ser	Gly	Val 195	Pro	Val	Ser	Asn	Phe 200	Ser	His	Leu	Ile	Glu 205	Gly	Phe	Ala
Phe 210	Ile	Lys	Ile	Ala	Ala 215	Arg	Ala	Asn	Phe	Glu 220	Leu	Gly	Val	Met	
Asp 225	Gly	Glu	Lys	Met	Glu 230	Ala	Leu	Cys	Gly	Ala 235	Cys	Val	Glu	Leu	Leu 240
Glu	Gly	Lys	Leu	His 245	Glu	His	Phe	Ala 250	Val	Asp	Met	Phe	Gln	Gly 255	Gly
Ala	Gly	Thr	Ser 260	Thr	Asn	Met	Asn	Ala 265	Asn	Glu	Val	Ile	Thr 270	Asn	Arg
Gly	Leu	Glu 275	Leu	Met	Gly	His	Glu 280	Lys	Gly	Glu	Tyr	Gln 285	Tyr	Leu	His
Pro 290	Asn	Asp	His	Ala	Asn	Cys 295	Ser	Gln	Ser	Thr	Asn 300	Asp	Thr	Tyr	Pro
Thr 305	Ala	Val	Lys	Leu	Ala 310	Val	Leu	Leu	Ser	His 315	Arg	Asn	Leu	Ala	Arg 320
Gly	Met	Glu	Asp	Leu 325	Lys	Asn	Ala	Leu	Leu 330	Gln	Lys	Ser	Val	Glu 335	Phe
Lys	Asp	Val	Leu 340	Lys	Met	Gly	Arg	Thr 345	Glu	Asn	Gln	Asp	Ala 350	Val	Pro
Met	Thr	Leu 355	Gly	Gln	Glu	Phe	Ser 360	Ala	Tyr	Ala	Val	Met 365	Val	Gly	Ser
Ala	Met 370	Arg	Ala	Ile	Glu	Gly 375	Ala	Ser	Glu	Glu	Phe 380	Met	His	Ile	Asn
Met 385	Gly	Ala	Thr	Ala	Ile 390	Gly	Thr	Gly	Ile	Asn 395	Cys	Pro	Leu	Gly	Tyr 400
Ala	Asp	Leu	Val	Thr 405	Glu	Lys	Leu	Val	Glu 410	Val	Ser	Gly	Phe	Pro 415	Leu
Lys	Arg	Ala	Gly 420	Asn	Leu	Val	Glu	Ala 425	Thr	Gln	Asn	Ala	Gly 430	Thr	Phe
Val	Gln	Met 435	Ser	Ala	Thr	Met	Lys 440	Arg	Ala	Ala	Val	Gln 445	Ile	Ser	Lys
Ile	Cys 450	Asn	Asp	Leu	Arg	Trp 455	Leu	Ser	Ser	Gly	Pro 460	Arg	Cys	Gly	Leu
Asn 465	Glu	Ile	Asn	Leu	Pro 470	Pro	Met	Gln	Pro	Gly 475	Ser	Ser	Ile	Met	Pro 480
Gly	Lys	Val	Asn	Pro 485	Val	Ile	Pro	Glu	Val 490	Val	Asn	Gln	Ile	Cys 495	Tyr
Gln	Val	Ile	Gly 500	Tyr	Asp	Thr	Val	Val 505	Ser	Met	Ala	Ala	Glu 510	Ser	Ser
Glu	Leu	Glu 515	Leu	Cys	Met	Ala	Glu 520	Pro	Ile	Ile	Ala	Tyr 525	Asp	Leu	Leu
His	Gly 530	Met	Met	Ile	Leu	Lys 535	Asn	Ala	Cys	Val	Thr 540	Leu	Ala	Ser	Arg
Cys 545	Ile	Val	Gly	Ile	Glu	Ala	Asn	Arg	Asp	Val 555	Cys	Arg	Ser	Tyr	Val 560
Glu	Asn	Ser	Ile	Gly 565	Leu	Val	Thr	Ala	Leu 570	Val	Pro	Val	Ile	Gly 575	Tyr
Glu	Pro	Ser	Ala 580	Ile	Ala	Lys	Glu 585	Ala	Leu	Lys	Thr	Gly 590	Gly	Ser	
Val	Tyr	Asn 595	Leu	Val	Leu	Glu	Lys 600	Gly	Leu	Leu	Thr	Lys 605	Lys	Glu	Leu
Asp	Asp	Met	Leu	Ser	Pro	Glu	Lys	Met	Thr	Asp	Pro	Arg	Asp	Ile	Pro

610
Gln His Leu
625

<210> 9677
<211> 1437
<212> DNA
<213> Yersinia pseudotuberculosis IP 32953

<220>
<221> CDS
<222> (1)..(1437)
<223> transl_table=11

```
<400> 9677
atg tca aat aac att cgt att gaa gaa gac ctg tta ggt aca cga gaa      48
Met Ser Asn Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Thr Arg Glu
   1           5           10           15
gtc ccc gca gag gct tac tac ggt gtt cat acc ctg cgt gcg att gaa      96
Val Pro Ala Glu Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Ile Glu
           20           25           30
aac ttc tat atc agt aac agt aaa atc agt gac gtg ccg gaa ttt gta     144
Asn Phe Tyr Ile Ser Asn Ser Lys Ile Ser Asp Val Pro Glu Phe Val
           35           40           45
cgt ggc atg gtc atg gta aaa aaa gcg gcg gca atg gct aac aaa gag     192
Arg Gly Met Val Met Val Lys Lys Ala Ala Ala Met Ala Asn Lys Glu
           50           55           60
ttg cat acc atc ccg cgt aaa att gca gac atc att att cag gca tgt     240
Leu His Thr Ile Pro Arg Lys Ile Ala Asp Ile Ile Ile Gln Ala Cys
           65           70           75
gat gaa gtt ctg gat aaa ggg aaa tgt atg gat cag ttc ccc gtt gat     288
Asp Glu Val Leu Asp Lys Gly Lys Cys Met Asp Gln Phe Pro Val Asp
           80           85           90
gtg ttc cag ggc ggc gca ggt acc tct ctc aat atg aac acc aac gag     336
Val Phe Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr Asn Glu
           95          100          105
gtc ttg gcc aat att ggc ctg gag ctg atg ggc cac caa aaa ggg gaa     384
Val Leu Ala Asn Ile Gly Leu Glu Leu Met Gly His Gln Lys Gly Glu
          110          115          120
tat cag tac ctt aac cct aac gac cat ctg aac aaa tgc cag tcc acc     432
Tyr Gln Tyr Leu Asn Pro Asn Asp His Leu Asn Lys Cys Gln Ser Thr
          125          130          135
aac gat gcc tac cca acc ggt ttc cgc att gcg gtc tac gcc tcc atc     480
Asn Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Ala Ser Ile
          140          145          150
ctc aag ttg atc gat gct atc aac caa tta ggc gaa ggt ttc ggt aga     528
Leu Lys Leu Ile Asp Ala Ile Asn Gln Leu Gly Glu Gly Phe Gly Arg
          155          160          165
aaa tct aaa gaa ttc gag aaa att ctg aaa atg ggc cgt acc caa tta     576
Lys Ser Lys Glu Phe Glu Lys Ile Leu Lys Met Gly Arg Thr Gln Leu
          170          175          180
cag gat gcc gta ccc atg act ctg ggc cag gaa ttc cgc gct ttc cag     624
Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Arg Ala Phe Gln
          185          190          195
gtg tta ttg aat gaa gaa acc aag aac ctg caa cgg acc gcc gag ttg     672
Val Leu Leu Asn Glu Glu Thr Lys Asn Leu Gln Arg Thr Ala Glu Leu
          200          205          210
cta ttg gaa gtc aac ctg ggt gcc act gcc atc ggc act gcg ctg aat     720
Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Ala Leu Asn
          215          220          225
aca cca gaa ggt tat tca caa ctt gcc gtg cag aaa ctg gca gaa atc     768
Thr Pro Glu Gly Tyr Ser Gln Leu Ala Val Gln Lys Leu Ala Glu Ile
          230          235          240
agt gga tta gcc tgt gtt cct gcc gaa gat ttg atc gaa gcg acc tct     816
Ser Gly Leu Ala Cys Val Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser
          245          250          255
gat tgc ggc gct tac gtg atg gta cac agc gcc cta aaa cgc cta gct     864
Asp Cys Gly Ala Tyr Val Met Val His Ser Ala Leu Lys Arg Leu Ala
          260          265          270
          275          280          285
```

PF59083SeqList PF59083.txt

gtt	aag	atg	tcc	aaa	atc	tgt	aac	gac	cta	cgt	ttg	ctc	tca	tct	ggc	912
Val	Lys	Met	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	
	290					295					300					
cca	cgt	act	ggg	ttg	aat	gaa	atc	aat	ctg	cca	gaa	ttg	cag	gcg	ggc	960
Pro	Arg	Thr	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	Ala	Gly	
305					310					315					320	
tct	tct	atc	atg	cct	gca	aaa	gtg	aac	ccg	gtg	atc	cct	gaa	gtt	gta	1008
Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	
				325					330					335		
aat	cag	gtt	tgt	ttt	aag	gtg	atc	ggc	aac	gat	act	tgc	att	act	atg	1056
Asn	Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Cys	Ile	Thr	Met	
			340					345					350			
gcg	gct	gaa	gcg	ggg	cag	ctt	cag	tta	aac	gtg	atg	gag	ccg	gtg	att	1104
Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile	
		355					360					365				
ggg	cag	gcc	atg	ttt	gag	tct	atc	cat	atc	ctg	act	aat	gcg	tgt	tac	1152
Gly	Gln	Ala	Met	Phe	Glu	Ser	Ile	His	Ile	Leu	Thr	Asn	Ala	Cys	Tyr	
						375					380					
aac	ctg	tta	gag	aag	tgc	atc	aat	ggc	att	acc	gct	aac	aaa	gag	gtc	1200
Asn	Leu	Leu	Glu	Lys	Cys	Ile	Asn	Gly	Ile	Thr	Ala	Asn	Lys	Glu	Val	
385					390					395					400	
tgc	gag	cg	tac	gtc	ttt	aac	tcc	ata	ggc	atc	gtc	act	tat	ctt	aac	1248
Cys	Glu	Arg	Tyr	Val	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	
				405					410					415		
ccg	ttc	att	ggc	cac	cat	aat	ggg	gac	att	gtg	ggg	aaa	atc	tgt	gcg	1296
Pro	Phe	Ile	Gly	His	His	Asn	Gly	Asp	Ile	Val	Gly	Lys	Ile	Cys	Ala	
			420					425					430			
gaa	acc	ggg	aaa	aat	gtg	cgg	gaa	gtg	gtt	ctg	gag	cg	ggg	ttg	tta	1344
Glu	Thr	Gly	Lys	Asn	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gly	Leu	Leu	
		435				440						445				
act	gaa	gcc	gaa	ctg	gac	gac	att	ttc	tct	gtt	gaa	aac	ctg	atg	cac	1392
Thr	Glu	Ala	Glu	Leu	Asp	Asp	Ile	Phe	Ser	Val	Glu	Asn	Leu	Met	His	
		450				455					460					
cca	gcc	tat	aaa	gcg	aaa	cgt	tat	acc	gat	gaa	aat	gaa	caa	taa		1437
Pro	Ala	Tyr	Lys	Ala	Lys	Arg	Tyr	Thr	Asp	Glu	Asn	Glu	Gln			
465					470					475						

<210> 9678

<211> 478

<212> PRT

<213> *Yersinia pseudotuberculosis* IP 32953

<400> 9678

Met	Ser	Asn	Asn	Ile	Arg	Ile	Glu	Glu	Asp	Leu	Leu	Gly	Thr	Arg	Glu	
1				5					10					15		
Val	Pro	Ala	Glu	Ala	Tyr	Tyr	Gly	Val	His	Thr	Leu	Arg	Ala	Ile	Glu	
			20					25					30			
Asn	Phe	Tyr	Ile	Ser	Asn	Ser	Lys	Ile	Ser	Asp	Val	Pro	Glu	Phe	Val	
		35					40					45				
Arg	Gly	Met	Val	Met	Val	Lys	Lys	Ala	Ala	Ala	Met	Ala	Asn	Lys	Glu	
	50					55					60					
Leu	His	Thr	Ile	Pro	Arg	Lys	Ile	Ala	Asp	Ile	Ile	Ile	Gln	Ala	Cys	
65					70				75						80	
Asp	Glu	Val	Leu	Asp	Lys	Gly	Lys	Cys	Met	Asp	Gln	Phe	Pro	Val	Asp	
			85						90					95		
Val	Phe	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Leu	Asn	Met	Asn	Thr	Asn	Glu	
			100					105					110			
Val	Leu	Ala	Asn	Ile	Gly	Leu	Glu	Leu	Met	Gly	His	Gln	Lys	Gly	Glu	
		115					120					125				
Tyr	Gln	Tyr	Leu	Asn	Pro	Asn	Asp	His	Leu	Asn	Lys	Cys	Gln	Ser	Thr	
		130				135					140					
Asn	Asp	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Ile	Ala	Val	Tyr	Ala	Ser	Ile	
145					150					155					160	
Leu	Lys	Leu	Ile	Asp	Ala	Ile	Asn	Gln	Leu	Gly	Glu	Gly	Phe	Gly	Arg	
			165						170					175		
Lys	Ser	Lys	Glu	Phe	Glu	Lys	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	
			180					185					190			
Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Arg	Ala	Phe	Gln	
		195					200					205				

PF59083SeqList PF59083.txt

Val Leu Leu Asn Glu Glu Thr Lys Asn Leu Gln Arg Thr Ala Glu Leu
 210 215 220
 Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Ala Leu Asn
 225 230 235 240
 Thr Pro Glu Gly Tyr Ser Gln Leu Ala Val Gln Lys Leu Ala Glu Ile
 245 250 255
 Ser Gly Leu Ala Cys Val Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser
 260 265 270
 Asp Cys Gly Ala Tyr Val Met Val His Ser Ala Leu Lys Arg Leu Ala
 275 280 285
 Val Lys Met Ser Lys Ile Cys Asn Asp Leu Arg Leu Ser Ser Gly
 290 295 300
 Pro Arg Thr Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly
 305 310 315 320
 Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val
 325 330 335
 Asn Gln Val Cys Phe Lys Val Ile Gly Asn Asp Thr Cys Ile Thr Met
 340 345 350
 Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile
 355 360 365
 Gly Gln Ala Met Phe Glu Ser Ile His Ile Leu Thr Asn Ala Cys Tyr
 370 375 380
 Asn Leu Leu Glu Lys Cys Ile Asn Gly Ile Thr Ala Asn Lys Glu Val
 385 390 395 400
 Cys Glu Arg Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn
 405 410 415
 Pro Phe Ile Gly His His Asn Gly Asp Ile Val Gly Lys Ile Cys Ala
 420 425 430
 Glu Thr Gly Lys Asn Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu
 435 440 445
 Thr Glu Ala Glu Leu Asp Asp Ile Phe Ser Val Glu Asn Leu Met His
 450 455 460
 Pro Ala Tyr Lys Ala Lys Arg Tyr Thr Asp Glu Asn Glu Gln
 465 470 475

<210> 9679

<211> 1410

<212> DNA

<213> Symbiobacterium thermophilum IAM 14863

<220>

<221> CDS

<222> (1)..(1410)

<223> transl_table=11

<400> 9679

atg	cag	cag	acg	cg	acc	gaa	cgg	gat	ctg	ctg	ggc	gaa	aaa	cag	gtt	48
Met	Gln	Gln	Thr	Arg	Thr	Glu	Arg	Asp	Leu	Leu	Gly	Glu	Lys	Gln	Val	
1				5					10					15		
ccc	gca	gac	gcc	tac	tac	ggc	atc	cag	acg	acg	cgt	gcg	ctg	gag	aac	96
Pro	Ala	Asp	Ala	Tyr	Tyr	Gly	Ile	Gln	Thr	Thr	Arg	Ala	Leu	Glu	Asn	
			20					25					30			
ttc	cg	att	acc	ggc	cag	cgg	ctg	cac	cct	gcc	ctg	gtg	cg	ggc	ctc	144
Phe	Arg	Ile	Thr	Gly	Gln	Arg	Leu	His	Pro	Ala	Leu	Val	Arg	Gly	Leu	
		35					40					45				
gcc	cag	gtg	aag	aag	gcc	gcg	gcc	cag	gcg	aat	cac	cag	ctg	gga	tac	192
Ala	Gln	Val	Lys	Lys	Ala	Ala	Ala	Gln	Ala	Asn	His	Gln	Leu	Gly	Tyr	
		50				55				60						
ttg	ccg	gac	gac	gtc	gcc	cgt	gcc	atc	gtg	cag	gcg	tgc	gac	gag	atc	240
Leu	Pro	Asp	Asp	Val	Ala	Arg	Ala	Ile	Val	Gln	Ala	Cys	Asp	Glu	Ile	
		65			70					75					80	
ctc	gcg	ggc	cg	ctg	gcc	gac	cag	ttc	ccc	atc	gat	ccg	gta	cag	ggc	288
Leu	Ala	Gly	Arg	Leu	Ala	Asp	Gln	Phe	Pro	Ile	Asp	Pro	Val	Gln	Gly	
				85					90					95		
ggc	gcc	ggg	acg	tcc	gcc	aac	atg	aac	gcc	aac	gag	gtg	atc	gcc	aac	336
Gly	Ala	Gly	Thr	Ser	Ala	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	
			100					105					110			
cg	gcc	atc	gag	atc	ctg	ggg	ggg	cgt	aag	ggc	gac	tac	agc	ctg	gtc	384
Arg	Ala	Ile	Glu	Ile	Leu	Gly	Gly	Arg	Lys	Gly	Asp	Tyr	Ser	Leu	Val	

PF59083SeqList PF59083.txt

		115				120				125							
tcc	ccc	aac	gac	cac	gtg	aac	ttc	gcc	cag	tcc	acc	aac	gac	gcc	ttc		432
Ser	Pro	Asn	Asp	His	Val	Asn	Phe	Ala	Gln	Ser	Thr	Asn	Asp	Ala	Phe		
	130					135				140							
ccc	acc	gcc	ctg	cgg	ctg	gcg	ctc	atg	gag	cgg	gcg	gac	gtg	ctg	gtg		480
Pro	Thr	Ala	Leu	Arg	Leu	Ala	Leu	Met	Glu	Arg	Ala	Asp	Val	Leu	Val		
145					150					155					160		
gag	agc	ctg	gtc	ggg	ctg	gag	gag	gcc	ctg	cgc	gcc	aag	gcc	gcc	gag		528
Glu	Ser	Leu	Val	Gly	Leu	Glu	Glu	Ala	Leu	Arg	Ala	Lys	Ala	Ala	Glu		
				165					170					175			
ttc	gac	gac	gtg	gtg	aag	gtc	ggc	cgc	acc	cac	ctg	cag	gac	gcc	gtg		576
Phe	Asp	Asp	Val	Val	Lys	Val	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Val		
			180					185					190				
ccg	atc	cgg	ctg	ggg	cag	gag	ttt	tcg	gcc	tgg	tgc	gcg	gcg	gtg	gag		624
Pro	Ile	Arg	Leu	Gly	Gln	Glu	Phe	Ser	Ala	Trp	Cys	Ala	Ala	Val	Glu		
		195				200						205					
cgg	ggg	cgg	cgg	cgc	atc	cag	cag	gct	gtg	gag	gcc	ctg	tgc	gag	gtc		672
Arg	Gly	Arg	Arg	Arg	Ile	Gln	Gln	Ala	Val	Glu	Ala	Leu	Cys	Glu	Val		
	210				215					220							
aac	atg	ggc	gcg	acc	gcg	gtg	ggg	acg	ggc	ctc	aac	gcc	gac	ccg	gcg		720
Asn	Met	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Ala	Asp	Pro	Ala		
225					230				235						240		
tac	ccg	ccg	ctg	gtc	atc	gag	ttg	ctc	agc	cgc	aac	acc	ggg	cgg	agc		768
Tyr	Pro	Pro	Leu	Val	Ile	Glu	Leu	Leu	Ser	Arg	Asn	Thr	Gly	Arg	Ser		
				245					250					255			
ctc	cgt	ccg	ccg	gct	gac	ctc	gtg	gac	gcc	acc	cag	aac	gtc	gac	ccg		816
Leu	Arg	Pro	Pro	Ala	Asp	Leu	Val	Asp	Ala	Thr	Gln	Asn	Val	Asp	Pro		
			260					265					270				
ctg	gtg	gcc	ctc	agc	ggc	agc	ctg	aag	gcg	ctg	gcg	gtg	agc	ctc	tcc		864
Leu	Val	Ala	Leu	Ser	Gly	Ser	Leu	Lys	Ala	Leu	Ala	Val	Ser	Leu	Ser		
		275				280						285					
aag	atc	gcc	aac	gac	atc	cgg	ctg	atg	gcc	tcg	ggg	ccg	cgc	tgc	ggg		912
Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	Met	Ala	Ser	Gly	Pro	Arg	Cys	Gly		
	290				295					300							
ctc	tac	gag	atc	agg	ctg	ccg	gag	atg	cag	ccg	ggc	tcc	tcc	atc	atg		960
Leu	Tyr	Glu	Ile	Arg	Leu	Pro	Glu	Met	Gln	Pro	Gly	Ser	Ser	Ile	Met		
305					310					315					320		
ccc	ggc	aag	gtg	aac	ccc	gtc	atg	gcg	gag	gtg	ctg	aac	cag	acc	tgc		1008
Pro	Gly	Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Val	Leu	Asn	Gln	Thr	Cys		
				325					330					335			
ttc	ctg	gtg	atc	ggc	ctg	gac	ctg	acg	gtg	acc	ctc	gcg	ggc	gag	gcc		1056
Phe	Leu	Val	Ile	Gly	Leu	Asp	Leu	Thr	Val	Thr	Leu	Ala	Gly	Glu	Ala		
			340					345					350				
ggc	cag	ctg	gag	ctg	aac	gtg	atg	gag	ccg	gtg	atg	ggc	cac	gcc	ctc		1104
Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Met	Gly	His	Ala	Leu		
		355				360						365					
ttc	acc	agc	atc	gac	gcc	ctg	gag	agc	gtc	gtg	cgg	ctg	ttc	acc	gac		1152
Phe	Thr	Ser	Ile	Asp	Ala	Leu	Glu	Ser	Val	Val	Arg	Leu	Phe	Thr	Asp		
	370				375					380							
cgg	tgc	gtg	cgg	ggc	atc	cag	gcc	aac	cgg	gag	cgc	tgc	gag	gag	ctg		1200
Arg	Cys	Val	Arg	Gly	Ile	Gln	Ala	Asn	Arg	Glu	Arg	Cys	Glu	Glu	Leu		
385					390				395						400		
gtc	aac	cgg	tcc	atc	ggg	ctg	gtg	acc	gcc	atc	aac	ccc	atc	gtc	ggg		1248
Val	Asn	Arg	Ser	Ile	Gly	Leu	Val	Thr	Ala	Ile	Asn	Pro	Ile	Val	Gly		
				405				410						415			
tac	aag	aac	gcc	tct	gag	gtg	gcg	cgc	gag	gcc	acg	ctc	acg	ggc	cgc		1296
Tyr	Lys	Asn	Ala	Ser	Glu	Val	Ala	Arg	Glu	Ala	Thr	Leu	Thr	Gly	Arg		
			420					425				430					
ccg	gtc	cgg	gag	atc	gtg	ctg	gag	aag	ggt	ctg	ctc	act	gcc	gag	gag		1344
Pro	Val	Arg	Glu	Ile	Val	Leu	Glu	Lys	Gly	Leu	Leu	Thr	Ala	Glu	Glu		
		435				440						445					
atc	gac	gag	atc	ctg	tcg	ccc	aag	cac	ctg	acg	acc	atg	ggg	atc	gcc		1392
Ile	Asp	Glu	Ile	Leu	Ser	Pro	Lys	His	Leu	Thr	Thr	Met	Gly	Ile	Ala		
	450				455						460						
cgg	cgg	acc	cac	gac	tga												1410
Arg	Arg	Thr	His	Asp													
465																	

<210> 9680

PF59083SeqList PF59083.txt

<211> 469

<212> PRT

<213> Symbiobacterium thermophilum IAM 14863

<400> 9680

```

Met Gln Gln Thr Arg Thr Glu Arg Asp Leu Leu Gly Glu Lys Gln Val
1      5      10      15
Pro Ala Asp Ala Tyr Tyr Gly Ile Gln Thr Thr Arg Ala Leu Glu Asn
      20      25      30
Phe Arg Ile Thr Gly Gln Arg Leu His Pro Ala Leu Val Arg Gly Leu
      35      40      45
Ala Gln Val Lys Lys Ala Ala Ala Gln Ala Asn His Gln Leu Gly Tyr
      50      55      60
Leu Pro Asp Asp Val Ala Arg Ala Ile Val Gln Ala Cys Asp Glu Ile
65      70      75      80
Leu Ala Gly Arg Leu Ala Asp Gln Phe Pro Ile Asp Pro Val Gln Gly
      85      90      95
Gly Ala Gly Thr Ser Ala Asn Met Asn Ala Asn Glu Val Ile Ala Asn
      100      105      110
Arg Ala Ile Glu Ile Leu Gly Gly Arg Lys Gly Asp Tyr Ser Leu Val
      115      120      125
Ser Pro Asn Asp His Val Asn Phe Ala Gln Ser Thr Asn Asp Ala Phe
      130      135      140
Pro Thr Ala Leu Arg Leu Ala Leu Met Glu Arg Ala Asp Val Leu Val
145      150      155      160
Glu Ser Leu Val Gly Leu Glu Glu Ala Leu Arg Ala Lys Ala Ala Glu
      165      170      175
Phe Asp Asp Val Val Lys Val Gly Arg Thr His Leu Gln Asp Ala Val
      180      185      190
Pro Ile Arg Leu Gly Gln Glu Phe Ser Ala Trp Cys Ala Ala Val Glu
      195      200      205
Arg Gly Arg Arg Arg Ile Gln Gln Ala Val Glu Ala Leu Cys Glu Val
      210      215      220
Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn Ala Asp Pro Ala
225      230      235      240
Tyr Pro Pro Leu Val Ile Glu Leu Leu Ser Arg Asn Thr Gly Arg Ser
      245      250      255
Leu Arg Pro Pro Ala Asp Leu Val Asp Ala Thr Gln Asn Val Asp Pro
      260      265      270
Leu Val Ala Leu Ser Gly Ser Leu Lys Ala Leu Ala Val Ser Leu Ser
      275      280      285
Lys Ile Ala Asn Asp Ile Arg Leu Met Ala Ser Gly Pro Arg Cys Gly
      290      295      300
Leu Tyr Glu Ile Arg Leu Pro Glu Met Gln Pro Gly Ser Ser Ile Met
305      310      315      320
Pro Gly Lys Val Asn Pro Val Met Ala Glu Val Leu Asn Gln Thr Cys
      325      330      335
Phe Leu Val Ile Gly Leu Asp Leu Thr Val Thr Leu Ala Gly Glu Ala
      340      345      350
Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Met Gly His Ala Leu
      355      360      365
Phe Thr Ser Ile Asp Ala Leu Glu Ser Val Val Arg Leu Phe Thr Asp
      370      375      380
Arg Cys Val Arg Gly Ile Gln Ala Asn Arg Glu Arg Cys Glu Glu Leu
385      390      395      400
Val Asn Arg Ser Ile Gly Leu Val Thr Ala Ile Asn Pro Ile Val Gly
      405      410      415
Tyr Lys Asn Ala Ser Glu Val Ala Arg Glu Ala Thr Leu Thr Gly Arg
      420      425      430
Pro Val Arg Glu Ile Val Leu Glu Lys Gly Leu Leu Thr Ala Glu Glu
      435      440      445
Ile Asp Glu Ile Leu Ser Pro Lys His Leu Thr Thr Met Gly Ile Ala
450      455      460
Arg Arg Thr His Asp
465

```

<210> 9681

<211> 1389

<212> DNA

PF59083SeqList PF59083.txt

<213> Anaplasma marginale str. St. Maries

<220>

<221> CDS

<222> (1)..(1389)

<223> transl_table=11

<400> 9681

atg ggg gtg agg att gag tct gac agc atg ggt aac att gag gtg ccg	48
Met Gly Val Arg Ile Glu Ser Asp Ser Met Gly Asn Ile Glu Val Pro	
1 5 10 15	
gct gaa cgc tat tgg ggt gca caa aca cag cgc tcc atg atg aac ttt	96
Ala Glu Arg Tyr Trp Gly Ala Gln Thr Gln Arg Ser Met Met Asn Phe	
20 25 30	
gca att gga gag gaa aaa atg ccc cgg ccc ttg ata tgg gcg ctg ggt	144
Ala Ile Gly Glu Glu Lys Met Pro Arg Pro Leu Ile Trp Ala Leu Gly	
35 40 45	
gtg gtg aag ctg gcg gct gcc cgg gta aac gct aga aaa gga agc ata	192
Val Val Lys Leu Ala Ala Ala Arg Val Asn Ala Arg Lys Gly Ser Ile	
50 55 60	
gaa aag tct gtg gga gag gca att tgt gct gct gcg cag gaa gtt ata	240
Glu Lys Ser Val Gly Glu Ala Ile Cys Ala Ala Ala Gln Glu Val Ile	
65 70 75 80	
gat ggc aag atg gat ggg gaa ttt ccc ctg gtg gtg tgg cag act ggt	288
Asp Gly Lys Met Asp Gly Glu Phe Pro Leu Val Val Trp Gln Thr Gly	
85 90 95	
tct ggc acc caa acc aac atg aac gcc aac gaa gta ata gca aac cgg	336
Ser Gly Thr Gln Thr Asn Met Asn Ala Asn Glu Val Ile Ala Asn Arg	
100 105 110	
gcc ata gag atg ctt ggg ggg aaa gtt ggt agc aag tct ccc gta cac	384
Ala Ile Glu Met Leu Gly Gly Lys Val Gly Ser Lys Ser Pro Val His	
115 120 125	
ccg aat gac cat gtc aac cac tct caa tct tca aat gat gta ttt ccc	432
Pro Asn Asp His Val Asn His Ser Gln Ser Ser Asn Asp Val Phe Pro	
130 135 140	
act gcc atg cac att gcc gcc gtg gcc gag gtg gaa cgg cgc tta ctg	480
Thr Ala Met His Ile Ala Ala Val Ala Glu Val Glu Arg Arg Leu Leu	
145 150 155 160	
ccc gcg ctg gag aca ctt cgc agc gcg ttg gag gcg aaa gtt gtg gca	528
Pro Ala Leu Glu Thr Leu Arg Ser Ala Leu Glu Ala Lys Val Val Ala	
165 170 175	
ttt tcg gac ata gta aaa acg ggt cgc acc cac ctc cag gat gca gta	576
Phe Ser Asp Ile Val Lys Thr Gly Arg Thr His Leu Gln Asp Ala Val	
180 185 190	
cct ctc acg ctt ggt cag gag ttt tcg ggg tac gaa tgc caa gtg aga	624
Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Glu Cys Gln Val Arg	
195 200 205	
aag gga ata gaa aga gtc aag tcc tca atg gtg gat gtt tat cag ctt	672
Lys Gly Ile Glu Arg Val Lys Ser Ser Met Val Asp Val Tyr Gln Leu	
210 215 220	
gca cag ggg ggt aca ggt gtt ggc acg ggt ttg aac acc aag aaa ggc	720
Ala Gln Gly Gly Thr Gly Val Gly Thr Gly Leu Asn Thr Lys Lys Gly	
225 230 235 240	
ttt gct gaa gag ttt gca aaa gag gtt gcg ggc atc acc ggt atg aag	768
Phe Ala Glu Glu Phe Ala Lys Glu Val Ala Gly Ile Thr Gly Met Lys	
245 250 255	
ttt ata acc gcg gag aac aaa ttc gag gcg ctt gct acg cat gat gcc	816
Phe Ile Thr Ala Glu Asn Lys Phe Glu Ala Leu Ala Thr His Asp Ala	
260 265 270	
atg gta caa cta agc ggc gcg ctc aat acg ctt gcc gtc agt tgc atg	864
Met Val Gln Leu Ser Gly Ala Leu Asn Thr Leu Ala Val Ser Cys Met	
275 280 285	
aaa ata gcg aat gac atc cgg ctg ctt gca tct ggg ccc agg tgc gga	912
Lys Ile Ala Asn Asp Ile Arg Leu Leu Ala Ser Gly Pro Arg Cys Gly	
290 295 300 305	
ata ggg gag atc atc ctt ccc gcg aat gag cct ggg tcg tca atc atg	960
Ile Gly Glu Ile Ile Leu Pro Ala Asn Glu Pro Gly Ser Ser Ile Met	
310 315 320	
ccg ggt aag gtg aac ccg acg cag tgc gaa gca ctc acc atg gtt tgc	1008

PF59083SeqList PF59083.txt

Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	
				325					330					335		
gcg	cag	gtt	atg	ggg	aat	cac	gtt	gca	gtt	tct	gta	ggg	ggg	tcc	aac	1056
Ala	Gln	Val	Met	Gly	Asn	His	Val	Ala	Val	Ser	Val	Gly	Gly	Ser	Asn	
			340					345					350			
gga	cac	ctt	gag	ctg	aac	gta	ttc	aag	cct	atg	att	gcg	tat	aac	gtt	1104
Gly	His	Leu	Glu	Leu	Asn	Val	Phe	Lys	Pro	Met	Ile	Ala	Tyr	Asn	Val	
		355					360					365				
cta	aac	tct	gtc	cga	ttg	ttg	gca	gat	gct	tgt	gaa	agc	ttt	gcg	acg	1152
Leu	Asn	Ser	Val	Arg	Leu	Leu	Ala	Asp	Ala	Cys	Glu	Ser	Phe	Ala	Thr	
		370				375					380					
aaa	tgc	gta	agc	ggc	ata	gag	gcc	gat	aaa	gaa	cgt	ata	gcc	gtc	atg	1200
Lys	Cys	Val	Ser	Gly	Ile	Glu	Ala	Asp	Lys	Glu	Arg	Ile	Ala	Val	Met	
385				390					395						400	
ctg	ggg	cag	tct	ctc	atg	ctg	gtt	act	gcg	cta	aac	agg	cat	ata	ggg	1248
Leu	Gly	Gln	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Arg	His	Ile	Gly	
			405					410						415		
tat	gac	aac	gcc	gca	aag	atc	tcc	aag	ttt	gcg	ttt	gag	aat	cgt	gtg	1296
Tyr	Asp	Asn	Ala	Ala	Lys	Ile	Ser	Lys	Phe	Ala	Phe	Glu	Asn	Arg	Val	
			420				425						430			
acg	ctt	aag	gat	gcg	gct	gca	aaa	ttg	ggg	tta	gta	gat	ggg	gag	gag	1344
Thr	Leu	Lys	Asp	Ala	Ala	Ala	Lys	Leu	Gly	Leu	Val	Asp	Gly	Ala	Glu	
		435				440						445				
ttt	gac	gcg	ata	gtt	gat	ccc	agg	aag	atg	gtc	tct	cct	gac	tga		1389
Phe	Asp	Ala	Ile	Val	Asp	Pro	Arg	Lys	Met	Val	Ser	Pro	Asp			
	450					455					460					

<210> 9682

<211> 462

<212> PRT

<213> Anaplasma marginale str. St. Maries

<400> 9682

Met	Gly	Val	Arg	Ile	Glu	Ser	Asp	Ser	Met	Gly	Asn	Ile	Glu	Val	Pro	
1				5					10					15		
Ala	Glu	Arg	Tyr	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Met	Met	Asn	Phe	
			20					25					30			
Ala	Ile	Gly	Glu	Glu	Lys	Met	Pro	Arg	Pro	Leu	Ile	Trp	Ala	Leu	Gly	
		35					40					45				
Val	Val	Lys	Leu	Ala	Ala	Ala	Arg	Val	Asn	Ala	Arg	Lys	Gly	Ser	Ile	
	50					55				60						
Glu	Lys	Ser	Val	Gly	Glu	Ala	Ile	Cys	Ala	Ala	Ala	Gln	Glu	Val	Ile	
65				70					75						80	
Asp	Gly	Lys	Met	Asp	Gly	Glu	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	
			85					90					95			
Ser	Gly	Thr	Gln	Thr	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	
			100				105						110			
Ala	Ile	Glu	Met	Leu	Gly	Gly	Lys	Val	Gly	Ser	Lys	Ser	Pro	Val	His	
		115				120						125				
Pro	Asn	Asp	His	Val	Asn	His	Ser	Gln	Ser	Ser	Asn	Asp	Val	Phe	Pro	
	130					135					140					
Thr	Ala	Met	His	Ile	Ala	Ala	Val	Ala	Glu	Val	Glu	Arg	Arg	Leu	Leu	
145					150				155					160		
Pro	Ala	Leu	Glu	Thr	Leu	Arg	Ser	Ala	Leu	Glu	Ala	Lys	Val	Val	Ala	
			165					170						175		
Phe	Ser	Asp	Ile	Val	Lys	Thr	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Val	
		180					185						190			
Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Glu	Cys	Gln	Val	Arg	
		195					200					205				
Lys	Gly	Ile	Glu	Arg	Val	Lys	Ser	Ser	Met	Val	Asp	Val	Tyr	Gln	Leu	
	210					215					220					
Ala	Gln	Gly	Gly	Thr	Gly	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	
225					230					235					240	
Phe	Ala	Glu	Glu	Phe	Ala	Lys	Glu	Val	Ala	Gly	Ile	Thr	Gly	Met	Lys	
			245					250						255		
Phe	Ile	Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Thr	His	Asp	Ala	
		260					265						270			
Met	Val	Gln	Leu	Ser	Gly	Ala	Leu	Asn	Thr	Leu	Ala	Val	Ser	Cys	Met	
		275				280						285				

PF59083SeqList PF59083.txt

Lys Ile Ala Asn Asp Ile Arg Leu Leu Ala Ser Gly Pro Arg Cys Gly
 290 295 300
 Ile Gly Glu Ile Ile Leu Pro Ala Asn Glu Pro Gly Ser Ser Ile Met
 305 310 315 320
 Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys
 325 330 335
 Ala Gln Val Met Gly Asn His Val Ala Val Ser Val Gly Gly Ser Asn
 340 345 350
 Gly His Leu Glu Leu Asn Val Phe Lys Pro Met Ile Ala Tyr Asn Val
 355 360 365
 Leu Asn Ser Val Arg Leu Leu Ala Asp Ala Cys Glu Ser Phe Ala Thr
 370 375 380
 Lys Cys Val Ser Gly Ile Glu Ala Asp Lys Glu Arg Ile Ala Val Met
 385 390 395 400
 Leu Gly Gln Ser Leu Met Leu Val Thr Ala Leu Asn Arg His Ile Gly
 405 410 415
 Tyr Asp Asn Ala Ala Lys Ile Ser Lys Phe Ala Phe Glu Asn Arg Val
 420 425 430
 Thr Leu Lys Asp Ala Ala Ala Lys Leu Gly Leu Val Asp Gly Ala Glu
 435 440 445
 Phe Asp Ala Ile Val Asp Pro Arg Lys Met Val Ser Pro Asp
 450 455 460

<210> 9683

<211> 1371

<212> DNA

<213> Silicibacter pomeroyi DSS-3

<220>

<221> CDS

<222> (1)..(1371)

<223> transl_table=11

<400> 9683

atg gac acc acc gcc agc cgc acc gaa cat gac agt atc ggc gcc tgc	48
Met Asp Thr Thr Ala Ser Arg Thr Glu His Asp Ser Ile Gly Ala Cys	
1 5 10 15	
acc atc ccc cag ggc gcg ccc tgg ggc tca caa acc caa cgc gcg atc	96
Thr Ile Pro Gln Gly Ala Pro Trp Gly Ser Gln Thr Gln Arg Ala Ile	
20 25 30	
gag aat ttc ccg atc acc gga ata ccg atc agc cac tat ccc gaa atc	144
Glu Asn Phe Pro Ile Thr Gly Ile Pro Ile Ser His Tyr Pro Glu Ile	
35 40 45	
gtg gtg gcg ctg gcg cag gtc aaa aag gcc tgc gcc ctg acc aac gcc	192
Val Val Ala Leu Ala Gln Val Lys Lys Ala Cys Ala Leu Thr Asn Ala	
50 55 60	
gaa ctg ggc gcg ctg acc ccg gac aag gcg gcg gtg atc gca tgc gtc	240
Glu Leu Gly Ala Leu Thr Pro Asp Lys Ala Ala Val Ile Ala Ser Val	
65 70 75 80	
tgc gac cgg atc atc gcc ggt cag cat cac gag gcg ttt tgc gtc gac	288
Cys Asp Arg Ile Ile Ala Gly Gln His His Glu Ala Phe Cys Val Asp	
85 90 95	
gtg atg cag ggt ggg gcc ggg acc tcg acc aac atg aat gcc aac gag	336
Val Met Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu	
100 105 110	
gtg atc gcc aac ctg ggt ctg atc gtt ttg ggc ggc agc tac ggc gac	384
Val Ile Ala Asn Leu Gly Leu Ile Val Leu Gly Gly Ser Tyr Gly Asp	
115 120 125	
tat ggc cac ctg cat ccc aat gac gac gtc aac cgc tcg caa tcg acc	432
Tyr Gly His Leu His Pro Asn Asp Asp Val Asn Arg Ser Gln Ser Thr	
130 135 140	
aac gat gtc tat ccc acg gcg atc cgt ctt gcg acg ctg tcc aag gcg	480
Asn Asp Val Tyr Pro Thr Ala Ile Arg Leu Ala Thr Leu Ser Lys Ala	
145 150 155 160	
cgg gtg ctg agt gcg gcg ctg cgc gat ctg gtt cag gcc ttt cac gac	528
Arg Val Leu Ser Ala Ala Leu Arg Asp Leu Val Gln Ala Phe His Asp	
165 170 175	
aag ggt gat gag ttt gcc cat atc aac aag gtg ggc cgt acc cag ttg	576
Lys Gly Asp Glu Phe Ala His Ile Asn Lys Val Gly Arg Thr Gln Leu	

PF59083SeqList PF59083.txt

180															185															190															
cag	gac	gcg	gtg	ccg	atg	acc	ttg	ggg	cag	gaa	ttt	cac	agc	ttt	gcc	624	Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	His	Ser	Phe	Ala													
195															200															205															
aat	act	ctg	gcc	gaa	gat	atc	gac	cgg	atc	acc	gat	ctg	ggc	cga	ctg	672	Asn	Thr	Leu	Ala	Glu	Asp	Ile	Asp	Arg	Ile	Thr	Asp	Leu	Gly	Arg	Leu													
210															215															220															
ctg	gcc	gag	gtc	aat	ctg	ggc	ggc	acc	gcc	atc	ggc	acc	cgg	atc	aac	720	Leu	Ala	Glu	Val	Asn	Leu	Gly	Gly	Thr	Ala	Ile	Gly	Thr	Arg	Ile	Asn													
225															230															235															
acg	ccc	gag	gga	tat	ggc	ccg	ctc	gtg	gta	gag	aaa	ctg	gcc	gat	atc	768	Thr	Pro	Glu	Gly	Tyr	Gly	Pro	Leu	Val	Val	Glu	Lys	Leu	Ala	Asp	Ile													
245															250															255															
acg	ggg	ctg	gcg	ctg	tct	ccg	gcc	cgc	gac	ctg	atc	gag	gct	tct	tcg	816	Thr	Gly	Leu	Ala	Leu	Ser	Pro	Ala	Arg	Asp	Leu	Ile	Glu	Ala	Ser	Ser													
260															265															270															
gat	ctt	ggc	gcc	ttc	gtg	atg	ttt	tca	ggc	gcg	ctc	aaa	cgg	gtg	gcg	864	Asp	Leu	Gly	Ala	Phe	Val	Met	Phe	Ser	Gly	Ala	Leu	Lys	Arg	Val	Ala													
275															280															285															
atc	aaa	ctt	tcc	aag	atc	tgc	aac	gac	ctg	cgc	ctg	ctc	agc	tcg	ggc	912	Ile	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Ser	Ser	Gly														
290															295															300															
ccg	cgc	gcc	ggg	ctg	ggg	gaa	atc	atc	ctg	ccc	ccc	gca	cag	gcc	ggg	960	Pro	Arg	Ala	Gly	Leu	Gly	Glu	Ile	Ile	Leu	Pro	Pro	Ala	Gln	Ala	Gly													
305															310															315															
tcc	tcg	atc	atg	ccg	ggc	aag	gtc	aat	ccg	gtg	atc	ccc	gag	gtg	gtc	1008	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val													
325															330															335															
aac	cag	atc	tgc	tat	cag	gcc	atc	ggc	aac	gac	ctg	acc	gtg	acc	atg	1056	Asn	Gln	Ile	Cys	Tyr	Gln	Ala	Ile	Gly	Asn	Asp	Leu	Thr	Val	Thr	Met													
340															345															350															
gcg	gcc	gag	gcc	ggg	caa	ttg	cag	ctg	aac	gcg	atg	gag	ccg	gtg	atc	1104	Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Ala	Met	Glu	Pro	Val	Ile													
355															360															365															
ttt	tac	aag	gtc	atg	gaa	acc	atg	acg	acg	ctg	acg	ggg	ggc	atg	aac	1152	Phe	Tyr	Lys	Val	Met	Glu	Thr	Met	Thr	Thr	Leu	Thr	Gly	Gly	Met	Asn													
370															375															380															
gtg	ctc	aac	aat	cgc	tgc	gtg	cgg	ggg	atc	cgg	gcg	gat	gag	aaa	cgc	1200	Val	Leu	Asn	Asn	Arg	Cys	Val	Arg	Gly	Ile	Arg	Ala	Asp	Glu	Lys	Arg													
385															390															395															
tgt	gcc	gag	ctg	ctg	ggc	ggc	agt	ctg	gtg	ctg	gcg	acg	ctg	ctg	gcg	1248	Cys	Ala	Glu	Leu	Leu	Gly	Gly	Ser	Leu	Val	Leu	Ala	Thr	Leu	Leu	Ala													
405															410															415															
ccg	gtc	atc	ggc	tat	gat	gcg	gcg	gcc	aaa	gtg	tcc	aaa	cgc	gcc	cgg	1296	Pro	Val	Ile	Gly	Tyr	Asp	Ala	Ala	Ala	Lys	Val	Ser	Lys	Arg	Ala	Arg													
420															425															430															
gcc	gaa	ggg	atc	acc	ctg	cgc	gag	gct	tgt	ctg	aaa	cag	ggg	ctg	gac	1344	Ala	Glu	Gly	Ile	Thr	Leu	Arg	Glu	Ala	Cys	Leu	Lys	Gln	Gly	Leu	Asp													
435															440															445															
gcg	gcg	ttg	gtg	gat	tct	ctg	cta	tga								1371	Ala	Ala	Leu	Val	Asp	Ser	Leu	Leu																					
450															455																														

<210> 9684

<211> 456

<212> PRT

<213> Silicibacter pomeroyi DSS-3

<400> 9684

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

PF59083SeqList PF59083.txt

Cys Asp Arg Ile Ile Ala Gly Gln His His Glu Ala Phe Cys Val Asp
 85 90 95
 Val Met Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu
 100 105 110
 Val Ile Ala Asn Leu Gly Leu Ile Val Leu Gly Gly Ser Tyr Gly Asp
 115 120 125
 Tyr Gly His Leu His Pro Asn Asp Asp Val Asn Arg Ser Gln Ser Thr
 130 135 140
 Asn Asp Val Tyr Pro Thr Ala Ile Arg Leu Ala Thr Leu Ser Lys Ala
 145 150 155 160
 Arg Val Leu Ser Ala Ala Leu Arg Asp Leu Val Gln Ala Phe His Asp
 165 170 175
 Lys Gly Asp Glu Phe Ala His Ile Asn Lys Val Gly Arg Thr Gln Leu
 180 185 190
 Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe His Ser Phe Ala
 195 200 205
 Asn Thr Leu Ala Glu Asp Ile Asp Arg Ile Thr Asp Leu Gly Arg Leu
 210 215 220
 Leu Ala Glu Val Asn Leu Gly Gly Thr Ala Ile Gly Thr Arg Ile Asn
 225 230 235 240
 Thr Pro Glu Gly Tyr Gly Pro Leu Val Val Glu Lys Leu Ala Asp Ile
 245 250 255
 Thr Gly Leu Ala Leu Ser Pro Ala Arg Asp Leu Ile Glu Ala Ser Ser
 260 265 270
 Asp Leu Gly Ala Phe Val Met Phe Ser Gly Ala Leu Lys Arg Val Ala
 275 280 285
 Ile Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly
 290 295 300
 Pro Arg Ala Gly Leu Gly Glu Ile Ile Leu Pro Ala Gln Ala Gly
 305 310 315 320
 Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Val
 325 330 335
 Asn Gln Ile Cys Tyr Gln Ala Ile Gly Asn Asp Leu Thr Val Thr Met
 340 345 350
 Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Ala Met Glu Pro Val Ile
 355 360 365
 Phe Tyr Lys Val Met Glu Thr Met Thr Thr Leu Thr Gly Gly Met Asn
 370 375 380
 Val Leu Asn Asn Arg Cys Val Arg Gly Ile Arg Ala Asp Glu Lys Arg
 385 390 395 400
 Cys Ala Glu Leu Leu Gly Gly Ser Leu Val Leu Ala Thr Leu Leu Ala
 405 410 415
 Pro Val Ile Gly Tyr Asp Ala Ala Ala Lys Val Ser Lys Arg Ala Arg
 420 425 430
 Ala Glu Gly Ile Thr Leu Arg Glu Ala Cys Leu Lys Gln Gly Leu Asp
 435 440 445
 Ala Ala Leu Val Asp Ser Leu Leu
 450 455

<210> 9685

<211> 1413

<212> DNA

<213> Bacillus clausii KSM-K16

<220>

<221> CDS

<222> (1)..(1413)

<223> transl_table=11

<400> 9685

atg gag tac cgg gtt gaa cga gac tta cta gga gaa aaa caa gta ccg
 Met Glu Tyr Arg Val Glu Arg Asp Leu Leu Gly Glu Lys Gln Val Pro
 1 5 10 15
 aaa cat gct tat tat ggc atc caa tcg ctg cgg gca aag gat aat ttt
 Lys His Ala Tyr Tyr Gly Ile Gln Ser Leu Arg Ala Lys Asp Asn Phe
 20 25 30
 ccg att acc ggc tat ccg ccc cac cct gaa ctt att cgc gct ttc ggc
 Pro Ile Thr Gly Tyr Pro Pro His Pro Glu Leu Ile Arg Ala Phe Gly
 35 40 45

48

96

144

PF59083SeqList PF59083.txt

tat	gtg	aaa	aaa	gcg	gct	gcc	ctt	gca	aac	cgg	gat	gtc	ggt	gta	ctg	192
Tyr	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Arg	Asp	Val	Gly	Val	Leu	
	50					55				60						
cgc	ccc	cac	att	gct	gaa	gcg	att	att	aag	gca	agc	gat	gaa	gta	att	240
Arg	Pro	His	Ile	Ala	Glu	Ala	Ile	Ile	Lys	Ala	Ser	Asp	Glu	Val	Ile	
	65				70					75					80	
gaa	ggg	cgt	ttg	aat	gat	cat	ttt	att	gtc	gat	tcg	atc	caa	gga	ggc	288
Glu	Gly	Arg	Leu	Asn	Asp	His	Phe	Ile	Val	Asp	Ser	Ile	Gln	Gly	Gly	
				85					90					95		
gcc	ggc	acg	tcg	ttt	aat	atg	aat	gcc	aat	gaa	gtc	att	gct	aac	cgg	336
Ala	Gly	Thr	Ser	Phe	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	
			100					105					110			
gcg	att	gaa	att	ctt	ggc	ggc	gaa	aaa	ggc	gat	tat	tta	aaa	gtc	agt	384
Ala	Ile	Glu	Ile	Leu	Gly	Gly	Glu	Lys	Gly	Asp	Tyr	Leu	Lys	Val	Ser	
		115					120					125				
ccc	aac	aca	cac	gtc	aac	atg	gcc	cag	tct	acc	aat	gat	tca	ttt	ccg	432
Pro	Asn	Thr	His	Val	Asn	Met	Ala	Gln	Ser	Thr	Asn	Asp	Ser	Phe	Pro	
	130					135				140						
acg	gcg	att	cat	att	gcc	gct	tta	aat	atg	aca	aag	ggc	ttg	acg	gaa	480
Thr	Ala	Ile	His	Ile	Ala	Ala	Leu	Asn	Met	Thr	Lys	Gly	Leu	Thr	Glu	
	145				150					155					160	
gaa	ttg	cag	aaa	ttg	atc	aac	gaa	atg	gaa	gcg	aaa	gcc	gaa	gaa	ttt	528
Glu	Leu	Gln	Lys	Leu	Ile	Asn	Glu	Met	Glu	Ala	Lys	Ala	Glu	Glu	Phe	
				165					170					175		
gac	agc	gtc	cta	aaa	atg	ggg	cgg	acc	cac	caa	gat	gca	gtc	cct		576
Asp	Ser	Val	Leu	Lys	Met	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Val	Pro	
			180					185				190				
att	cga	cta	ggg	cag	gaa	ttt	ggc	tcg	tac	cgc	aga	gtg	cta	gcc	cgt	624
Ile	Arg	Leu	Gly	Gln	Glu	Phe	Gly	Ser	Tyr	Arg	Arg	Val	Leu	Ala	Arg	
		195					200					205				
gat	cta	aaa	cgg	gta	agc	cgt	tcg	gca	gac	cac	ctc	cac	gac	atc	aat	672
Asp	Leu	Lys	Arg	Val	Ser	Arg	Ser	Ala	Asp	His	Leu	His	Asp	Ile	Asn	
	210					215				220						
atg	ggt	gca	acc	gct	gta	gga	acg	ggt	ttg	aac	gcc	aaa	ccg	gaa	tac	720
Met	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Ala	Lys	Pro	Glu	Tyr	
	225				230					235					240	
att	gaa	aaa	ggt	gca	aaa	cat	ttg	gct	gac	ttg	act	gag	ctg	ccg	ttg	768
Ile	Glu	Lys	Val	Ala	Lys	His	Leu	Ala	Asp	Leu	Thr	Glu	Leu	Pro	Leu	
				245					250					255		
aaa	acg	gcg	gag	gat	ctt	gtc	gat	gcc	acc	caa	aat	aca	gat	gcc	tat	816
Lys	Thr	Ala	Glu	Asp	Leu	Val	Asp	Ala	Thr	Gln	Asn	Thr	Asp	Ala	Tyr	
			260					265					270			
aca	gag	ctt	tct	agt	tcg	tta	aaa	att	tta	gct	att	aat	tta	tcg	aaa	864
Thr	Glu	Leu	Ser	Ser	Ser	Leu	Lys	Ile	Leu	Ala	Ile	Asn	Leu	Ser	Lys	
		275					280					285				
atc	gca	aat	gac	tta	cgt	tta	atg	agc	tcg	ggc	ccg	cgg	acc	gga	ttg	912
Ile	Ala	Asn	Asp	Leu	Arg	Leu	Met	Ser	Ser	Gly	Pro	Arg	Thr	Gly	Leu	
	290				295					300						
aat	gaa	atc	aat	ttg	ccg	ccg	cga	cag	ccg	ggt	tca	tcg	atc	atg	cct	960
Asn	Glu	Ile	Asn	Leu	Pro	Pro	Arg	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	
	305				310					315					320	
gga	aaa	gta	aat	ccg	ggt	atg	tgt	gaa	gtc	att	aac	cag	ctt	tct	ttt	1008
Gly	Lys	Val	Asn	Pro	Val	Met	Cys	Glu	Val	Ile	Asn	Gln	Leu	Ser	Phe	
				325					330					335		
caa	ggt	atc	ggc	aat	gac	cat	acg	atc	agc	ctt	gct	tca	gaa	gcg	ggc	1056
Gln	Val	Ile	Gly	Asn	Asp	His	Thr	Ile	Ser	Leu	Ala	Ser	Glu	Ala	Gly	
			340					345					350			
caa	ctt	gaa	cta	aac	gtg	atg	gaa	cct	gta	ctc	ggt	ttt	aat	tta	ttg	1104
Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Leu	Val	Phe	Asn	Leu	Leu	
		355					360					365				
caa	tca	tta	acg	gtg	cta	caa	aac	ggt	atg	cgc	gtc	ttt	aaa	gat	tac	1152
Gln	Ser	Leu	Thr	Val	Leu	Gln	Asn	Gly	Met	Arg	Val	Phe	Lys	Asp	Tyr	
	370				375					380						
gca	att	gcc	ggc	att	acc	gct	aac	gtg	gag	cga	tgc	cgg	gaa	ctt	gta	1200
Ala	Ile	Ala	Gly	Ile	Thr	Ala	Asn	Val	Glu	Arg	Cys	Arg	Glu	Leu	Val	
				390						395					400	
gaa	cat	agc	gtc	ggt	att	gta	acg	gca	atc	aat	ccc	cat	gtc	ggc	tat	1248
Glu	His	Ser	Val	Gly	Ile	Val	Thr	Ala	Ile	Asn	Pro	His	Val	Gly	Tyr	
				405					410					415		

PF59083SeqList PF59083.txt

gaa	gta	gct	act	cgt	gta	gct	aaa	gaa	gca	att	gaa	aca	ggg	cgg	ccg		1296
Glu	Val	Ala	Thr	Arg	Val	Ala	Lys	Glu	Ala	Ile	Glu	Thr	Gly	Arg	Pro		
			420					425					430				
gtc	cgg	gaa	att	tgt	ctt	gaa	cgg	ggc	atc	ctt	tca	gag	gaa	gaa	ttg		1344
Val	Arg	Glu	Ile	Cys	Leu	Glu	Arg	Gly	Ile	Leu	Ser	Glu	Glu	Glu	Leu		
		435					440					445					
aat	gaa	att	ctt	gat	cca	aaa	gaa	atg	aca	aaa	ccc	ggg	atc	gcg	ggc		1392
Asn	Glu	Ile	Leu	Asp	Pro	Lys	Glu	Met	Thr	Lys	Pro	Gly	Ile	Ala	Gly		
	450					455					460						
tcc	cgt	ttt	ttg	ccg	tta	taa											1413
Ser	Arg	Phe	Leu	Pro	Leu												
465					470												

<210> 9686

<211> 470

<212> PRT

<213> Bacillus clausii KSM-K16

<400> 9686

Met	Glu	Tyr	Arg	Val	Glu	Arg	Asp	Leu	Leu	Gly	Glu	Lys	Gln	Val	Pro		
1				5					10					15			
Lys	His	Ala	Tyr	Tyr	Gly	Ile	Gln	Ser	Leu	Arg	Ala	Lys	Asp	Asn	Phe		
			20					25					30				
Pro	Ile	Thr	Gly	Tyr	Pro	Pro	His	Pro	Glu	Leu	Ile	Arg	Ala	Phe	Gly		
		35					40					45					
Tyr	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Arg	Asp	Val	Gly	Val	Leu		
	50				55						60						
Arg	Pro	His	Ile	Ala	Glu	Ala	Ile	Ile	Lys	Ala	Ser	Asp	Glu	Val	Ile		
65					70				75						80		
Glu	Gly	Arg	Leu	Asn	Asp	His	Phe	Ile	Val	Asp	Ser	Ile	Gln	Gly	Gly		
			85					90					95				
Ala	Gly	Thr	Ser	Phe	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg		
		100						105					110				
Ala	Ile	Glu	Ile	Leu	Gly	Gly	Glu	Lys	Gly	Asp	Tyr	Leu	Lys	Val	Ser		
		115					120					125					
Pro	Asn	Thr	His	Val	Asn	Met	Ala	Gln	Ser	Thr	Asn	Asp	Ser	Phe	Pro		
	130				135						140						
Thr	Ala	Ile	His	Ile	Ala	Ala	Leu	Asn	Met	Thr	Lys	Gly	Leu	Thr	Glu		
145					150					155					160		
Glu	Leu	Gln	Lys	Leu	Ile	Asn	Glu	Met	Glu	Ala	Lys	Ala	Glu	Glu	Phe		
			165					170					175				
Asp	Ser	Val	Leu	Lys	Met	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Val	Pro		
		180						185					190				
Ile	Arg	Leu	Gly	Gln	Glu	Phe	Gly	Ser	Tyr	Arg	Arg	Val	Leu	Ala	Arg		
		195					200					205					
Asp	Leu	Lys	Arg	Val	Ser	Arg	Ser	Ala	Asp	His	Leu	His	Asp	Ile	Asn		
	210					215					220						
Met	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Ala	Lys	Pro	Glu	Tyr		
225					230					235					240		
Ile	Glu	Lys	Val	Ala	Lys	His	Leu	Ala	Asp	Leu	Thr	Glu	Leu	Pro	Leu		
			245					250					255				
Lys	Thr	Ala	Glu	Asp	Leu	Val	Asp	Ala	Thr	Gln	Asn	Thr	Asp	Ala	Tyr		
		260						265					270				
Thr	Glu	Leu	Ser	Ser	Ser	Leu	Lys	Ile	Leu	Ala	Ile	Asn	Leu	Ser	Lys		
		275					280						285				
Ile	Ala	Asn	Asp	Leu	Arg	Leu	Met	Ser	Ser	Gly	Pro	Arg	Thr	Gly	Leu		
	290					295						300					
Asn	Glu	Ile	Asn	Leu	Pro	Pro	Arg	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro		
305					310					315					320		
Gly	Lys	Val	Asn	Pro	Val	Met	Cys	Glu	Val	Ile	Asn	Gln	Leu	Ser	Phe		
			325					330					335				
Gln	Val	Ile	Gly	Asn	Asp	His	Thr	Ile	Ser	Leu	Ala	Ser	Glu	Ala	Gly		
		340						345					350				
Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Leu	Val	Phe	Asn	Leu	Leu		
		355					360					365					
Gln	Ser	Leu	Thr	Val	Leu	Gln	Asn	Gly	Met	Arg	Val	Phe	Lys	Asp	Tyr		
	370					375					380						
Ala	Ile	Ala	Gly	Ile	Thr	Ala	Asn	Val	Glu	Arg	Cys	Arg	Glu	Leu	Val		
385					390					395					400		

PF59083SeqList PF59083.txt

Glu His Ser Val Gly Ile Val Thr Ala Ile Asn Pro His Val Gly Tyr
 405 410 415
 Glu Val Ala Thr Arg Val Ala Lys Glu Ala Ile Glu Thr Gly Arg Pro
 420 425 430
 Val Arg Glu Ile Cys Leu Glu Arg Gly Ile Leu Ser Glu Glu Leu
 435 440 445
 Asn Glu Ile Leu Asp Pro Lys Glu Met Thr Lys Pro Gly Ile Ala Gly
 450 455 460
 Ser Arg Phe Leu Pro Leu
 465 470

<210> 9687

<211> 1398

<212> DNA

<213> Neisseria gonorrhoeae FA 1090

<220>

<221> CDS

<222> (1)..(1398)

<223> transl_table=11

<400> 9687

atg act gtc cgt atc gaa cac gat tta ttg ggc gac cgc gag att ccc	48
Met Thr Val Arg Ile Glu His Asp Leu Leu Gly Asp Arg Glu Ile Pro	
1 5 10 15	
gcc gaa gtg tat tgg ggc atc cac acc ctg cgc gcc att gaa aac ttt	96
Ala Glu Val Tyr Trp Gly Ile His Thr Leu Arg Ala Ile Glu Asn Phe	
20 25 30	
aaa atc tcc aca caa aaa att tcc gac gtg ccg cag ttt gtc cgc agt	144
Lys Ile Ser Thr Gln Lys Ile Ser Asp Val Pro Gln Phe Val Arg Ser	
35 40 45	
ata gtg atg gtg aaa aaa gca acc gcg cag gca aac ggc gaa ttg ggt	192
Ile Val Met Val Lys Lys Ala Thr Ala Gln Ala Asn Gly Glu Leu Gly	
50 55 60	
gca gta aaa ccc gaa atc gcc gcc att gaa aag gct tgc gac gaa	240
Ala Val Lys Pro Glu Ile Ala Ala Ile Glu Lys Ala Cys Asp Glu	
65 70 75 80	
gtt ctg ctg aac aac cgc tgc ctc gac caa ttc ccg tcc gac gtg tat	288
Val Leu Leu Asn Asn Arg Cys Leu Asp Gln Phe Pro Ser Asp Val Tyr	
85 90 95	
cag ggc ggg gcg gga act tcg gtc aat atg aac acc aac gaa gtc atc	336
Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Ile	
100 105 110	
gcc aac ctt gca ttg gaa gcc ttg ggc tat gag aaa ggc cgc tac gac	384
Ala Asn Leu Ala Leu Glu Ala Leu Gly Tyr Glu Lys Gly Arg Tyr Asp	
115 120 125	
atc gtc aat ccg atg gat cac gtc aac gcc agc caa tcc acc aac gat	432
Ile Val Asn Pro Met Asp His Val Asn Ala Ser Gln Ser Thr Asn Asp	
130 135 140	
gcc tat ccc acg ggc ttc cgc arg ctt gcc gtg tat tac agc atc ggc gaa	480
Ala Tyr Pro Thr Gly Phe Arg Leu Ala Val Tyr Tyr Ser Ile Gly Glu	
145 150 155 160	
ttg ctc gac aaa ctg acc gta ttg aaa aac gcc ttt gcc gcc aaa gcc	528
Leu Leu Asp Lys Leu Thr Val Leu Lys Asn Ala Phe Ala Lys Ala	
165 170 175	
gaa gcg ttt aaa gac gtt ttg aaa atg ggt cgc acc cag ctt caa gat	576
Glu Ala Phe Lys Asp Val Leu Lys Met Gly Arg Thr Gln Leu Gln Asp	
180 185 190	
gcc gta ccg atg acg gca ggc cag gaa ttc caa tct ttc caa gta ttg	624
Ala Val Pro Met Thr Ala Gly Gln Glu Phe Gln Ser Phe Gln Val Leu	
195 200 205	
ttg gaa gag gaa atc ctc aac ctt gac cgc acc cgc caa ctg ctc ttg	672
Leu Glu Glu Glu Ile Leu Asn Leu Asp Arg Thr Arg Gln Leu Leu Leu	
210 215 220	
gaa gtc aat ttg ggc gca acg gca atc ggc acg gtg aac acg ccc	720
Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Val Asn Thr Pro	
225 230 235 240	
aaa ggc tac gcc gaa ctg gtg gtc aaa aaa ctc tcc gaa gtc agc ggc	768
Lys Gly Tyr Ala Glu Leu Val Val Lys Lys Leu Ser Glu Val Ser Gly	

PF59083SeqList PF59083.txt

245	250	255	
ttg cct tgc aaa ctg act gaa aac ctg atc gaa gcg acc tcc gac tgc			816
Leu Pro Cys Lys Leu Thr Glu Asn Leu Ile Glu Ala Thr Ser Asp Cys			
260	265	270	
ggt gca tat gtg atg gta cac ggc gca ttg aaa cgc acg gcc gtc aaa			864
Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Thr Ala Val Lys			
275	280	285	
ctc tct aaa atc tgc aac gat ttg cgc ctt ctc tct tcc ggt ccg cgc			912
Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg			
290	295	300	
gcc ggt ttg aaa gaa atc aac ctg ccc gaa ttg cag gcc ggt tct tcc			960
Ala Gly Leu Lys Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly Ser Ser			
305	310	315	
atc atg cct gcc aaa gtc aat ccc gtg att ccc gaa gtc gtc aac caa			1008
Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln			
325	330	335	
gtc tgc ttc aaa gtc atc ggc aac gat acg acg att acc ttc gcc gcc			1056
Val Cys Phe Lys Val Ile Gly Asn Asp Thr Thr Ile Thr Phe Ala Ala			
340	345	350	
gaa tcc ggg caa ctg caa tta aac gtt atg gag ccg gtc atc gcc caa			1104
Glu Ser Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Ala Gln			
355	360	365	
tgt atg ttt gaa acc att tcc ctc ttg ggc aat gcc gca gtc aac cta			1152
Cys Met Phe Glu Thr Ile Ser Leu Leu Gly Asn Ala Ala Val Asn Leu			
370	375	380	
tcc gac aaa tgc gtc aaa ggc att acg gtc aac cgc gaa atc tgc gag			1200
Ser Asp Lys Cys Val Lys Gly Ile Thr Val Asn Arg Glu Ile Cys Glu			
385	390	395	
cgg tat gtc ttc aac tcc atc ggt ttg gtc act tat ctg aat ccg tac			1248
Arg Tyr Val Phe Asn Ser Ile Gly Leu Val Thr Tyr Leu Asn Pro Tyr			
405	410	415	
atc ggc cac cgc aac ggc gac ttg gtc ggc aaa atc tgc gcc caa acc			1296
Ile Gly His Arg Asn Gly Asp Leu Val Gly Lys Ile Cys Ala Gln Thr			
420	425	430	
ggc aaa ggc gtg cgc gaa gtc gta ctg gag cgc ggc ctg tta agc gaa			1344
Gly Lys Gly Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu Ser Glu			
435	440	445	
gaa gaa atc aac cgc atc ctc tcc ccc gag aac ctg atg aat cct cat			1392
Glu Glu Ile Asn Arg Ile Leu Ser Pro Glu Asn Leu Met Asn Pro His			
450	455	460	
ctg taa			1398
Leu			
465			

<210> 9688

<211> 465

<212> PRT

<213> Neisseria gonorrhoeae FA 1090

<400> 9688

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

PF59083SeqList PF59083.txt

145 150 155 160
 Leu Leu Asp Lys Leu Thr Val Leu Lys Asn Ala Phe Ala Ala Lys Ala
 165 170 175
 Glu Ala Phe Lys Asp Val Leu Lys Met Gly Arg Thr Gln Leu Gln Asp
 180 185 190
 Ala Val Pro Met Thr Ala Gly Gln Phe Gln Ser Phe Gln Val Leu
 195 200 205
 Leu Glu Glu Glu Ile Leu Asn Leu Asp Arg Thr Arg Gln Leu Leu Leu
 210 215 220
 Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Val Asn Thr Pro
 225 230 235 240
 Lys Gly Tyr Ala Glu Leu Val Val Lys Lys Leu Ser Glu Val Ser Gly
 245 250 255
 Leu Pro Cys Lys Leu Thr Glu Asn Leu Ile Glu Ala Thr Ser Asp Cys
 260 265 270
 Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Thr Ala Val Lys
 275 280 285
 Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg
 290 295 300
 Ala Gly Leu Lys Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly Ser Ser
 305 310 315 320
 Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln
 325 330 335
 Val Cys Phe Lys Val Ile Gly Asn Asp Thr Thr Ile Thr Phe Ala Ala
 340 345 350
 Glu Ser Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Ala Gln
 355 360 365
 Cys Met Phe Glu Thr Ile Ser Leu Leu Gly Asn Ala Ala Val Asn Leu
 370 375 380
 Ser Asp Lys Cys Val Lys Gly Ile Thr Val Asn Arg Glu Ile Cys Glu
 385 390 395 400
 Arg Tyr Val Phe Asn Ser Ile Gly Leu Val Thr Tyr Leu Asn Pro Tyr
 405 410 415
 Ile Gly His Arg Asn Gly Asp Leu Val Gly Lys Ile Cys Ala Gln Thr
 420 425 430
 Gly Lys Gly Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu Ser Glu
 435 440 445
 Glu Glu Ile Asn Arg Ile Leu Ser Pro Glu Asn Leu Met Asn Pro His
 450 455 460
 Leu
 465

<210> 9689
 <211> 1458
 <212> DNA
 <213> Colwellia psychrerythraea 34H

<220>
 <221> CDS
 <222> (1)..(1458)
 <223> transl_table=11

<400> 9689
 atg tct aag aaa cag gtt act aaa gct caa act ata act gcg cca aaa 48
 Met Ser Lys Lys Gln Val Thr Lys Ala Gln Thr Ile Thr Ala Pro Lys
 1 5 10 15
 gaa cga ata gaa aaa gat tta cta ggt gaa aga agt ttg cct gtt gat 96
 Glu Arg Ile Glu Lys Asp Leu Leu Gly Glu Arg Ser Leu Pro Val Asp
 20 25 30
 gtc tat tat ggt gta caa aca tta cgg gca acg gaa aac ttt aat att 144
 Val Tyr Tyr Gly Val Gln Thr Leu Arg Ala Thr Glu Asn Phe Asn Ile
 35 40 45
 acc tct att tgt gta ggt gac ttt ccc gcc cta gtt aaa gcc tta gct 192
 Thr Ser Ile Cys Val Gly Asp Phe Pro Ala Leu Val Lys Ala Leu Ala
 50 55 60
 atg gta aaa aag gcc tgc gct ttg gct aat aaa aaa tta aac tta ctt 240
 Met Val Lys Lys Ala Cys Ala Leu Ala Asn Lys Lys Leu Asn Leu Leu
 65 70 75 80
 gaa aat aac aaa gca gaa gct ata aca cag gcc tgt gac gaa gtt atc 288
 85 90 95 100
 Seite 10164

PF59083SeqList PF59083.txt

Glu	Asn	Asn	Lys	Ala	Glu	Ala	Ile	Thr	Gln	Ala	Cys	Asp	Glu	Val	Ile	
85									90					95		
agt	ggt	aaa	ttt	gat	aat	caa	ttt	gtg	gtc	gat	atg	atc	caa	gga	gga	336
Ser	Gly	Lys	Phe	Asp	Asn	Gln	Phe	Val	Val	Asp	Met	Ile	Gln	Gly	Gly	
		100						105					110			
gct	ggt	act	tca	acc	aac	atg	aac	gcc	aat	gaa	gtt	ata	gca	aat	aga	384
Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	
		115					120					125				
gca	tta	gaa	att	ctt	ggc	cat	gaa	aag	ggc	tgt	tac	gac	ata	att	agt	432
Ala	Leu	Glu	Ile	Leu	Gly	His	Glu	Lys	Gly	Cys	Tyr	Asp	Ile	Ile	Ser	
	130					135					140					
cca	aat	aac	cat	ggt	aat	ttg	tca	caa	tct	acc	aat	gat	ggt	tat	cca	480
Pro	Asn	Asn	His	Val	Asn	Leu	Ser	Gln	Ser	Thr	Asn	Asp	Val	Tyr	Pro	
145					150					155					160	
aca	gcc	tta	cgt	ttg	gca	tta	att	atg	tcg	aca	cct	gag	ctt	tac	gag	528
Thr	Ala	Leu	Arg	Leu	Ala	Leu	Ile	Met	Ser	Thr	Pro	Glu	Leu	Tyr	Glu	
				165				170						175		
tct	ata	gct	tta	ttg	ggt	tat	cag	tgc	aag	caa	aaa	gcc	gta	gaa	ttt	576
Ser	Ile	Ala	Leu	Leu	Gly	Tyr	Gln	Cys	Lys	Gln	Lys	Ala	Val	Glu	Phe	
			180					185					190			
tcc	agt	gtg	att	aaa	atg	ggt	cga	acg	caa	tta	caa	gat	gcc	gta	cct	624
Ser	Ser	Val	Ile	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	
		195					200					205				
atg	act	ttg	ggc	caa	gag	ttt	gaa	gca	tac	tac	gcc	aca	ctg	aaa	gaa	672
Met	Thr	Leu	Gly	Gln	Glu	Phe	Glu	Ala	Tyr	Tyr	Ala	Thr	Leu	Lys	Glu	
	210					215					220					
gat	ttg	gat	atg	tta	aag	gcg	ggt	act	gat	aac	ttt	aga	gaa	atc	aat	720
Asp	Leu	Asp	Met	Leu	Lys	Ala	Val	Thr	Asp	Asn	Phe	Arg	Glu	Ile	Asn	
225					230					235					240	
tta	ggc	gct	aca	gcg	ata	ggt	aca	gga	att	aat	act	gac	cct	gaa	tat	768
Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Thr	Asp	Pro	Glu	Tyr	
				245				250						255		
tca	agc	tta	ggt	att	gaa	gag	tta	tgc	tgg	att	gcc	gac	ata	cat	ttc	816
Ser	Ser	Leu	Val	Ile	Glu	Glu	Leu	Cys	Trp	Ile	Ala	Asp	Ile	His	Phe	
			260					265					270			
att	aga	gca	acc	aac	tta	att	gaa	gcc	aca	agt	gat	atg	ggg	gca	ttt	864
Ile	Arg	Ala	Thr	Asn	Leu	Ile	Glu	Ala	Thr	Ser	Asp	Met	Gly	Ala	Phe	
		275					280					285				
att	acc	cta	tca	agt	atg	cta	aaa	aga	act	gcc	ata	aaa	ggt	tca	aaa	912
Ile	Thr	Leu	Ser	Ser	Met	Leu	Lys	Arg	Thr	Ala	Ile	Lys	Val	Ser	Lys	
		290				295					300					
atg	tgt	aat	gat	cta	cgt	tta	atg	agc	agc	ggt	cct	aga	gct	ggc	ttg	960
Met	Cys	Asn	Asp	Leu	Arg	Leu	Met	Ser	Ser	Gly	Pro	Arg	Ala	Gly	Leu	
305					310					315					320	
aat	gag	att	aac	ctg	cca	gct	atg	caa	cca	ggc	tca	tca	atc	atg	cca	1008
Asn	Glu	Ile	Asn	Leu	Pro	Ala	Met	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	
				325					330					335		
ggc	aag	gta	aac	cct	ggt	atc	cct	gaa	gta	gta	aat	caa	gtc	gct	tat	1056
Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln	Val	Ala	Tyr	
			340					345					350			
gaa	ggt	ata	ggc	aat	gac	ttg	gct	ata	act	atg	gca	gca	gaa	gcc	ggt	1104
Glu	Val	Ile	Gly	Asn	Asp	Leu	Ala	Ile	Thr	Met	Ala	Ala	Glu	Ala	Gly	
		355					360					365				
caa	ctg	cag	tta	aac	ggt	atg	gag	cct	gta	att	gct	ttt	aat	cta	tta	1152
Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile	Ala	Phe	Asn	Leu	Leu	
		370				375					380					
aga	tcc	atc	aaa	ttc	tta	acc	aac	gct	ttt	aat	gct	ctt	gcc	act	cgc	1200
Arg	Ser	Ile	Lys	Phe	Leu	Thr	Asn	Ala	Phe	Asn	Ala	Leu	Ala	Thr	Arg	
385					390					395					400	
tgt	att	tca	ggt	atc	act	gct	aac	gaa	gag	cat	tgt	aaa	tca	atg	gtt	1248
Cys	Ile	Ser	Gly	Ile	Thr	Ala	Asn	Glu	Glu	His	Cys	Lys	Ser	Met	Val	
				405				410						415		
tat	aac	agt	att	ggt	att	ggt	acc	gct	atc	aat	cct	tat	ttg	ggt	tat	1296
Tyr	Asn	Ser	Ile	Gly	Ile	Val	Thr	Ala	Ile	Asn	Pro	Tyr	Leu	Gly	Tyr	
			420					425					430			
gaa	gta	tcg	acc	cgt	att	gca	aaa	gag	gca	tta	gca	aca	ggg	gag	aat	1344
Glu	Val	Ser	Thr	Arg	Ile	Ala	Lys	Glu	Ala	Leu	Ala	Thr	Gly	Glu	Asn	
		435					440					445				
att	atc	aat	ttg	att	aaa	cga	gat	ggt	tta	tta	act	gag	aag	caa	ctt	1392

PF59083SeqList PF59083.txt

Ile	Ile	Asn	Leu	Ile	Lys	Arg	Asp	Gly	Leu	Leu	Thr	Glu	Lys	Gln	Leu	
450						455					460					
gct	gat	att	ctt	aac	cct	gaa	aat	atg	act	cag	cct	aga	cga	caa	ttt	1440
Ala	Asp	Ile	Leu	Asn	Pro	Glu	Asn	Met	Thr	Gln	Pro	Arg	Arg	Gln	Phe	
465					470					475					480	
tct	tcc	gat	aaa	aaa	tag											1458
Ser	Ser	Asp	Lys	Lys												
				485												

<210> 9690
 <211> 485
 <212> PRT
 <213> Colwellia psychrerythraea 34H

<400> 9690

Met	Ser	Lys	Lys	Gln	Val	Thr	Lys	Ala	Gln	Thr	Ile	Thr	Ala	Pro	Lys	
1				5					10					15		
Glu	Arg	Ile	Glu	Lys	Asp	Leu	Leu	Gly	Glu	Arg	Ser	Leu	Pro	Val	Asp	
			20					25					30			
Val	Tyr	Tyr	Gly	Val	Gln	Thr	Leu	Arg	Ala	Thr	Glu	Asn	Phe	Asn	Ile	
			35				40					45				
Thr	Ser	Ile	Cys	Val	Gly	Asp	Phe	Pro	Ala	Leu	Val	Lys	Ala	Leu	Ala	
	50				55						60					
Met	Val	Lys	Lys	Ala	Cys	Ala	Leu	Ala	Asn	Lys	Lys	Leu	Asn	Leu	Leu	
65					70					75					80	
Glu	Asn	Asn	Lys	Ala	Glu	Ala	Ile	Thr	Gln	Ala	Cys	Asp	Glu	Val	Ile	
			85						90					95		
Ser	Gly	Lys	Phe	Asp	Asn	Gln	Phe	Val	Val	Asp	Met	Ile	Gln	Gly	Gly	
			100				105						110			
Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	
		115					120					125				
Ala	Leu	Glu	Ile	Leu	Gly	His	Glu	Lys	Gly	Cys	Tyr	Asp	Ile	Ile	Ser	
	130					135					140					
Pro	Asn	Asn	His	Val	Asn	Leu	Ser	Gln	Ser	Thr	Asn	Asp	Val	Tyr	Pro	
145					150					155					160	
Thr	Ala	Leu	Arg	Leu	Ala	Leu	Ile	Met	Ser	Thr	Pro	Glu	Leu	Tyr	Glu	
			165						170					175		
Ser	Ile	Ala	Leu	Leu	Gly	Tyr	Gln	Cys	Lys	Gln	Lys	Ala	Val	Glu	Phe	
			180					185					190			
Ser	Ser	Val	Ile	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	
		195					200					205				
Met	Thr	Leu	Gly	Gln	Glu	Phe	Glu	Ala	Tyr	Tyr	Ala	Thr	Leu	Lys	Glu	
	210					215					220					
Asp	Leu	Asp	Met	Leu	Lys	Ala	Val	Thr	Asp	Asn	Phe	Arg	Glu	Ile	Asn	
225					230					235					240	
Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Thr	Asp	Pro	Glu	Tyr	
			245						250					255		
Ser	Ser	Leu	Val	Ile	Glu	Glu	Leu	Cys	Trp	Ile	Ala	Asp	Ile	His	Phe	
		260						265					270			
Ile	Arg	Ala	Thr	Asn	Leu	Ile	Glu	Ala	Thr	Ser	Asp	Met	Gly	Ala	Phe	
		275					280					285				
Ile	Thr	Leu	Ser	Ser	Met	Leu	Lys	Arg	Thr	Ala	Ile	Lys	Val	Ser	Lys	
	290					295					300					
Met	Cys	Asn	Asp	Leu	Arg	Leu	Met	Ser	Ser	Gly	Pro	Arg	Ala	Gly	Leu	
305					310					315					320	
Asn	Glu	Ile	Asn	Leu	Pro	Ala	Met	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	
			325						330					335		
Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln	Val	Ala	Tyr	
			340					345					350			
Glu	Val	Ile	Gly	Asn	Asp	Leu	Ala	Ile	Thr	Met	Ala	Ala	Glu	Ala	Gly	
		355					360					365				
Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile	Ala	Phe	Asn	Leu	Leu	
	370					375					380					
Arg	Ser	Ile	Lys	Phe	Leu	Thr	Asn	Ala	Phe	Asn	Ala	Leu	Ala	Thr	Arg	
385					390					395					400	
Cys	Ile	Ser	Gly	Ile	Thr	Ala	Asn	Glu	Glu	His	Cys	Lys	Ser	Met	Val	
			405						410					415		
Tyr	Asn	Ser	Ile	Gly	Ile	Val	Thr	Ala	Ile	Asn	Pro	Tyr	Leu	Gly	Tyr	
			420					425					430			

PF59083SeqList PF59083.txt

Glu Val Ser Thr Arg Ile Ala Lys Glu Ala Leu Ala Thr Gly Glu Asn
 435 440 445
 Ile Ile Asn Leu Ile Lys Arg Asp Gly Leu Leu Thr Glu Lys Gln Leu
 450 455 460
 Ala Asp Ile Leu Asn Pro Glu Asn Met Thr Gln Pro Arg Arg Gln Phe
 465 470 475 480
 Ser Ser Asp Lys Lys
 485

<210> 9691
 <211> 1425
 <212> DNA
 <213> Dechloromonas aromatica RCB

<220>
 <221> CDS
 <222> (1)..(1425)
 <223> transl_table=11

<400> 9691
 atg acc acc act ccc ttc cgc ctc gag cat gac ctg ctt ggt gac cgc 48
 Met Thr Thr Thr Pro Phe Arg Leu Glu His Asp Leu Leu Gly Asp Arg
 1 5 10 15
 gag gtt ccg acc gcc gcc tac tac ggg gta cac acc ctg cga gcc ctt 96
 Glu Val Pro Thr Ala Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Leu
 20 25 30
 gag aat ttc ccg atc acc ggc atc tcg atc gcc gtc tat ccc gac ctg 144
 Glu Asn Phe Pro Ile Thr Gly Ile Ser Ile Ala Val Tyr Pro Asp Leu
 35 40 45
 atc cgc gcc ctg gcc cag atc aag gcc gcc gcc cag gcc aac cag 192
 Ile Arg Ala Leu Ala Gln Ile Lys Lys Ala Ala Ala Gln Ala Asn Gln
 50 55 60
 caa ctc ggc ctg ctc gat gcc cgg cgc gcc ggc gcc atc gcc gaa gcc 240
 Gln Leu Gly Leu Leu Asp Ala Arg Arg Ala Gly Ala Ile Ala Glu Ala
 65 70 75 80
 tgc ggc gag atc atc gac ggc cag tgg cac aac cag ttc gtc gtc gat 288
 Cys Gly Glu Ile Ile Asp Gly Gln Trp His Asn Gln Phe Val Val Asp
 85 90 95
 gtc att cag ggc ggc gcc ggc acc tcg acc aac atg aat gcc aac gag 336
 Val Ile Gln Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu
 100 105 110
 gtg atc gcc aac cgt gcg ctg gaa ctg ctc ggc aag acg cgc gcc gac 384
 Val Ile Ala Asn Arg Ala Leu Glu Leu Leu Gly Lys Thr Arg Gly Asp
 115 120 125
 tac aag acg ctg cac ccg aac gaa cac gtc aac atg agc cag tcg acc 432
 Tyr Lys Thr Leu His Pro Asn Glu His Val Asn Met Ser Gln Ser Thr
 130 135 140
 aac gac gtc tat ccg acg gcg ctg aag ctg gcc acc tat gtc ggc atc 480
 Asn Asp Val Tyr Pro Thr Ala Leu Lys Leu Ala Thr Tyr Val Gly Ile
 145 150 155 160
 ttc cgc ctg gtc gag gcc atg gct tat ctg cgc aaa gct ttc gag cgc 528
 Phe Arg Leu Val Glu Ala Met Ala Tyr Leu Arg Lys Ala Phe Glu Arg
 165 170 175
 aag gcc gac gag ttc gcc gac gtg ctg aag atg ggc cgt acc cag ttg 576
 Lys Ala Asp Glu Phe Ala Asp Val Leu Lys Met Gly Arg Thr Gln Leu
 180 185 190
 cag gac gcc gtg ccg atg acc ctc ggc cag gag ttc tcg acc tac gcc 624
 Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Ser Thr Tyr Ala
 195 200 205
 gtg atg ttg ggc gag gac gaa gaa cgc ctg aag gaa gcc gca ctg ctc 672
 Val Met Leu Gly Glu Asp Glu Glu Arg Leu Lys Glu Ala Ala Leu Leu
 210 215 220
 atc cgc gaa atg aat ctc ggt gcc acc gcc att ggc acc ggc atc aac 720
 Ile Arg Glu Met Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Ile Asn
 225 230 235 240
 gcc cac ccg gac tac gcc ccg ctg gtc tgc cgc aag ctg gcc gaa atc 768
 Ala His Pro Asp Tyr Ala Pro Leu Val Cys Arg Lys Leu Ala Glu Ile
 245 250 255
 agc ggc atc ccg gtc gtc acc gcg ccc aac ctg atc gag gcg acg cag 816

PF59083SeqList PF59083.txt

Ser	Gly	Ile	Pro	Val	Val	Thr	Ala	Pro	Asn	Leu	Ile	Glu	Ala	Thr	Gln	
			260					265					270			
gat	tgc	ggc	agc	ttc	gtg	caa	ctg	tcc	ggc	gtc	ctg	aag	cgc	gtc	gcc	864
Asp	Cys	Gly	Ser	Phe	Val	Gln	Leu	Ser	Gly	Val	Leu	Lys	Arg	Val	Ala	
		275					280					285				
gtc	aag	cta	tcc	aag	gtc	tgc	aac	gac	ctg	cgc	ctg	ctc	tct	tcc	ggc	912
Val	Lys	Leu	Ser	Lys	Val	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	
	290					295					300					
ccg	cgt	gcc	ggc	ttc	aac	gag	atc	aat	ctg	ccg	ccg	cgc	cag	gcc	ggt	960
Pro	Arg	Ala	Gly	Phe	Asn	Glu	Ile	Asn	Leu	Pro	Pro	Arg	Gln	Ala	Gly	
					310					315					320	
tcg	tcg	atc	atg	ccg	ggc	aag	gtc	aat	ccg	gtg	atc	ccg	gaa	gtg	gtc	1008
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	
				325					330					335		
aac	cag	atc	gcc	ttc	gaa	gtg	atc	ggc	aac	gac	acc	acc	gtc	act	ttc	1056
Asn	Gln	Ile	Ala	Phe	Glu	Val	Ile	Gly	Asn	Asp	Thr	Thr	Val	Thr	Phe	
			340					345					350			
gcc	gcc	gaa	gcc	ggc	cag	ctg	cag	ctc	aat	gcc	ttc	gag	ccg	atc	atc	1104
Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Ala	Phe	Glu	Pro	Ile	Ile	
		355				360						365				
gcc	cac	agc	ctg	ttc	aag	agc	gcc	ctg	cac	ctg	acc	aac	ggc	tgc	cgc	1152
Ala	His	Ser	Leu	Phe	Lys	Ser	Ala	Leu	His	Leu	Thr	Asn	Gly	Cys	Arg	
	370					375					380					
gtg	ctg	gcc	gac	cat	tgc	gtc	aat	ggc	atc	acc	gcc	aac	cgc	gat	cag	1200
Val	Leu	Ala	Asp	His	Cys	Val	Asn	Gly	Ile	Thr	Ala	Asn	Arg	Asp	Gln	
					390					395					400	
ctg	cgc	gaa	tcg	gtc	gag	cgc	tcg	atc	ggc	atc	gtc	acc	gcc	ctc	aac	1248
Leu	Arg	Glu	Ser	Val	Glu	Arg	Ser	Ile	Gly	Ile	Val	Thr	Ala	Leu	Asn	
				405					410					415		
ccg	tac	att	ggc	tac	gcc	aac	gcc	acc	gaa	gtc	gct	gcc	gaa	gcc	ttc	1296
Pro	Tyr	Ile	Gly	Tyr	Ala	Asn	Ala	Thr	Glu	Val	Ala	Ala	Glu	Ala	Phe	
			420					425					430			
cgt	agc	ggg	cgc	ggc	gtg	gcc	gag	gtg	gtc	atc	gaa	cgc	ggc	ctg	atg	1344
Arg	Ser	Gly	Arg	Gly	Val	Ala	Glu	Val	Val	Ile	Glu	Arg	Gly	Leu	Met	
		435				440						445				
agc	ccg	gaa	cag	ctg	gcc	gaa	gtg	ctg	cgt	ccc	gag	gtg	ctg	acc	cgc	1392
Ser	Pro	Glu	Gln	Leu	Ala	Glu	Val	Leu	Arg	Pro	Glu	Val	Leu	Thr	Arg	
		450				455					460					
cca	caa	gtc	atc	ccc	ctg	cct	gtc	gcc	gcc	tga						1425
Pro	Gln	Val	Ile	Pro	Leu	Pro	Val	Ala	Ala							
					470											

<210> 9692

<211> 474

<212> PRT

<213> Dechloromonas aromatica RCB

<400> 9692

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

PF59083SeqList PF59083.txt

165 170 175
 Lys Ala Asp Glu Phe Ala Asp Val Leu Lys Met Gly Arg Thr Gln Leu
 180 185 190
 Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Ser Thr Tyr Ala
 195 200 205
 Val Met Leu Gly Glu Asp Glu Arg Leu Lys Glu Ala Ala Leu Leu
 210 215 220
 Ile Arg Glu Met Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Ile Asn
 225 230 235 240
 Ala His Pro Asp Tyr Ala Pro Leu Val Cys Arg Lys Leu Ala Glu Ile
 245 250 255
 Ser Gly Ile Pro Val Val Thr Ala Pro Asn Leu Ile Glu Ala Thr Gln
 260 265 270
 Asp Cys Gly Ser Phe Val Gln Leu Ser Gly Val Leu Lys Arg Val Ala
 275 280 285
 Val Lys Leu Ser Lys Val Cys Asn Asp Leu Arg Leu Ser Ser Gly
 290 295 300
 Pro Arg Ala Gly Phe Asn Glu Ile Asn Leu Pro Pro Arg Gln Ala Gly
 305 310 315 320
 Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Val
 325 330 335
 Asn Gln Ile Ala Phe Glu Val Ile Gly Asn Asp Thr Thr Val Thr Phe
 340 345 350
 Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Ala Phe Glu Pro Ile Ile
 355 360 365
 Ala His Ser Leu Phe Lys Ser Ala Leu His Leu Thr Asn Gly Cys Arg
 370 375 380
 Val Leu Ala Asp His Cys Val Asn Gly Ile Thr Ala Asn Arg Asp Gln
 385 390 395 400
 Leu Arg Glu Ser Val Glu Arg Ser Ile Gly Ile Val Thr Ala Leu Asn
 405 410 415
 Pro Tyr Ile Gly Tyr Ala Asn Ala Thr Glu Val Ala Ala Glu Ala Phe
 420 425 430
 Arg Ser Gly Arg Gly Val Ala Glu Val Val Ile Glu Arg Gly Leu Met
 435 440 445
 Ser Pro Glu Gln Leu Ala Glu Val Leu Arg Pro Glu Val Leu Thr Arg
 450 455 460
 Pro Gln Val Ile Pro Leu Pro Val Ala Ala
 465 470

<210> 9693

<211> 1428

<212> DNA

<213> Ralstonia eutropha JMP134

<220>

<221> CDS

<222> (1)..(1428)

<223> transl_table=11

<400> 9693

atg	act	gcc	gga	ccc	ttc	aga	acc	gaa	cat	gac	ctg	ctg	ggc	gac	cgg	48
Met	Thr	Ala	Gly	Pro	Phe	Arg	Thr	Glu	His	Asp	Leu	Leu	Gly	Asp	Arg	
1				5				10					15			
gaa	gtc	ccg	gcc	cag	gct	tac	tac	ggt	gtc	cac	acc	ctg	cgc	gcc	gtc	96
Glu	Val	Pro	Ala	Gln	Ala	Tyr	Tyr	Gly	Val	His	Thr	Leu	Arg	Ala	Val	
			20					25					30			
gag	aac	ttc	ccg	atc	acg	ggc	acg	cca	att	tcc	atc	tac	ccg	gaa	ctg	144
Glu	Asn	Phe	Pro	Ile	Thr	Gly	Thr	Pro	Ile	Ser	Ile	Tyr	Pro	Glu	Leu	
			35				40					45				
atc	aag	gcg	ctg	gcc	gcg	atc	aag	caa	gcc	gcg	gcg	caa	gcg	aac	cat	192
Ile	Lys	Ala	Leu	Ala	Ala	Ile	Lys	Gln	Ala	Ala	Ala	Gln	Ala	Asn	His	
	50				55			60								
gag	ctt	gag	ctg	cta	gac	cag	gca	cgc	tgc	gac	gcg	atc	gtc	gct	gcc	240
Glu	Leu	Glu	Leu	Leu	Asp	Gln	Ala	Arg	Cys	Asp	Ala	Ile	Val	Ala	Ala	
	65				70			75							80	
tgt	cag	gaa	ctg	atg	gcc	gga	aag	ctg	cac	gat	cag	ttc	gtg	gtc	gac	288
Cys	Gln	Glu	Leu	Met	Ala	Gly	Lys	Leu	His	Asp	Gln	Phe	Val	Val	Asp	
				85				90						95		

PF59083SeqList PF59083.txt																
gtg	atc	cag	ggc	ggc	gct	ggc	acc	tcg	aca	aac	atg	aac	gcc	aat	gag	336
Val	Ile	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	
			100					105					110			
gtc	atc	gcc	aat	cgc	gcg	ctc	gag	ctt	ctc	ggg	cat	cag	aag	ggc	gag	384
Val	Ile	Ala	Asn	Arg	Ala	Leu	Glu	Leu	Leu	Gly	His	Gln	Lys	Gly	Glu	
			115				120					125				
tac	cag	cac	ctg	cat	ccg	aac	gaa	cac	gtc	aat	atc	ggc	cag	agc	acc	432
Tyr	Gln	His	Leu	His	Pro	Asn	Glu	His	Val	Asn	Ile	Gly	Gln	Ser	Thr	
			130			135				140						
aac	gat	gtc	tat	ccg	acc	gcg	ttg	aag	gtc	gcg	aca	tgg	ttc	ggc	atc	480
Asn	Asp	Val	Tyr	Pro	Thr	Ala	Leu	Lys	Val	Ala	Thr	Trp	Phe	Gly	Ile	
145					150				155						160	
cgt	ggg	ctt	gtg	gag	gcc	atg	gcg	gta	ctg	cgc	cag	gcg	ttc	gag	gcg	528
Arg	Gly	Leu	Val	Glu	Ala	Met	Ala	Val	Leu	Arg	Gln	Ala	Phe	Glu	Ala	
			165					170						175		
aag	gcc	gag	gag	ttc	gcc	cac	atc	atc	aag	atg	ggc	cgc	acg	caa	ttg	576
Lys	Ala	Glu	Glu	Phe	Ala	His	Ile	Ile	Lys	Met	Gly	Arg	Thr	Gln	Leu	
			180				185						190			
cag	gat	gcg	gtg	ccg	atg	acg	ctc	ggc	cag	gaa	ttc	agc	acc	tat	gcc	624
Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Thr	Tyr	Ala	
			195				200					205				
gtg	atg	ctc	ggc	gaa	gac	gag	gcg	cgc	ttg	cgt	gaa	gcc	gcg	atg	ctg	672
Val	Met	Leu	Gly	Glu	Asp	Glu	Ala	Arg	Leu	Arg	Glu	Ala	Ala	Met	Leu	
			210			215				220						
atc	tgc	gag	atc	aac	ctc	ggc	gcc	acc	gcc	att	ggc	acc	ggc	att	acc	720
Ile	Cys	Glu	Ile	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Thr	
225					230				235						240	
gcg	cac	cca	tcc	tat	gcg	ccg	gtg	gtg	ctg	cgg	cgg	ctg	cgc	gac	atc	768
Ala	His	Pro	Ser	Tyr	Ala	Pro	Val	Val	Leu	Arg	Arg	Leu	Arg	Asp	Ile	
			245						250					255		
act	ggc	att	ccg	ctt	gag	aca	gcg	cca	aac	ctg	atc	gaa	gct	acg	cag	816
Thr	Gly	Ile	Pro	Leu	Glu	Thr	Ala	Pro	Asn	Leu	Ile	Glu	Ala	Thr	Gln	
			260				265					270				
gat	tgc	ggc	gcc	ttc	gtg	caa	ctg	tcc	ggc	gtg	cta	aaa	cgc	gtt	gcg	864
Asp	Cys	Gly	Ala	Phe	Val	Gln	Leu	Ser	Gly	Val	Leu	Lys	Arg	Val	Ala	
			275				280					285				
gtg	aag	ctt	tca	aag	acc	tgc	aac	gac	ctg	cgg	ctg	ttg	tcg	agc	ggc	912
Val	Lys	Leu	Ser	Lys	Thr	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	
			290			295				300						
ccg	cgt	gcg	ggg	ctg	tgc	gaa	atc	aac	ctg	ccg	ccg	atg	cag	gcc	ggc	960
Pro	Arg	Ala	Gly	Leu	Cys	Glu	Ile	Asn	Leu	Pro	Pro	Met	Gln	Ala	Gly	
305					310				315						320	
tcc	agc	atc	atg	ccc	ggc	aag	gtg	aat	ccg	gtg	atc	ccc	gaa	gtc	gtg	1008
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	
			325						330					335		
aac	cag	att	gcc	ttc	gag	gtc	atc	ggc	aac	gac	gtg	acg	gtc	agc	ttc	1056
Asn	Gln	Ile	Ala	Phe	Glu	Val	Ile	Gly	Asn	Asp	Val	Thr	Val	Ser	Phe	
			340				345					350				
gca	gcc	gaa	gcc	ggc	cag	ctg	cag	ctc	aat	gcg	ttc	gag	ccg	atc	att	1104
Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Ala	Phe	Glu	Pro	Ile	Ile	
			355				360					365				
gcc	cac	agc	ctg	ttc	aag	agc	gtc	agc	cat	ctg	cgc	aac	ggc	tgc	ctg	1152
Ala	His	Ser	Leu	Phe	Lys	Ser	Val	Ser	His	Leu	Arg	Asn	Gly	Cys	Leu	
			370			375				380						
acg	ctc	gcc	gag	cgt	tgc	gtc	aag	ggc	atc	acg	gca	aat	gca	gat	cgg	1200
Thr	Leu	Ala	Glu	Arg	Cys	Val	Lys	Gly	Ile	Thr	Ala	Asn	Ala	Asp	Arg	
385					390				395					400		
ctg	cgg	gct	acc	gtc	gag	aac	tcg	atc	ggg	atc	gtc	acg	gcg	ctc	aac	1248
Leu	Arg	Ala	Thr	Val	Glu	Asn	Ser	Ile	Gly	Ile	Val	Thr	Ala	Leu	Asn	
			405						410					415		
cct	tac	atc	ggc	tat	gcg	aac	gca	aca	gcc	gtc	gcg	cag	gaa	gcc	cac	1296
Pro	Tyr	Ile	Gly	Tyr	Ala	Asn	Ala	Thr	Ala	Val	Ala	Gln	Glu	Ala	His	
			420				425					430				
gcc	acc	ggc	ggc	agc	gtc	tat	gag	atc	gtg	ctg	cgc	aag	ggc	ctg	ttg	1344
Ala	Thr	Gly	Gly	Ser	Val	Tyr	Glu	Ile	Val	Leu	Arg	Lys	Gly	Leu	Leu	
			435			440						445				
tcg	aaa	gag	gag	ctt	gac	cac	atc	ctg	cgg	ccc	gag	acg	ctg	aca	cag	1392
Ser	Lys	Glu	Glu	Leu	Asp	His	Ile	Leu	Arg	Pro	Glu	Thr	Leu	Thr	Gln	
	450					455					460					

ccc gtg ccg ctc gat ctg cat ggg aag tcg cac tga
 Pro Val Pro Leu Asp Leu His Gly Lys Ser His
 465 470 475

<210> 9694

<211> 475

<212> PRT

<213> Ralstonia eutropha JMP134

<400> 9694

Met Thr Ala Gly Pro Phe Arg Thr Glu His Asp Leu Leu Gly Asp Arg
 1 5 10 15
 Glu Val Pro Ala Gln Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Val
 20 25 30
 Glu Asn Phe Pro Ile Thr Gly Thr Pro Ile Ser Ile Tyr Pro Glu Leu
 35 40 45
 Ile Lys Ala Leu Ala Ala Ile Lys Gln Ala Ala Ala Gln Ala Asn His
 50 55 60
 Glu Leu Glu Leu Leu Asp Gln Ala Arg Cys Asp Ala Ile Val Ala Ala
 65 70 75 80
 Cys Gln Glu Leu Met Ala Gly Lys Leu His Asp Gln Phe Val Val Asp
 85 90 95
 Val Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu
 100 105 110
 Val Ile Ala Asn Arg Ala Leu Glu Leu Leu Gly His Gln Lys Gly Glu
 115 120 125
 Tyr Gln His Leu His Pro Asn Glu His Val Asn Ile Gly Gln Ser Thr
 130 135 140
 Asn Asp Val Tyr Pro Thr Ala Leu Lys Val Ala Thr Trp Phe Gly Ile
 145 150 155 160
 Arg Gly Leu Val Glu Ala Met Ala Val Leu Arg Gln Ala Phe Glu Ala
 165 170 175
 Lys Ala Glu Glu Phe Ala His Ile Ile Lys Met Gly Arg Thr Gln Leu
 180 185 190
 Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Ser Thr Tyr Ala
 195 200 205 210
 Val Met Leu Gly Glu Asp Glu Ala Arg Leu Arg Glu Ala Ala Met Leu
 215 220 225
 Ile Cys Glu Ile Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Ile Thr
 230 235 240
 Ala His Pro Ser Tyr Ala Pro Val Val Leu Arg Arg Leu Arg Asp Ile
 245 250 255
 Thr Gly Ile Pro Leu Glu Thr Ala Pro Asn Leu Ile Glu Ala Thr Gln
 260 265 270
 Asp Cys Gly Ala Phe Val Gln Leu Ser Gly Val Leu Lys Arg Val Ala
 275 280 285
 Val Lys Leu Ser Lys Thr Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly
 290 295 300
 Pro Arg Ala Gly Leu Cys Glu Ile Asn Leu Pro Met Gln Ala Gly
 305 310 315 320
 Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Val
 325 330 335
 Asn Gln Ile Ala Phe Glu Val Ile Gly Asn Asp Val Thr Val Ser Phe
 340 345 350
 Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Ala Phe Glu Pro Ile Ile
 355 360 365
 Ala His Ser Leu Phe Lys Ser Val Ser His Leu Arg Asn Gly Cys Leu
 370 375 380
 Thr Leu Ala Glu Arg Cys Val Lys Gly Ile Thr Ala Asn Ala Asp Arg
 385 390 395 400
 Leu Arg Ala Thr Val Glu Asn Ser Ile Gly Ile Val Thr Ala Leu Asn
 405 410 415
 Pro Tyr Ile Gly Tyr Ala Asn Ala Thr Ala Val Ala Gln Glu Ala His
 420 425 430
 Ala Thr Gly Gly Ser Val Tyr Glu Ile Val Leu Arg Lys Gly Leu Leu
 435 440 445
 Ser Lys Glu Glu Leu Asp His Ile Leu Arg Pro Glu Thr Leu Thr Gln
 450 455 460
 Pro Val Pro Leu Asp Leu His Gly Lys Ser His

465

470

475

<210> 9695
 <211> 1401
 <212> DNA
 <213> *Thiobacillus denitrificans* ATCC 25259

<220>
 <221> CDS
 <222> (1)..(1401)
 <223> transl_table=11

<400> 9695
 atg aat gaa ttc cgc acc gag aag gac tcg ctc ggc gaa gtc cgg gtt 48
 Met Asn Glu Phe Arg Thr Glu Lys Asp Ser Leu Gly Glu Val Arg Val
 1 5 10 15
 ccc cga gac gcg tgg tac ggc gcc cag acc gca cgg gcc gtg agc aat 96
 Pro Arg Asp Ala Trp Tyr Gly Ala Gln Thr Ala Arg Ala Val Ser Asn
 20 25 30
 ttt ccc att tcg ggc cgc gcg ccg gat aag gat ttc gta cta gcg cac 144
 Phe Pro Ile Ser Gly Arg Ala Pro Asp Lys Asp Phe Val Leu Ala His
 35 40 45
 gtg cgt ata aag ctc gca gcg gca cgc gcg aat tgc cag cca ggg tgg 192
 Val Arg Ile Lys Leu Ala Ala Ala Arg Ala Asn Cys Gln Pro Gly Trp
 50 55 60
 ctg ccg gaa ctc aag cgc gac gca atc gtc gcg gcc tgc gag cag atc 240
 Leu Pro Glu Leu Lys Arg Asp Ala Ile Val Ala Ala Cys Glu Gln Ile
 65 70 75 80
 ctc gcg ggc gcg cac ctc gac cag ttc gtc gtt gac cgc ttc cag gcg 288
 Leu Ala Gly Ala His Leu Asp Gln Phe Val Val Asp Arg Phe Gln Ala
 85 90 95
 ggt gcg ggc acg agc cac aac atg aac agc aac gag gtc atc gcg aac 336
 Gly Ala Gly Thr Ser His Asn Met Asn Ser Asn Glu Val Ile Ala Asn
 100 105 110
 ctt gcc aac gtc gcg ctc ggc ggc gaa aag ggc cgc tac tcg ccg gtc 384
 Leu Ala Asn Val Ala Leu Gly Gly Glu Lys Gly Arg Tyr Ser Pro Val
 115 120 125
 aac ccg aac gac gac gtc aac atg ggg cag tcg acc aac gac acg atc 432
 Asn Pro Asn Asp Asp Val Asn Met Gly Gln Ser Thr Asn Asp Thr Ile
 130 135 140
 ccg acc gcg ata cgt ctc gca gtg ttg gcg aag ctg ccc cgc ctg gtc 480
 Pro Thr Ala Ile Arg Leu Ala Val Leu Ala Lys Leu Pro Arg Leu Val
 145 150 155 160
 gcc gcc gtg cgc ggc atg gcc ggt gaa ttt tcg cgg ctg gcc gag cgc 528
 Ala Ala Val Arg Met Ala Gly Glu Phe Ser Arg Leu Ala Glu Arg
 165 170 175
 gaa aag gac acg gtg aaa tcg ggc cgg acg cat ttg cag gat gcc gtg 576
 Glu Lys Asp Thr Val Lys Ser Gly Arg Thr His Leu Gln Asp Ala Val
 180 185 190
 ccg acg acg ctc ggc cag gaa ttc gac ggc tac gcg tgg acg ctg gcg 624
 Pro Thr Thr Leu Gly Gln Glu Phe Asp Gly Tyr Ala Trp Thr Leu Ala
 195 200 205
 cgt tgt gcg gcg gcg ctc gaa gcc gtg cgc ccg gcc ctg tgc gaa atc 672
 Arg Cys Ala Ala Ala Leu Glu Ala Val Arg Pro Ala Leu Cys Glu Ile
 210 215 220
 ggc ctc ggc ggc tcg gcg gcc ggg acg gga ctg aac acc tcg ccc gat 720
 Gly Leu Gly Gly Ser Ala Ala Gly Thr Gly Leu Asn Thr Ser Pro Asp
 225 230 235 240
 tat ccg gac cgc gtc gcg gcg gaa ctc gcc gcg ctg acc ggc gaa tcg 768
 Tyr Pro Asp Arg Val Ala Ala Glu Leu Ala Leu Thr Gly Glu Ser
 245 250 255
 att cgc gcc ggc caa ctc gtc gcg cag atg cag tcg atg aac gac ctt 816
 Ile Arg Ala Gly Gln Leu Val Ala Gln Met Gln Ser Met Asn Asp Leu
 260 265 270
 gcg cgg ctg tcc ggc gaa atc cgc aat ctc gcg ctc gaa ctc acg cgc 864
 Ala Arg Leu Ser Gly Glu Ile Arg Asn Leu Ala Leu Glu Leu Thr Arg
 275 280 285
 att tcc aac gac ctg gcg ctg ctt gcc tcg ggg ccg cgt acc ggc ctc 912
 Ile Ser Asn Asp Leu Arg Leu Leu Ala Ser Gly Pro Arg Thr Gly Leu

PF59083SeqList PF59083.txt

290	295	300	
ggc gaa atc cag ctg ccg ccg gtg cag ccc ggc tcg tcg atc atg ccg			960
Gly Glu Ile Gln Leu Pro Pro Val Gln Pro Gly Ser Ser Ile Met Pro			
305	310	315	320
ggc aag gtc aac ccg gtc atg ttc gaa atg ctg aac cag gtc tgc ttc			1008
Gly Lys Val Asn Pro Val Met Phe Glu Met Leu Asn Gln Val Cys Phe			
	325	330	335
cag gtg ctc ggg cag gat gcg gcg gtc tcc tac atg gtg cag gca ggc			1056
Gln Val Leu Gly Gln Asp Ala Ala Val Ser Tyr Met Val Gln Ala Gly			
	340	345	350
cag ctc gag ctc aac gtg atg atg ccg gcg ctc ggt tcg gcg ctt ttc			1104
Gln Leu Glu Leu Asn Val Met Met Pro Ala Leu Gly Ser Ala Leu Phe			
	355	360	365
gac gcc atg gac tgg ctg acc aac gca atc gac gcc gcc acc gag aag			1152
Asp Ala Met Asp Trp Leu Thr Asn Ala Ile Asp Ala Ala Thr Glu Lys			
	370	375	380
aac ctc aag ggc atc gtc gcc aac cgg gag cgc tgt gcg ttt ttc atc			1200
Asn Leu Lys Gly Ile Val Ala Asn Arg Glu Arg Cys Ala Phe Phe Ile			
	385	390	400
cac cag agc gtc gcg ctc gcc acg ctc ctg aac acc gcg atc ggc tac			1248
His Gln Ser Val Ala Leu Ala Thr Leu Leu Asn Thr Arg Ile Gly Tyr			
	405	410	415
atg gag gcc gcc gag gtc gcc aag gaa tcc gaa aaa acc ggc cgc ccg			1296
Met Glu Ala Ala Glu Val Ala Lys Glu Ser Glu Lys Thr Gly Arg Pro			
	420	425	430
gtc cgc gac atc gtc gcg cag cgc gcg ctg atg gat gcc gcc gag ttc			1344
Val Arg Asp Ile Val Ala Gln Arg Ala Leu Met Asp Ala Ala Glu Phe			
	435	440	445
gac gcg ctc gtg ctc gcc gcg gcg cat ggc gtg ggt agc ggg ggc ggc			1392
Asp Ala Leu Val Leu Ala Ala His Gly Val Gly Ser Gly Gly Gly			
	450	455	460
ggc ggc tga			1401
Gly Gly			
465			

<210> 9696

<211> 466

<212> PRT

<213> Thiobacillus denitrificans ATCC 25259

<400> 9696

Met Asn Glu Phe Arg Thr Glu Lys Asp Ser Leu Gly Glu Val Arg Val	
1 5 10 15	
Pro Arg Asp Ala Trp Tyr Gly Ala Gln Thr Ala Arg Ala Val Ser Asn	
20 25 30	
Phe Pro Ile Ser Gly Arg Ala Pro Asp Lys Asp Phe Val Leu Ala His	
35 40 45	
Val Arg Ile Lys Leu Ala Ala Arg Ala Asn Cys Gln Pro Gly Trp	
50 55 60	
Leu Pro Glu Leu Lys Arg Asp Ala Ile Val Ala Cys Glu Gln Ile	
65 70 75 80	
Leu Ala Gly Ala His Leu Asp Gln Phe Val Val Asp Arg Phe Gln Ala	
85 90 95	
Gly Ala Gly Thr Ser His Asn Met Asn Ser Asn Glu Val Ile Ala Asn	
100 105 110	
Leu Ala Asn Val Ala Leu Gly Gly Glu Lys Gly Arg Tyr Ser Pro Val	
115 120 125	
Asn Pro Asn Asp Asp Val Asn Met Gly Gln Ser Thr Asn Asp Thr Ile	
130 135 140	
Pro Thr Ala Ile Arg Leu Ala Val Leu Ala Lys Leu Pro Arg Leu Val	
145 150 155 160	
Ala Ala Val Arg Gly Met Ala Gly Glu Phe Ser Arg Leu Ala Glu Arg	
165 170 175	
Glu Lys Asp Thr Val Lys Ser Gly Arg Thr His Leu Gln Asp Ala Val	
180 185 190	
Pro Thr Thr Leu Gly Gln Glu Phe Asp Gly Tyr Ala Trp Thr Leu Ala	
195 200 205	
Arg Cys Ala Ala Ala Leu Glu Ala Val Arg Pro Ala Leu Cys Glu Ile	
210 215 220	

PF59083SeqList PF59083.txt

Gly Leu Gly Gly Ser Ala Ala Gly Thr Gly Leu Asn Thr Ser Pro Asp
 225 230 235 240
 Tyr Pro Asp Arg Val Ala Ala Glu Leu Ala Ala Leu Thr Gly Glu Ser
 245 250 255
 Ile Arg Ala Gly Gln Leu Val Ala Gln Met Gln Ser Met Asn Asp Leu
 260 265 270
 Ala Arg Leu Ser Gly Glu Ile Arg Asn Leu Ala Leu Glu Leu Thr Arg
 275 280 285
 Ile Ser Asn Asp Leu Arg Leu Leu Ala Ser Gly Pro Arg Thr Gly Leu
 290 295 300
 Gly Glu Ile Gln Leu Pro Val Gln Pro Gly Ser Ser Ile Met Pro
 305 310 315 320
 Gly Lys Val Asn Pro Val Met Phe Glu Met Leu Asn Gln Val Cys Phe
 325 330 335
 Gln Val Leu Gly Gln Asp Ala Ala Val Ser Tyr Met Val Gln Ala Gly
 340 345 350
 Gln Leu Glu Leu Asn Val Met Met Pro Ala Leu Gly Ser Ala Leu Phe
 355 360 365
 Asp Ala Met Asp Trp Leu Thr Asn Ala Ile Asp Ala Ala Thr Glu Lys
 370 375 380
 Asn Leu Lys Gly Ile Val Ala Asn Arg Glu Arg Cys Ala Phe Phe Ile
 385 390 395 400
 His Gln Ser Val Ala Leu Ala Thr Leu Leu Asn Thr Arg Ile Gly Tyr
 405 410 415
 Met Glu Ala Ala Glu Val Ala Lys Glu Ser Glu Lys Thr Gly Arg Pro
 420 425 430
 Val Arg Asp Ile Val Ala Gln Arg Ala Leu Met Asp Ala Ala Glu Phe
 435 440 445
 Asp Ala Leu Val Leu Ala Ala Ala His Gly Val Gly Ser Gly Gly Gly
 450 455 460
 Gly Gly
 465

<210> 9697

<211> 1416

<212> DNA

<213> Anabaena variabilis ATCC 29413

<220>

<221> CDS

<222> (1)..(1416)

<223> transl_table=11

<400> 9697

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

PF59083SeqList PF59083.txt

Lys	Arg	Val	Ser	Pro	Asn	Asp	His	Val	Asn	Tyr	Gly	Gln	Ser	Thr	Asn	
130						135					140					
gat	gtt	att	cct	act	gca	att	cgc	atc	ggc	ggc	tta	ttg	gca	ctg	acc	480
Asp	Val	Ile	Pro	Thr	Ala	Ile	Arg	Ile	Gly	Gly	Leu	Leu	Ala	Leu	Thr	
145					150				155						160	
aaa	aca	tta	cag	cca	gca	tta	gaa	aaa	gcg	atc	gct	gct	tta	gaa	cac	528
Lys	Thr	Leu	Gln	Pro	Ala	Leu	Glu	Lys	Ala	Ile	Ala	Ala	Leu	Glu	His	
				165					170					175		
aaa	gct	gta	gaa	ttt	caa	gat	att	gtc	aaa	tcc	ggc	aga	acc	cat	tta	576
Lys	Ala	Val		Phe	Gln	Asp	Ile	Val	Lys	Ser	Gly	Arg	Thr	His	Leu	
			180					185					190			
cag	gat	gcc	gtt	ccc	gtc	cgc	ttg	ggg	gat	aat	ttc	gcc	gct	tggt	gcg	624
Gln	Asp	Ala	Val	Pro	Val	Arg	Leu	Gly	Asp	Asn	Phe	Ala	Ala	Trp	Ala	
		195					200				205					
cat	atc	ctc	tca	gaa	cat	caa	aac	cgc	att	tac	acc	gcc	tct	gga	gac	672
His	Ile	Leu	Ser	Glu	His	Gln	Asn	Arg	Ile	Tyr	Thr	Ala	Ser	Gly	Asp	
		210				215					220					
ttg	atg	gta	ctc	ggg	tta	ggg	agg	gcg	gcg	gga	aca	ggc	tta	aac		720
Leu	Met	Val	Leu	Gly	Leu	Gly	Gly	Ser	Ala	Ala	Gly	Thr	Gly	Leu	Asn	
225					230					235				240		
acc	cat	ccc	caa	tac	cgc	gcc	cgt	gtg	gtt	gaa	gta	ttg	gca	gaa	cta	768
Thr	His	Pro	Gln	Tyr	Arg	Ala	Arg	Val	Val	Glu	Val	Leu	Ala	Glu	Leu	
				245				250						255		
ctc	aac	tta	cca	ctc	caa	ccc	gca	ccc	cat	ctc	atg	gct	gct	atg	cag	816
Leu	Asn	Leu	Pro	Leu	Gln	Pro	Ala	Pro	His	Leu	Met	Ala	Ala	Met	Gln	
			260				265						270			
agt	atg	tcc	cca	ttt	gtg	aac	gtt	tcc	ggg	gca	ata	cgc	aac	cta	gcc	864
Ser	Met	Ser	Pro	Phe	Val	Asn	Val	Ser	Gly	Ala	Ile	Arg	Asn	Leu	Ala	
		275				280						285				
cag	gat	tta	gca	aaa	atc	tct	cac	gat	tta	cgg	ctg	atg	gac	tcc	ggg	912
Gln	Asp	Leu	Ala	Lys	Ile	Ser	His	Asp	Leu	Arg	Leu	Met	Asp	Ser	Gly	
		290				295					300					
cca	aaa	act	ggc	ttg	aaa	gaa	att	caa	tta	ccc	cca	gta	caa	ccc	ggg	960
Pro	Lys	Thr	Gly	Leu	Lys	Glu	Ile	Gln	Leu	Pro	Pro	Val	Gln	Pro	Gly	
305					310					315					320	
tcc	tca	atc	atg	cca	ggc	aaa	tat	aac	ccc	gtc	atg	gca	gag	atg	aca	1008
Ser	Ser	Ile	Met	Pro	Gly	Lys	Tyr	Asn	Pro	Val	Met	Ala	Glu	Met	Thr	
				325				330						335		
tcg	atg	gtg	tgt	ttc	cag	gtg	atg	ggg	tac	gat	cag	gcg	atc	gct	ctt	1056
Ser	Met	Val	Cys	Phe	Gln	Val	Met	Gly	Tyr	Asp	Gln	Ala	Ile	Ala	Leu	
			340					345					350			
gca	gcc	caa	gcc	gga	caa	tta	gaa	tta	aac	gtg	atg	atg	ccg	ttg	att	1104
Ala	Ala	Gln	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Met	Pro	Leu	Ile	
		355				360						365				
gcc	tat	gat	tta	att	cac	agc	atc	gaa	att	ctg	ggg	tca	act	atc	gcc	1152
Ala	Tyr	Asp	Leu	Ile	His	Ser	Ile	Glu	Ile	Leu	Gly	Ser	Thr	Ile	Ala	
		370				375					380					
gcc	ctc	aca	gaa	cgc	tgt	att	caa	gga	att	acc	gcc	aac	aaa	gaa	cgg	1200
Ala	Leu	Thr	Glu	Arg	Cys	Ile	Gln	Gly	Ile	Thr	Ala	Asn	Lys	Glu	Arg	
385					390					395					400	
tgt	tta	gcc	tac	gcc	gaa	ggc	agt	tta	gct	tta	gtt	act	gcc	ctc	aac	1248
Cys	Leu	Ala	Tyr	Ala	Glu	Gly	Ser	Leu	Ala	Leu	Val	Thr	Ala	Leu	Asn	
			405					410						415		
act	cat	att	ggg	tat	tta	aat	gcc	gca	gat	gtt	gcc	aaa	gaa	tct	tta	1296
Thr	His	Ile	Gly	Tyr	Leu	Asn	Ala	Ala	Asp	Val	Ala	Lys	Glu	Ser	Leu	
			420				425						430			
aac	aca	gga	aaa	tct	cta	cgg	cag	att	gtg	tta	gaa	aaa	gga	ctg	atg	1344
Asn	Thr	Gly	Lys	Ser	Leu	Arg	Gln	Ile	Val	Leu	Glu	Lys	Gly	Leu	Met	
		435				440						445				
agc	gaa	gca	gag	tta	gcc	act	gtg	cta	aat	cta	gaa	gaa	atg	agt	agt	1392
Ser	Glu	Ala	Glu	Leu	Ala	Thr	Val	Leu	Asn	Leu	Glu	Glu	Met	Ser	Ser	
		450				455					460					
ata	ttg	cca	ctc	cag	gca	gag	taa									1416
Ile	Leu	Pro	Leu	Gln	Ala	Glu										
465					470											

<210> 9698

<211> 471

<212> PRT

<213> *Anabaena variabilis* ATCC 29413

<400> 9698

```

Met Thr Thr Asn Thr Asp Phe Arg Ile Glu Arg Asp Ser Met Gly Asp
1      5      10      15
Arg Gln Ile Ala Ser Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg Ala
      20      25      30
Ile Glu Asn Phe Pro Ile Ser Gly Leu Lys Pro Leu Pro Thr Tyr Val
      35      40      45
Asp Ala Gly Leu Leu Ile Lys Lys Ala Thr Ala Ile Val Asn Gly Glu
      50      55      60
Leu Gly Cys Ile Pro Gln Asp Ile Ser Gln Ala Ile Val Gln Ala Thr
65      70      75      80
Asp Glu Ile Leu Ala Gly Lys Leu Arg Asp Gln Phe Val Val Asp Val
      85      90      95
Tyr Gln Ala Gly Ala Gly Thr Ser His His Met Asn Ile Asn Glu Val
      100      105      110
Leu Ala Asn Arg Ala Leu Glu Ile Leu Gly Glu Glu Lys Gly Asn Tyr
      115      120      125
Lys Arg Val Ser Pro Asn Asp His Val Asn Tyr Gly Gln Ser Thr Asn
130      135      140
Asp Val Ile Pro Thr Ala Ile Arg Ile Gly Gly Leu Leu Ala Leu Thr
145      150      155      160
Lys Thr Leu Gln Pro Ala Leu Glu Lys Ala Ile Ala Ala Leu Glu His
      165      170      175
Lys Ala Val Glu Phe Gln Asp Ile Val Lys Ser Gly Arg Thr His Leu
      180      185      190
Gln Asp Ala Val Pro Val Arg Leu Gly Asp Asn Phe Ala Ala Trp Ala
      195      200      205
His Ile Leu Ser Glu His Gln Asn Arg Ile Tyr Thr Ala Ser Gly Asp
210      215      220
Leu Met Val Leu Gly Leu Gly Gly Ser Ala Ala Gly Thr Gly Leu Asn
225      230      235      240
Thr His Pro Gln Tyr Arg Ala Arg Val Val Glu Val Leu Ala Glu Leu
      245      250      255
Leu Asn Leu Pro Leu Gln Pro Ala Pro His Leu Met Ala Ala Met Gln
      260      265      270
Ser Met Ser Pro Phe Val Asn Val Ser Gly Ala Ile Arg Asn Leu Ala
      275      280      285
Gln Asp Leu Ala Lys Ile Ser His Asp Leu Arg Leu Met Asp Ser Gly
290      295      300
Pro Lys Thr Gly Leu Lys Glu Ile Gln Leu Pro Pro Val Gln Pro Gly
305      310      315      320
Ser Ser Ile Met Pro Gly Lys Tyr Asn Pro Val Met Ala Glu Met Thr
      325      330      335
Ser Met Val Cys Phe Gln Val Met Gly Tyr Asp Gln Ala Ile Ala Leu
      340      345      350
Ala Ala Gln Ala Gly Gln Leu Glu Leu Asn Val Met Met Pro Leu Ile
      355      360      365
Ala Tyr Asp Leu Ile His Ser Ile Glu Ile Leu Gly Ser Thr Ile Ala
370      375      380
Ala Leu Thr Glu Arg Cys Ile Gln Gly Ile Thr Ala Asn Lys Glu Arg
385      390      395      400
Cys Leu Ala Tyr Ala Glu Gly Ser Leu Ala Leu Val Thr Ala Leu Asn
      405      410      415
Thr His Ile Gly Tyr Leu Asn Ala Ala Asp Val Ala Lys Glu Ser Leu
      420      425      430
Asn Thr Gly Lys Ser Leu Arg Gln Ile Val Leu Glu Lys Gly Leu Met
435      440      445
Ser Glu Ala Glu Leu Ala Thr Val Leu Asn Leu Glu Met Ser Ser
450      455      460
Ile Leu Pro Leu Gln Ala Glu
465      470

```

<210> 9699

<211> 1425

<212> DNA

<213> *Desulfovibrio desulfuricans* G20

PF59083SeqList PF59083.txt

<220>
 <221> CDS
 <222> (1)..(1425)
 <223> transl_table=11

<400> 9699

atg acc tac cgt acg gaa cat gac agt ctt ggc gaa cgc aag gtt ccc	48
Met Thr Tyr Arg Thr Glu His Asp Ser Leu Gly Glu Arg Lys Val Pro	
1 5 10 15	
gca cag gct tac tac ggc att cag aca ctg agg gct ctg gag aat ttt	96
Ala Gln Ala Tyr Tyr Gly Ile Gln Thr Leu Arg Ala Leu Glu Asn Phe	
20 25 30	
gaa atc aca act att cct gtt tcg cat tac agc agg ttc ata cag gcg	144
Glu Ile Thr Thr Ile Pro Val Ser His Tyr Ser Arg Phe Ile Gln Ala	
35 40 45	
ctg gct gtg gtt aaa aaa gct gcg gcc atg gcc aat atg gag ttg gga	192
Leu Ala Val Val Lys Lys Ala Ala Ala Met Ala Asn Met Glu Leu Gly	
50 55 60	
gaa ctc gat tcc gcc gtc ggc gaa gct att atc cat gcc tgc aaa gac	240
Glu Leu Asp Ser Ala Val Gly Glu Ala Ile Ile His Ala Cys Lys Asp	
65 70 75 80	
gtg cgg cag ggc aag ctg gat gac cag ttt gta gtg gat gtc att cag	288
Val Arg Gln Gly Lys Leu Asp Asp Gln Phe Val Val Asp Val Ile Gln	
85 90 95	
ggc ggg gcg gga acg tcg gta aac atg aac gcc aat gaa gtg atc tgc	336
Gly Gly Ala Gly Thr Ser Val Asn Met Asn Ala Asn Glu Val Ile Cys	
100 105 110	
aac agg gct ctt gag ctg agc ggg cat gaa aaa ggg agg tat gac att	384
Asn Arg Ala Leu Glu Leu Ser Gly His Glu Lys Gly Arg Tyr Asp Ile	
115 120 125	
atc cat ccg ctc aat cat gtg aat ctt tcg cag tcc acc aat gat gtt	432
Ile His Pro Leu Asn His Val Asn Leu Ser Gln Ser Thr Asn Asp Val	
130 135 140	
tac ccc acg gct ttg cgc ata gcg ctt gtg tgg tac agc cgc gaa ctg	480
Tyr Pro Thr Ala Leu Arg Ile Ala Leu Val Trp Tyr Ser Arg Glu Leu	
145 150 155 160	
ctg cac ggg ctg cgc gaa ctg cgc gac gct ttg agc cgc aaa ggt gca	528
Leu His Gly Leu Arg Glu Leu Arg Asp Ala Leu Ser Arg Lys Gly Ala	
165 170 175	
gaa ttc ggc aat gtc att aaa atg gcc cgc aca cag ctg cag gat gcc	576
Glu Phe Gly Asn Val Ile Lys Met Ala Arg Thr Gln Leu Gln Asp Ala	
180 185 190	
gtt ccc atc acg ctc gga gcc gag ttt gcg gca tat gct gtt acc gtc	624
Val Pro Ile Thr Leu Gly Ala Glu Phe Ala Ala Tyr Ala Val Thr Val	
195 200 205	
aat gaa gac att gac cgt ctg gaa gag gtg atg cgc ctg ctt tgc gaa	672
Asn Glu Asp Ile Asp Arg Leu Glu Glu Val Met Arg Leu Leu Cys Glu	
210 215 220	
gtc aat ctg ggg gct acg gca gtg gga aca ggc atc aat tcc gtt ccg	720
Val Asn Leu Gly Ala Thr Ala Val Gly Thr Gly Ile Asn Ser Val Pro	
225 230 235 240	
ggc tac gga gcc cgc gcc tgc gcc att ctg gct gat gtg aca ggc ctg	768
Gly Tyr Gly Ala Arg Ala Cys Ala Ile Leu Ala Asp Val Thr Gly Leu	
245 250 255	
ccc ata tct cag tcg gcg aat ctg gta gaa gca acc agc gat gcc ggc	816
Pro Ile Ser Gln Ser Ala Asn Leu Val Glu Ala Thr Ser Asp Ala Gly	
260 265 270	
gca tat gtg act ctt tca gga ctg ctg aaa cgc acc agt gtg aaa ctt	864
Ala Tyr Val Thr Leu Ser Gly Leu Leu Lys Arg Thr Ser Val Lys Leu	
275 280 285	
tca aag ata tgt aat gat ctc aga ttg atg tct tca ggg ccg ttt acc	912
Ser Lys Ile Cys Asn Asp Leu Arg Leu Met Ser Ser Gly Pro Phe Thr	
290 295 300	
ggc ctg cac gaa atc aat ctg ccg ccg gtg cag ccc gga tca tcc ata	960
Gly Leu His Glu Ile Asn Leu Pro Pro Val Gln Pro Gly Ser Ser Ile	
305 310 315 320	
atg ccg ggc aag gtc aac cct gtc att cct gaa gtg gtc acc cag ata	1008
Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Val Thr Gln Ile	
325 330 335	

PF59083SeqList PF59083.txt

tgc	tac	cag	att	atc	ggc	aat	gac	atg	aca	gtg	acc	atg	gct	gcg	gag	1056
Cys	Tyr	Gln	Ile	Ile	Gly	Asn	Asp	Met	Thr	Val	Thr	Met	Ala	Ala	Glu	
		340						345					350			
gca	ggg	cag	ctt	gag	ctt	aat	gtt	ttc	gga	ccc	att	atc	gca	ttt	aat	1104
Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Phe	Gly	Pro	Ile	Ile	Ala	Phe	Asn	
		355						360					365			
ctg	ttt	cag	tca	ctg	gaa	att	ctg	acc	aga	ggg	gtg	cac	acc	ctg	aga	1152
Leu	Phe	Gln	Ser	Leu	Glu	Ile	Leu	Thr	Arg	Gly	Val	His	Thr	Leu	Arg	
	370					375					380					
aag	cgg	tgc	atc	gag	ggc	ata	acc	gct	aat	gat	gag	cgt	tgt	ctt	gaa	1200
Lys	Arg	Cys	Ile	Glu	Gly	Ile	Thr	Ala	Asn	Asp	Glu	Arg	Cys	Leu	Glu	
385					390					395					400	
ttg	ctc	aaa	ggg	tct	ctg	ggg	gtg	gtg	acg	gct	tta	gct	ccc	gcc	ata	1248
Leu	Leu	Lys	Gly	Ser	Leu	Gly	Val	Val	Thr	Ala	Leu	Ala	Pro	Ala	Ile	
				405					410					415		
gga	tat	gag	gcg	gct	gca	aaa	gtg	gtc	aaa	cag	gca	cag	gaa	acg	cg	1296
Gly	Tyr	Glu	Ala	Ala	Ala	Lys	Val	Val	Lys	Gln	Ala	Gln	Glu	Thr	Arg	
		420						425					430			
aag	cct	gtg	gga	cag	gtg	ctt	gac	gag	cag	ggg	ctt	atg	acc	gcc	gaa	1344
Lys	Pro	Val	Gly	Gln	Val	Leu	Asp	Glu	Gln	Gly	Leu	Met	Thr	Ala	Glu	
		435					440						445			
gag	tat	aac	gag	ctg	ctg	gat	ccg	agc	aag	atg	ctt	gct	ccg	aga	aag	1392
Glu	Tyr	Asn	Glu	Leu	Leu	Asp	Pro	Ser	Lys	Met	Leu	Ala	Pro	Arg	Lys	
	450					455					460					
ttg	ccg	aac	cgt	aaa	gcg	gca	gag	gat	aaa	tga						1425
Leu	Pro	Asn	Arg	Lys	Ala	Ala	Glu	Asp	Lys							
465					470											

<210> 9700

<211> 474

<212> PRT

<213> Desulfovibrio desulfuricans G20

<400> 9700

Met	Thr	Tyr	Arg	Thr	Glu	His	Asp	Ser	Leu	Gly	Glu	Arg	Lys	Val	Pro	
1				5					10					15		
Ala	Gln	Ala	Tyr	Tyr	Gly	Ile	Gln	Thr	Leu	Arg	Ala	Leu	Glu	Asn	Phe	
			20					25					30			
Glu	Ile	Thr	Thr	Ile	Pro	Val	Ser	His	Tyr	Ser	Arg	Phe	Ile	Gln	Ala	
		35					40					45				
Leu	Ala	Val	Val	Lys	Lys	Ala	Ala	Ala	Met	Ala	Asn	Met	Glu	Leu	Gly	
	50					55					60					
Glu	Leu	Asp	Ser	Ala	Val	Gly	Glu	Ala	Ile	Ile	His	Ala	Cys	Lys	Asp	
65					70				75					80		
Val	Arg	Gln	Gly	Lys	Leu	Asp	Asp	Gln	Phe	Val	Val	Asp	Val	Ile	Gln	
			85					90						95		
Gly	Gly	Ala	Gly	Thr	Ser	Val	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Cys	
		100					105						110			
Asn	Arg	Ala	Leu	Glu	Leu	Ser	Gly	His	Glu	Lys	Gly	Arg	Tyr	Asp	Ile	
		115					120						125			
Ile	His	Pro	Leu	Asn	His	Val	Asn	Leu	Ser	Gln	Ser	Thr	Asn	Asp	Val	
	130					135					140					
Tyr	Pro	Thr	Ala	Leu	Arg	Ile	Ala	Leu	Val	Trp	Tyr	Ser	Arg	Glu	Leu	
145					150					155				160		
Leu	His	Gly	Leu	Arg	Glu	Leu	Arg	Asp	Ala	Leu	Ser	Arg	Lys	Gly	Ala	
			165						170					175		
Glu	Phe	Gly	Asn	Val	Ile	Lys	Met	Ala	Arg	Thr	Gln	Leu	Gln	Asp	Ala	
		180						185					190			
Val	Pro	Ile	Thr	Leu	Gly	Ala	Glu	Phe	Ala	Ala	Tyr	Ala	Val	Thr	Val	
		195					200					205				
Asn	Glu	Asp	Ile	Asp	Arg	Leu	Glu	Glu	Val	Met	Arg	Leu	Leu	Cys	Glu	
	210					215					220					
Val	Asn	Leu	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Ser	Val	Pro	
225					230					235					240	
Gly	Tyr	Gly	Ala	Arg	Ala	Cys	Ala	Ile	Leu	Ala	Asp	Val	Thr	Gly	Leu	
			245						250					255		
Pro	Ile	Ser	Gln	Ser	Ala	Asn	Leu	Val	Glu	Ala	Thr	Ser	Asp	Ala	Gly	
		260						265					270			
Ala	Tyr	Val	Thr	Leu	Ser	Gly	Leu	Leu	Lys	Arg	Thr	Ser	Val	Lys	Leu	

PF59083SeqList PF59083.txt

```

      275      280      285
Ser Lys Ile Cys Asn Asp Leu Arg Leu Met Ser Ser Gly Pro Phe Thr
  290      295      300
Gly Leu His Glu Ile Asn Leu Pro Pro Val Gln Pro Gly Ser Ser Ile
  305      310      315
Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val Val Thr Gln Ile
      325      330      335
Cys Tyr Gln Ile Ile Gly Asn Asp Met Thr Val Thr Met Ala Ala Glu
      340      345      350
Ala Gly Gln Leu Glu Leu Asn Val Phe Gly Pro Ile Ile Ala Phe Asn
      355      360      365
Leu Phe Gln Ser Leu Glu Ile Leu Thr Arg Gly Val His Thr Leu Arg
      370      375      380
Lys Arg Cys Ile Glu Gly Ile Thr Ala Asn Asp Glu Arg Cys Leu Glu
  385      390      395
Leu Leu Lys Gly Ser Leu Gly Val Val Thr Ala Leu Ala Pro Ala Ile
      405      410      415
Gly Tyr Glu Ala Ala Ala Lys Val Val Lys Gln Ala Gln Glu Thr Arg
      420      425      430
Lys Pro Val Gly Gln Val Leu Asp Glu Gln Gly Leu Met Thr Ala Glu
      435      440      445
Glu Tyr Asn Glu Leu Leu Asp Pro Ser Lys Met Leu Ala Pro Arg Lys
      450      455      460
Leu Pro Asn Arg Lys Ala Ala Glu Asp Lys
  465      470

```

<210> 9701

<211> 1431

<212> DNA

<213> Moorella thermoacetica ATCC 39073

<220>

<221> CDS

<222> (1)..(1431)

<223> transl_table=11

<400> 9701

```

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

```

PF59083SeqList PF59083.txt

```

165      170      175
gcc ggg gtg gtc aaa atc ggt cgt acc gag ctc cag gac gcc gtg ccg      576
Ala Gly Val Val Lys Ile Gly Arg Thr Glu Leu Gln Asp Ala Val Pro
180      185      190
gta acc ctg ggg cag gaa ttc ggc gct tac gcc cag gcc att tcc cgg      624
Val Thr Leu Gly Gln Glu Phe Gly Ala Tyr Ala Gln Ala Ile Ser Arg
195      200      205
gac cgc tgg cgc ctc tat aaa gtt gaa gag cgc ctg cgc cag gta aac      672
Asp Arg Trp Arg Leu Tyr Lys Val Glu Glu Arg Leu Arg Gln Val Asn
210      215      220
ctg ggt ggc acc gcc acc ggc acc ggc ctt aac gcc ccc ctg aag tac      720
Leu Gly Gly Thr Ala Thr Gly Thr Gly Leu Asn Ala Pro Leu Lys Tyr
225      230      235
atc tac ctg gtc aac gac tac ctg cgc cgc ctt aca gga ata ggc ctg      768
Ile Tyr Leu Val Asn Asp Tyr Leu Arg Arg Leu Thr Gly Ile Gly Leu
240      245      250
gcc cgg gcg gag aat atg att gac gcc acc cag aat atg gac gtc ttt      816
Ala Arg Ala Glu Asn Met Ile Asp Ala Thr Gln Asn Met Asp Val Phe
255      260      265
gtg gag gtc tct ggt ctg gtc aag gct gcc gcc gtt acc atg cac aaa      864
Val Glu Val Ser Gly Leu Val Lys Ala Ala Ala Val Thr Met His Lys
270      275      280
ata gcc tcc gac ctg cgt ttt atg gcc gcc ggc ccc cgg ggc ggc ccg      912
Ile Ala Ser Asp Leu Arg Phe Met Ala Ala Gly Pro Arg Gly Gly Pro
285      290      295
gcg gag atc aat ttg ccg gaa cgc cag gcg gga tcc tcc atc atg ccc      960
Ala Glu Ile Asn Leu Pro Glu Arg Gln Ala Gly Ser Ser Ile Met Pro
300      305      310
ggc aaa gtc aat ccc gtc atc ccg gag atg gtc agc cag gta gcc atg      1008
Gly Lys Val Asn Pro Val Ile Pro Glu Met Val Ser Gln Val Ala Met
315      320      325
cag gtc atg gcc aat gat tac ttg atc gcc atg gct gcc agt cag ggc      1056
Gln Val Met Ala Asn Asp Tyr Leu Ile Ala Met Ala Ala Ser Gln Gly
330      335      340
cag ctg gag ctc aat ccc ttt gcc ccc ctt att gcc cat acc ttg ctg      1104
Gln Leu Glu Leu Asn Pro Phe Ala Pro Leu Ile Ala His Thr Leu Leu
345      350      355
gaa tcc ctg gcc atg ctg gcg gca gcg gcc cgg ata ttc cgc acc gag      1152
Glu Ser Leu Ala Met Leu Ala Ala Ala Ala Arg Ile Phe Arg Thr Glu
360      365      370
tgt atc acg ggt ata acc gcc aac ccc gag cgc tgc cag gaa ctc ctg      1200
Cys Ile Thr Gly Ile Thr Ala Asn Pro Glu Arg Cys Gln Glu Leu Leu
375      380      385
gcc gtg agc ccg gcc ctg gct acg gcc ctg ctg ccc tat att ggc tac      1248
Ala Val Ser Pro Ala Leu Ala Thr Ala Leu Pro Tyr Ile Gly Tyr
390      395      400
gag aag gcc acg gaa gta gtg cgg gaa gcc gtg gtt tcc ggc cga tca      1296
Glu Lys Ala Thr Glu Val Val Arg Glu Ala Val Val Ser Gly Arg Ser
405      410      415
ata aaa gaa ata gtt cta gaa gaa ggg tat ttg acc tct gac gaa ctg      1344
Ile Lys Glu Ile Val Leu Glu Glu Gly Tyr Leu Thr Ser Asp Glu Leu
420      425      430
gaa aac gtc tta acc ccg gcc gcc atg acc aaa ccg gga acc gtc gga      1392
Glu Asn Val Leu Thr Pro Ala Ala Met Thr Lys Pro Gly Thr Val Gly
435      440      445
gcc gta aag cag gga ata aag gag aag gga aaa gcg taa      1431
Ala Val Lys Gln Gly Ile Lys Glu Lys Gly Lys Ala
450      455      460
465      470      475

```

<210> 9702

<211> 476

<212> PRT

<213> Moorella thermoacetica ATCC 39073

<400> 9702

```

Met Ser Thr Arg Gln Glu His Asp Leu Leu Gly Thr Arg Glu Val Pro
1      5      10      15
Ala Thr Ala Tyr Gly Ile His Thr Leu Arg Ala Ala Glu Asn Phe
20      25      30

```

PF59083SeqList PF59083.txt

```

Asn Val Ser Arg Ala Arg Val His Pro Glu Leu Ile Lys Ala Leu Ala
    35      40      45
Thr Val Lys Glu Ala Ala Ala Arg Ala Asn Leu Asp Leu Gly Tyr Leu
    50      55      60
Pro Ala Glu Lys Gly Arg Ala Ile Ile Thr Ala Cys Gln Glu Val Ala
65      70      75      80
Arg Gly Glu Leu Ala Asp Gln Phe Phe Leu Asp Ala Tyr Gln Gly Gly
    85      90      95
Ala Gly Thr Ser Thr Asn Met Asn Val Asn Glu Val Ile Ala Asn Arg
    100     105     110
Ala Leu Glu Ile Leu Gly Arg Pro Lys Gly Asp Tyr Ala Thr Ile His
    115     120     125
Pro Ile Asp His Val Asn Leu His Gln Ser Thr Asn Asp Val Tyr Pro
    130     135     140
Thr Ala Met Arg Val Ala Ala Ile Arg Leu Leu Leu Pro Leu Ala Asp
145     150     155     160
Glu Leu Ala Lys Leu Gln Glu Ala Leu Gln Glu Lys Glu Ala Ala Phe
    165     170     175
Ala Gly Val Val Lys Ile Gly Arg Thr Glu Leu Gln Asp Ala Val Pro
    180     185     190
Val Thr Leu Gly Gln Glu Phe Gly Ala Tyr Ala Gln Ala Ile Ser Arg
    195     200     205
Asp Arg Trp Arg Leu Tyr Lys Val Glu Glu Arg Leu Arg Gln Val Asn
    210     215     220
Leu Gly Gly Thr Ala Thr Gly Thr Gly Leu Asn Ala Pro Leu Lys Tyr
225     230     235     240
Ile Tyr Leu Val Asn Asp Tyr Leu Arg Arg Leu Thr Gly Ile Gly Leu
    245     250     255
Ala Arg Ala Glu Asn Met Ile Asp Ala Thr Gln Asn Met Asp Val Phe
    260     265     270
Val Glu Val Ser Gly Leu Val Lys Ala Ala Ala Val Thr Met His Lys
    275     280     285
Ile Ala Ser Asp Leu Arg Phe Met Ala Ala Gly Pro Arg Gly Gly Pro
    290     295     300
Ala Glu Ile Asn Leu Pro Glu Arg Gln Ala Gly Ser Ser Ile Met Pro
305     310     315     320
Gly Lys Val Asn Pro Val Ile Pro Glu Met Val Ser Gln Val Ala Met
    325     330     335
Gln Val Met Ala Asn Asp Tyr Leu Ile Ala Met Ala Ala Ser Gln Gly
    340     345     350
Gln Leu Glu Leu Asn Pro Phe Ala Pro Leu Ile Ala His Thr Leu Leu
    355     360     365
Glu Ser Leu Ala Met Leu Ala Ala Ala Ala Arg Ile Phe Arg Thr Glu
    370     375     380
Cys Ile Thr Gly Ile Thr Ala Asn Pro Glu Arg Cys Gln Glu Leu Leu
385     390     395     400
Ala Val Ser Pro Ala Leu Ala Thr Ala Leu Leu Pro Tyr Ile Gly Tyr
    405     410     415
Glu Lys Ala Thr Glu Val Val Arg Glu Ala Val Val Ser Gly Arg Ser
    420     425     430
Ile Lys Glu Ile Val Leu Glu Glu Gly Tyr Leu Thr Ser Asp Glu Leu
    435     440     445
Glu Asn Val Leu Thr Pro Ala Ala Met Thr Lys Pro Gly Thr Val Gly
    450     455     460
Ala Val Lys Gln Gly Ile Lys Glu Lys Gly Lys Ala
465     470     475

```

<210> 9703

<211> 1428

<212> DNA

<213> Desulfitobacterium hafniense Y51

<220>

<221> CDS

<222> (1)..(1428)

<223> transl_table=11

<400> 9703

atg gtg cgc aag gaa aag gac ttg ctc gga gtt atg gaa gta ccg gaa
Seite 10181

PF59083SeqList PF59083.txt

Met	Val	Arg	Lys	Glu	Lys	Asp	Leu	Leu	Gly	Val	Met	Glu	Val	Pro	Glu	
1				5					10					15		
gac	gtc	tat	tat	gga	ata	cag	acc	tta	aga	gct	cgt	gaa	aac	ttc	ccg	96
Asp	Val	Tyr	Tyr	Gly	Ile	Gln	Thr	Leu	Arg	Ala	Arg	Glu	Asn	Phe	Pro	
			20					25					30			
att	acg	gga	tat	cgc	cca	cac	cat	gaa	tta	atc	cgg	gga	ttg	ggt	ttg	144
Ile	Thr	Gly	Tyr	Arg	Pro	His	His	Glu	Leu	Ile	Arg	Gly	Leu	Gly	Leu	
		35					40					45				
gtg	aag	gct	gct	gcc	gct	caa	gcc	aat	atg	gac	atc	ggt	tcc	ttg	aac	192
Val	Lys	Ala	Ala	Ala	Ala	Gln	Ala	Asn	Met	Asp	Ile	Gly	Ser	Leu	Asn	
	50					55					60					
cac	gag	atc	ggc	gag	gct	gta	att	aaa	gca	tct	ctg	gaa	gtg	gcc	gag	240
His	Glu	Ile	Gly	Glu	Ala	Val	Ile	Lys	Ala	Ser	Leu	Glu	Val	Ala	Glu	
65				70					75					80		
ggt	gcc	ttt	aat	gac	cat	ttt	gtg	gtg	gat	gtc	att	caa	gga	gga	gca	288
Gly	Ala	Phe	Asn	Asp	His	Phe	Val	Val	Asp	Val	Ile	Gln	Gly	Gly	Ala	
			85					90					95			
gga	acc	tcg	att	aat	atg	aat	gct	aat	gaa	gtg	att	gct	aac	cgg	gct	336
Gly	Thr	Ser	Ile	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	Ala	
			100				105					110				
att	gag	att	ttg	gga	ggg	cga	aaa	ggg	gat	tac	tcc	cgg	ggt	cat	ccc	384
Ile	Glu	Ile	Leu	Gly	Gly	Arg	Lys	Gly	Asp	Tyr	Ser	Arg	Val	His	Pro	
		115				120					125					
aat	ggt	cat	ggt	aac	atg	gcg	cag	agc	acc	aat	gat	gta	ttt	ccc	aca	432
Asn	Val	His	Val	Asn	Met	Ala	Gln	Ser	Thr	Asn	Asp	Val	Phe	Pro	Thr	
	130					135					140					
gcc	atc	cgt	att	gcc	tgt	ctt	aat	gta	gca	gac	gat	ctc	ctt	cat	gcc	480
Ala	Ile	Arg	Ile	Ala	Cys	Leu	Asn	Val	Ala	Asp	Asp	Leu	Leu	His	Ala	
145				150					155					160		
tta	aat	gag	ttg	aag	agt	gct	ttt	caa	gag	aag	gcc	agg	gag	ttt	gac	528
Leu	Asn	Glu	Leu	Lys	Ser	Ala	Phe	Gln	Glu	Lys	Ala	Arg	Glu	Phe	Asp	
			165					170					175			
gga	gtc	atc	aag	atg	ggg	aga	acc	cat	ctt	cag	gat	gcg	ggt	cct	att	576
Gly	Val	Ile	Lys	Met	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Val	Pro	Ile	
		180					185					190				
cgc	tta	ggg	cag	gaa	ttc	gcc	gcc	tat	gga	caa	atg	ctg	gag	aga	gat	624
Arg	Leu	Gly	Gln	Glu	Phe	Ala	Ala	Tyr	Gly	Gln	Met	Leu	Glu	Arg	Asp	
		195				200					205					
ctg	cgc	agg	atc	act	gaa	gca	gcg	aag	tcc	tta	cat	agt	att	aat	atg	672
Leu	Arg	Arg	Ile	Thr	Glu	Ala	Ala	Lys	Ser	Leu	His	Ser	Ile	Asn	Met	
	210				215						220					
ggt	gca	aca	gct	gta	ggt	acc	ggg	ctg	aat	gct	gat	ccg	att	tat	att	720
Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Ala	Asp	Pro	Ile	Tyr	Ile	
225				230					235					240		
gag	gaa	ggt	tct	gag	aat	ctg	agg	aag	ggt	acc	ggg	ttg	ccg	tta	ttg	768
Glu	Glu	Val	Ser	Glu	Asn	Leu	Arg	Lys	Val	Thr	Gly	Leu	Pro	Leu	Leu	
			245					250				255				
cga	gcg	gat	aat	ctg	gta	gat	gcg	aca	cag	aac	acg	gat	gcc	ttt	ttg	816
Arg	Ala	Asp	Asn	Leu	Val	Asp	Ala	Thr	Gln	Asn	Thr	Asp	Ala	Phe	Leu	
		260					265					270				
gag	gtg	tcg	ggt	gct	ctt	aag	acc	ctg	gcc	ggt	aac	ctc	tct	aag	atc	864
Glu	Val	Ser	Gly	Ala	Leu	Lys	Thr	Leu	Ala	Val	Asn	Leu	Ser	Lys	Ile	
		275				280					285					
gcc	aat	gat	ctg	cgg	ctg	atg	gcc	tct	ggg	ccc	aga	acg	ggc	ttt	ggg	912
Ala	Asn	Asp	Leu	Arg	Leu	Met	Ala	Ser	Gly	Pro	Arg	Thr	Gly	Phe	Gly	
	290				295					300						
gaa	att	aat	ctt	cct	gct	atg	cag	ccg	ggg	tct	tct	att	atg	ccc	ggg	960
Glu	Ile	Asn	Leu	Pro	Ala	Met	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	
305				310					315					320		
aaa	gtc	aac	ccc	gtc	atg	gct	gag	gtg	gtc	aac	cag	gta	tcc	ttc	cag	1008
Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Val	Val	Asn	Gln	Val	Ser	Phe	Gln	
			325					330					335			
gta	cag	gga	aat	gat	ttt	acc	atc	gcc	tta	gcc	tgt	gga	gcg	ggg	cag	1056
Val	Gln	Gly	Asn	Asp	Phe	Thr	Ile	Ala	Leu	Ala	Cys	Gly	Ala	Gly	Gln	
		340					345					350				
ctg	gaa	ctc	aat	gtg	atg	gag	cct	gtg	gta	gtc	ttc	aat	ctg	ctc	caa	1104
Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Val	Val	Phe	Asn	Leu	Leu	Gln	
		355				360					365					
tct	ttg	gat	atc	ctc	cgc	aat	gtg	atc	aag	gtc	ttc	aaa	gag	cgc	tgt	1152

PF59083SeqList PF59083.txt

Ser	Leu	Asp	Ile	Leu	Arg	Asn	Val	Ile	Lys	Val	Phe	Lys	Glu	Arg	Cys	
370						375					380					
gtc	gat	ggg	ata	acc	gct	aat	gtg	gaa	cgc	tgt	cgg	gat	ctg	gtt	gaa	1200
Val	Asp	Gly	Ile	Thr	Ala	Asn	Val	Glu	Arg	Cys	Arg	Asp	Leu	Val	Glu	
385					390					395					400	
aac	agc	gtc	ggg	gtc	gtc	acc	gca	atc	aac	ccc	cat	gta	gga	tac	gaa	1248
Asn	Ser	Val	Gly	Val	Val	Thr	Ala	Ile	Asn	Pro	His	Val	Gly	Tyr	Glu	
				405					410					415		
gtc	gct	tcc	cga	atc	gcc	aag	gaa	gcc	ata	gtg	acc	gga	cgt	cct	gtc	1296
Val	Ala	Ser	Arg	Ile	Ala	Lys	Glu	Ala	Ile	Val	Thr	Gly	Arg	Pro	Val	
			420					425					430			
aga	gag	att	gtc	ctg	gaa	aga	gga	ctt	ttg	acc	tcc	gag	gag	ctg	gat	1344
Arg	Glu	Ile	Val	Leu	Glu	Arg	Gly	Leu	Leu	Thr	Ser	Glu	Glu	Leu	Asp	
		435					440					445				
ctt	ata	tta	aat	ccc	cac	gaa	atg	acc	aat	ccg	ggg	atc	agc	ggc	tcg	1392
Leu	Ile	Leu	Asn	Pro	His	Glu	Met	Thr	Asn	Pro	Gly	Ile	Ser	Gly	Ser	
450						455					460					
gag	ttg	ctt	aag	gga	gtg	ctt	ccc	cg	gg	cat	taa					1428
Glu	Leu	Leu	Lys	Gly	Val	Leu	Pro	Arg	Gly	His						
465					470					475						

<210> 9704

<211> 475

<212> PRT

<213> Desulfitobacterium hafniense Y51

<400> 9704

Met	Val	Arg	Lys	Glu	Lys	Asp	Leu	Leu	Gly	Val	Met	Glu	Val	Pro	Glu	
1				5					10					15		
Asp	Val	Tyr	Tyr	Gly	Ile	Gln	Thr	Leu	Arg	Ala	Arg	Glu	Asn	Phe	Pro	
			20					25					30			
Ile	Thr	Gly	Tyr	Arg	Pro	His	His	Glu	Leu	Ile	Arg	Gly	Leu	Gly	Leu	
		35				40						45				
Val	Lys	Ala	Ala	Ala	Ala	Gln	Ala	Asn	Met	Asp	Ile	Gly	Ser	Leu	Asn	
	50					55					60					
His	Glu	Ile	Gly	Glu	Ala	Val	Ile	Lys	Ala	Ser	Leu	Glu	Val	Ala	Glu	
65					70					75					80	
Gly	Ala	Phe	Asn	Asp	His	Phe	Val	Val	Asp	Val	Ile	Gln	Gly	Gly	Ala	
			85						90				95			
Gly	Thr	Ser	Ile	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	Ala	
			100					105					110			
Ile	Glu	Ile	Leu	Gly	Gly	Arg	Lys	Gly	Asp	Tyr	Ser	Arg	Val	His	Pro	
		115					120					125				
Asn	Val	His	Val	Asn	Met	Ala	Gln	Ser	Thr	Asn	Asp	Val	Phe	Pro	Thr	
	130					135					140					
Ala	Ile	Arg	Ile	Ala	Cys	Leu	Asn	Val	Ala	Asp	Asp	Leu	Leu	His	Ala	
145					150					155					160	
Leu	Asn	Glu	Leu	Lys	Ser	Ala	Phe	Gln	Glu	Lys	Ala	Arg	Glu	Phe	Asp	
			165						170					175		
Gly	Val	Ile	Lys	Met	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Val	Pro	Ile	
		180						185					190			
Arg	Leu	Gly	Gln	Glu	Phe	Ala	Ala	Tyr	Gly	Gln	Met	Leu	Glu	Arg	Asp	
		195				200						205				
Leu	Arg	Arg	Ile	Thr	Glu	Ala	Ala	Lys	Ser	Leu	His	Ser	Ile	Asn	Met	
	210					215					220					
Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Ala	Asp	Pro	Ile	Tyr	Ile	
225					230					235					240	
Glu	Glu	Val	Ser	Glu	Asn	Leu	Arg	Lys	Val	Thr	Gly	Leu	Pro	Leu	Leu	
			245						250					255		
Arg	Ala	Asp	Asn	Leu	Val	Asp	Ala	Thr	Gln	Asn	Thr	Asp	Ala	Phe	Leu	
			260					265					270			
Glu	Val	Ser	Gly	Ala	Leu	Lys	Thr	Leu	Ala	Val	Asn	Leu	Ser	Lys	Ile	
		275					280					285				
Ala	Asn	Asp	Leu	Arg	Leu	Met	Ala	Ser	Gly	Pro	Arg	Thr	Gly	Phe	Gly	
	290					295					300					
Glu	Ile	Asn	Leu	Pro	Ala	Met	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	
305					310					315					320	
Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Val	Val	Asn	Gln	Val	Ser	Phe	Gln	
			325						330					335		

PF59083SeqList PF59083.txt

Val Gln Gly Asn Asp Phe Thr Ile Ala Leu Ala Cys Gly Ala Gly Gln
 340 345 350
 Leu Glu Leu Asn Val Met Glu Pro Val Val Val Phe Asn Leu Leu Gln
 355 360 365
 Ser Leu Asp Ile Leu Arg Asn Val Ile Lys Val Phe Lys Glu Arg Cys
 370 375 380
 Val Asp Gly Ile Thr Ala Asn Val Glu Arg Cys Arg Asp Leu Val Glu
 385 390 395 400
 Asn Ser Val Gly Val Thr Ala Ile Asn Pro His Val Gly Tyr Glu
 405 410 415
 Val Ala Ser Arg Ile Ala Lys Glu Ala Ile Val Thr Gly Arg Pro Val
 420 425 430
 Arg Glu Ile Val Leu Glu Arg Gly Leu Leu Thr Ser Glu Glu Leu Asp
 435 440 445
 Leu Ile Leu Asn Pro His Glu Met Thr Asn Pro Gly Ile Ser Gly Ser
 450 455 460
 Glu Leu Leu Lys Gly Val Leu Pro Arg Gly His
 465 470 475

<210> 9705

<211> 1431

<212> DNA

<213> Acidobacteria bacterium Ellin345

<220>

<221> CDS

<222> (1)..(1431)

<223> transl_table=11

<400> 9705

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

PF59083SeqList PF59083.txt

gcc	gag	aag	tcg	gtg	cgt	gag	caa	tcg	gaa	ctt	ttg	cgt	gaa	ttg	gga	672
Ala	Glu	Lys	Ser	Val	Arg	Glu	Gln	Ser	Glu	Leu	Leu	Arg	Glu	Leu	Gly	
210						215					220					
ctc	ggt	gga	tcg	gca	gtg	gga	acg	ggg	atc	aat	acc	cat	ccc	gag	tat	720
Leu	Gly	Gly	Ser	Ala	Val	Gly	Thr	Gly	Ile	Asn	Thr	His	Pro	Glu	Tyr	
225					230					235					240	
cgc	gag	aag	gcg	att	cgc	aat	ctg	gcg	cgg	att	tcg	gga	cag	aaa	ctg	768
Arg	Glu	Lys	Ala	Ile	Arg	Asn	Leu	Ala	Arg	Ile	Ser	Gly	Gln	Lys	Leu	
			245					250						255		
gtg	gtg	gcg	gat	gat	atg	cgc	tac	gcg	atg	cag	tcg	aac	ctg	gcg	atg	816
Val	Val	Ala	Asp	Asp	Met	Arg	Tyr	Ala	Met	Gln	Ser	Asn	Leu	Ala	Met	
			260					265					270			
gcg	agt	gtg	agt	tcg	gcc	ctg	cga	aat	ctg	tcg	ctg	gag	atc	att	cgc	864
Ala	Ser	Val	Ser	Ser	Ala	Leu	Arg	Asn	Leu	Ser	Leu	Glu	Ile	Ile	Arg	
			275				280					285				
atc	agt	aac	gac	ctg	cga	ttg	att	gcg	tcg	gga	cct	aac	act	gga	ctg	912
Ile	Ser	Asn	Asp	Leu	Arg	Leu	Ile	Ala	Ser	Gly	Pro	Asn	Thr	Gly	Leu	
			290			295					300					
gcc	gag	atc	aat	ttg	ccg	gcg	ctg	cag	ccg	ggc	tcg	tca	att	atg	ccg	960
Ala	Glu	Ile	Asn	Leu	Pro	Ala	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	
305					310					315					320	
ggc	aag	atc	aat	ccg	gtg	atg	ccg	gaa	ttg	gcg	gcg	atg	gtg	tgc	ttc	1008
Gly	Lys	Ile	Asn	Pro	Val	Met	Pro	Glu	Leu	Ala	Ala	Met	Val	Cys	Phe	
				325				330						335		
cag	gtg	att	ggc	aac	gac	acg	gca	gtg	gcg	ttc	gcg	gtg	cag	gct	ggc	1056
Gln	Val	Ile	Gly	Asn	Asp	Thr	Ala	Val	Ala	Phe	Ala	Val	Gln	Ala	Gly	
			340					345					350			
caa	ctt	gaa	ttg	aac	gtg	atg	atg	ccg	acc	atg	gcg	tac	agc	gtg	ctg	1104
Gln	Leu	Glu	Leu	Asn	Val	Met	Met	Pro	Thr	Met	Ala	Tyr	Ser	Val	Leu	
			355			360						365				
caa	tcg	gtc	acg	atc	ctg	acg	aac	atg	gtg	cgg	gtg	ttc	acg	gag	aag	1152
Gln	Ser	Val	Thr	Ile	Leu	Thr	Asn	Met	Val	Arg	Val	Phe	Thr	Glu	Lys	
			370			375					380					
tgc	gtt	atc	gga	atc	act	gca	aac	gct	aag	cgc	aat	gag	atg	tac	gca	1200
Cys	Val	Ile	Gly	Ile	Thr	Ala	Asn	Ala	Lys	Arg	Asn	Glu	Met	Tyr	Ala	
385					390					395					400	
cag	agc	acg	gtg	tcg	ctg	gcg	acg	gcg	ttg	aat	ccg	tat	atc	ggc	tat	1248
Gln	Ser	Thr	Val	Ser	Leu	Ala	Thr	Ala	Leu	Asn	Pro	Tyr	Ile	Gly	Tyr	
			405					410						415		
gcg	aag	gcg	gcg	gag	atc	gcg	aaa	gaa	tcg	gtt	gcg	acc	ggc	agg	acg	1296
Ala	Lys	Ala	Ala	Glu	Ile	Ala	Lys	Glu	Ser	Val	Ala	Thr	Gly	Arg	Thr	
			420					425					430			
atc	atc	gag	att	gca	cga	gag	aag	aag	tac	ctg	agc	gaa	gag	cag	atc	1344
Ile	Ile	Glu	Ile	Ala	Arg	Glu	Lys	Lys	Tyr	Leu	Ser	Glu	Glu	Gln	Ile	
			435			440						445				
aaa	gag	atc	ctt	gat	cca	gcg	caa	atg	acg	gag	ccc	cgt	ctg	cca	tcg	1392
Lys	Glu	Ile	Leu	Asp	Pro	Ala	Gln	Met	Thr	Glu	Pro	Arg	Leu	Pro	Ser	
			450			455					460					
gag	gca	gcg	aag	gat	cgc	gac	aag	atc	aag	tta	cgc	tga				1431
Glu	Ala	Ala	Lys	Asp	Arg	Asp	Lys	Ile	Lys	Leu	Arg					
465					470					475						

<210> 9706

<211> 476

<212> PRT

<213> Acidobacteria bacterium Ellin345

<400> 9706

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

PF59083SeqList PF59083.txt

85 90 95
 Ala Gly Val Ser Phe His Ile Asn Ala Asn Glu Val Ile Ala Asn Arg
 100 105 110
 Ala Glu Glu Leu Thr Gly Gly Lys Leu Gly Glu Tyr Lys Ile Val His
 115 120 125
 Pro Asn Asp His Val Asn Tyr Gly Gln Ser Thr Asn Asp Val Phe Pro
 130 135 140
 Thr Ala Met Arg Leu Ala Thr Leu Leu Glu Leu Glu Lys Leu Tyr Pro
 145 150 155
 Val Leu Asp Gly Leu Ala Ser Ala Phe Gly Ala Lys Gly Lys Glu Phe
 165 170 175
 His Asp Ile Leu Lys Ser Gly Arg Thr His Met Gln Asp Ala Val Pro
 180 185 190
 Met Arg Leu Gly Gln Glu Phe Ala Ala Tyr Ala Gly Ala Val Arg Arg
 195 200 205
 Ala Glu Lys Ser Val Arg Glu Gln Ser Glu Leu Leu Arg Glu Leu Gly
 210 215 220
 Leu Gly Gly Ser Ala Val Gly Thr Gly Ile Asn Thr His Pro Glu Tyr
 225 230 235
 Arg Glu Lys Ala Ile Arg Asn Leu Ala Arg Ile Ser Gly Gln Lys Leu
 245 250 255
 Val Val Ala Asp Asp Met Arg Tyr Ala Met Gln Ser Asn Leu Ala Met
 260 265 270
 Ala Ser Val Ser Ser Ala Leu Arg Asn Leu Ser Leu Glu Ile Ile Arg
 275 280 285
 Ile Ser Asn Asp Leu Arg Leu Ile Ala Ser Gly Pro Asn Thr Gly Leu
 290 295 300
 Ala Glu Ile Asn Leu Pro Ala Leu Gln Pro Gly Ser Ser Ile Met Pro
 305 310 315
 Gly Lys Ile Asn Pro Val Met Pro Glu Leu Ala Ala Met Val Cys Phe
 325 330 335
 Gln Val Ile Gly Asn Asp Thr Ala Val Ala Phe Ala Val Gln Ala Gly
 340 345 350
 Gln Leu Glu Leu Asn Val Met Met Pro Thr Met Ala Tyr Ser Val Leu
 355 360 365
 Gln Ser Val Thr Ile Leu Thr Asn Met Val Arg Val Phe Thr Glu Lys
 370 375 380
 Cys Val Ile Gly Ile Thr Ala Asn Ala Lys Arg Asn Glu Met Tyr Ala
 385 390 395
 Gln Ser Thr Val Ser Leu Ala Thr Ala Leu Asn Pro Tyr Ile Gly Tyr
 405 410 415
 Ala Lys Ala Ala Glu Ile Ala Lys Glu Ser Val Ala Thr Gly Arg Thr
 420 425 430
 Ile Ile Glu Ile Ala Arg Glu Lys Tyr Leu Ser Glu Glu Gln Ile
 435 440 445
 Lys Glu Ile Leu Asp Pro Ala Gln Met Thr Glu Pro Arg Leu Pro Ser
 450 455 460
 Glu Ala Ala Lys Asp Arg Asp Lys Ile Lys Leu Arg
 465 470 475

<210> 9707

<211> 1389

<212> DNA

<213> Cytophaga hutchinsonii ATCC 33406

<220>

<221> CDS

<222> (1)..(1389)

<223> transl_table=11

<400> 9707

atg tct att cga att gaa aaa gat acc atg ggt ttg gtg gaa gtg ccg
 Met Ser Ile Arg Ile Glu Lys Asp Thr Met Gly Leu Val Glu Val Pro
 1 5 10 15

48

gca gat aaa tat tgg ggt gca caa acc caa cgt tcc ata gaa aat ttt
 Ala Asp Lys Tyr Trp Gly Ala Gln Thr Gln Arg Ser Ile Glu Asn Phe
 20 25 30

96

aaa atc ggt gat gct tca acg cgc atg ccg atc gaa atc ata cac gcc
 Lys Ile Gly Asp Ala Ser Thr Arg Met Pro Ile Glu Ile Ile His Ala

144

PF59083SeqList PF59083.txt

																35																	40																	45																																		
ttc	gct	atc	tta	aaa	aag	gca	gct	gca	caa	aca	aat	ctc	gaa	tta	ggg		192																																																																			
Phe	Ala	Ile	Leu	Lys	Lys	Ala	Ala	Ala	Gln	Thr	Asn	Leu	Glu	Leu	Gly																																																																					
																50																	55																	60																																		
att	tta	gat	aaa	gaa	aaa	gca	ggc	agt	atc	gca	gaa	gtc	tgc	gat	gaa		240																																																																			
Ile	Leu	Asp	Lys	Glu	Lys	Ala	Gly	Ser	Ile	Ala	Glu	Val	Cys	Asp	Glu																																																																					
																65																	70																	75																	80																	
att	ctg	gca	aaa	aaa	ctg	gat	gat	caa	ttt	ccg	ttg	gtt	gta	tggt	caa		288																																																																			
Ile	Leu	Ala	Lys	Lys	Leu	Asp	Asp	Gln	Phe	Pro	Leu	Val	Val	Trp	Gln																																																																					
																85																	90																	95																																		
aca	ggt	tcg	ggt	aca	caa	tca	aat	atg	aat	gtg	aat	gaa	gtg	att	gca		336																																																																			
Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Val	Asn	Glu	Val	Ile	Ala																																																																					
																100																	105																	110																																		
aac	cggt	gca	cat	ggt	ttg	ctt	ggc	gga	aat	tta	ctg	gat	gaa	aca	aaa		384																																																																			
Asn	Arg	Ala	His	Val	Leu	Leu	Gly	Gly	Asn	Leu	Leu	Asp	Glu	Thr	Lys																																																																					
																115																	120																	125																																		
aaa	att	cat	cca	aat	gat	gat	gta	aat	aaa	tcg	cag	tca	tca	aac	gac		432																																																																			
Lys	Ile	His	Pro	Asn	Asp	Asp	Val	Asn	Lys	Ser	Gln	Ser	Ser	Asn	Asp																																																																					
																130																	135																	140																																		
acg	ttt	ccc	acg	gct	atg	cac	att	gcc	gct	tgc	ctg	atg	tta	aaa	aaa		480																																																																			
Thr	Phe	Pro	Thr	Ala	Met	His	Ile	Ala	Ala	Cys	Leu	Met	Leu	Lys	Lys																																																																					
																145																	150																	155																	160																	
gta	acg	att	cca	gga	ata	gag	caa	ttg	cag	cat	acg	tta	cgg	aca	aaa		528																																																																			
Val	Thr	Ile	Pro	Gly	Ile	Glu	Gln	Leu	Gln	His	Thr	Leu	Arg	Thr	Lys																																																																					
																165																	170																	175																																		
aca	gaa	cag	ttt	aaa	gat	ggt	ggt	aaa	ata	ggc	cggt	acg	cat	ttc	atg		576																																																																			
Thr	Glu	Gln	Phe	Lys	Asp	Val	Val	Lys	Ile	Gly	Arg	Thr	His	Phe	Met																																																																					
																180																	185																	190																																		
gat	gca	acg	cct	ttg	aca	ttg	ggc	cag	gag	ttt	tcc	gga	tat	gct	gcg		624																																																																			
Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Ala	Ala																																																																					
																195																	200																	205																																		
caa	tta	agc	tat	gca	tta	aaa	gca	att	cac	aat	gcc	tcg	gca	cat	ctt		672																																																																			
Gln	Leu	Ser	Tyr	Ala	Leu	Lys	Ala	Ile	His	Asn	Ala	Ser	Ala	His	Leu																																																																					
																210																	215																	220																																		
tca	gaa	cta	gcg	ctg	gggt	gga	aca	gct	ggt	gggt	acg	gga	att	aat	gca		720																																																																			
Ser	Glu	Leu	Ala	Leu	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Ala																																																																					
																225																	230																	235																	240																	
ccc	aaa	gga	tat	gcg	gaa	cggt	ggt	gcc	ggg	cac	att	gct	gcg	ctc	aca		768																																																																			
Pro	Lys	Gly	Tyr	Ala	Glu	Arg	Val	Ala	Gly	His	Ile	Ala	Ala	Leu	Thr																																																																					
																245																	250																	255																																		
gggt	ttt	ccg	ttt	aca	tca	gca	ccc	aat	aaa	ttt	gaa	gca	ctt	gct	aca		816																																																																			
Gly</																																																																																				

PF59083SeqList PF59083.txt

<div> <div>405</div> <div>410</div> <div>415</div> </div>																
cat	att	ggt	tat	gat	aag	tct	gca	gaa	att	gca	aaa	cat	gcg	cat	aaa	1296
His	Ile	Gly	Tyr	Asp	Lys	Ser	Ala	Glu	Ile	Ala	Lys	His	Ala	His	Lys	
<div> <div>420</div> <div>425</div> <div>430</div> </div>																
gaa	aac	aca	agt	ctc	cgg	cag	gct	gca	tta	gca	tta	ggc	tat	gtt	acc	1344
Glu	Asn	Thr	Ser	Leu	Arg	Gln	Ala	Ala	Leu	Ala	Leu	Gly	Tyr	Val	Thr	
<div> <div>435</div> <div>440</div> <div>445</div> </div>																
aac	gaa	cag	ttt	gat	gcc	tgg	gta	aat	cct	aaa	aat	atg	atc	tag		1389
Asn	Glu	Gln	Phe	Asp	Ala	Trp	Val	Asn	Pro	Lys	Asn	Met	Ile			
<div> <div>450</div> <div>455</div> <div>460</div> </div>																

<210> 9708

<211> 462

<212> PRT

<213> *Cytophaga hutchinsonii* ATCC 33406

<400> 9708

Met 1	Ser	Ile	Arg	Ile 5	Glu	Lys	Asp	Thr	Met 10	Gly	Leu	Val	Glu	Val 15	Pro
Ala	Asp	Lys	Tyr 20	Trp	Gly	Ala	Gln	Thr 25	Gln	Arg	Ser	Ile	Glu 30	Asn	Phe
Lys	Ile	Gly 35	Asp	Ala	Ser	Thr	Arg 40	Met	Pro	Ile	Glu	Ile 45	Ile	His	Ala
Phe	Ala 50	Ile	Leu	Lys	Lys	Ala 55	Ala	Ala	Gln	Thr	Asn 60	Leu	Glu	Leu	Gly
Ile 65	Leu	Asp	Lys	Glu	Lys 70	Ala	Gly	Ser	Ile	Ala 75	Glu	Val	Cys	Asp	Glu 80
Ile	Leu	Ala	Lys	Lys 85	Leu	Asp	Asp	Gln	Phe 90	Pro	Leu	Val	Val	Trp 95	Gln
Thr	Gly	Ser	Gly 100	Thr	Gln	Ser	Asn	Met 105	Asn	Val	Asn	Glu	Val 110	Ile	Ala
Asn	Arg	Ala 115	His	Val	Leu	Leu	Gly 120	Gly	Asn	Leu	Leu	Asp 125	Glu	Thr	Lys
Lys	Ile 130	His	Pro	Asn	Asp	Asp 135	Val	Asn	Lys	Ser	Gln 140	Ser	Ser	Asn	Asp
Thr 145	Phe	Pro	Thr	Ala	Met 150	His	Ile	Ala	Ala	Cys 155	Leu	Met	Leu	Lys	Lys 160
Val	Thr	Ile	Pro	Gly 165	Ile	Glu	Gln	Leu	Gln 170	His	Thr	Leu	Arg	Thr 175	Lys
Thr	Glu	Gln	Phe 180	Lys	Asp	Val	Val	Lys 185	Ile	Gly	Arg	Thr	His 190	Phe	Met
Asp	Ala	Thr 195	Pro	Leu	Thr	Leu	Gly 200	Gln	Glu	Phe	Ser	Gly 205	Tyr	Ala	Ala
Gln	Leu 210	Ser	Tyr	Ala	Leu	Lys 215	Ala	Ile	His	Asn	Ala 220	Ser	Ala	His	Leu
Ser 225	Glu	Leu	Ala	Leu	Gly 230	Gly	Thr	Ala	Val	Gly 235	Thr	Gly	Ile	Asn	Ala 240
Pro	Lys	Gly	Tyr	Ala 245	Glu	Arg	Val	Ala	Gly 250	His	Ile	Ala	Ala	Leu 255	Thr
Gly	Phe	Pro	Phe 260	Thr	Ser	Ala	Pro	Asn 265	Lys	Phe	Glu	Ala	Leu 270	Ala	Thr
His	Asp	Ala 275	Leu	Val	Glu	Met	His 280	Gly	Ala	Leu	Lys	Thr 285	Ser	Ala	Val
Ser	Leu 290	Met	Lys	Ile	Ala	Asn 295	Asp	Ile	Arg	Met	Leu 300	Ala	Ser	Gly	Pro
Arg 305	Ser	Gly	Ile	Gly	Glu 310	Ile	His	Ile	Pro	Asp 315	Asn	Glu	Pro	Gly	Ser 320
Ser	Ile	Met	Pro	Gly 325	Lys	Val	Asn	Pro	Thr 330	Gln	Val	Glu	Ala	Leu 335	Thr
Met	Val	Cys	Ala 340	Gln	Val	Met	Gly	Asn 345	Asp	Val	Thr	Leu	Ser 350	Val	Ala
Gly	Ser	Met 355	Gly	Gln	Phe	Glu	Leu 360	Asn	Val	Phe	Lys	Pro 365	Val	Ile	Ile
Tyr	Asn 370	Phe	Leu	Gln	Ser	Ala 375	Arg	Leu	Ile	Gly	Asp 380	Ala	Cys	Val	Ser
Phe 385	Asn	Glu	Lys	Cys	Ala 390	Lys	Gly	Ile	Glu	Pro 395	Asn	Thr	Ala	Thr	Ile 400
Glu	Arg	Asn	Val	Glu 405	Asn	Ser	Leu	Met	Leu 410	Val	Thr	Ala	Leu	Asn 415	Pro

PF59083SeqList PF59083.txt

His Ile Gly Tyr Asp Lys Ser Ala Glu Ile Ala Lys His Ala His Lys
 420 425 430
 Glu Asn Thr Ser Leu Arg Gln Ala Ala Leu Ala Leu Gly Tyr Val Thr
 435 440 445
 Asn Glu Gln Phe Asp Ala Trp Val Asn Pro Lys Asn Met Ile
 450 455 460

<210> 9709
 <211> 1464
 <212> DNA
 <213> Rhodococcus sp. RHA1

<220>
 <221> CDS
 <222> (1)..(1464)
 <223> transl_table=11

<400> 9709
 ttg agc gac agc gat gtg cgg atc gag cac gat tcg atc gga gat ctg 48
 Met Ser Asp Ser Asp Val Arg Ile Glu His Asp Ser Ile Gly Asp Leu
 1 5 10 15
 gcg gta ccg gcg ggg gcg tac tac ggc gtc cac acc gcc agg gcg atg 96
 Ala Val Pro Ala Gly Ala Tyr Tyr Gly Val His Thr Ala Arg Ala Met
 20 25 30
 gac aat ttc gcg atc acc ggg tct gcc atc ggt cag tac ccg gca ctg 144
 Asp Asn Phe Ala Ile Thr Gly Ser Ala Ile Gly Gln Tyr Pro Ala Leu
 35 40 45
 gtc gcg gcg ttg gcg acc gtg aaa cag gct gcc tgc ctg gcg aac cgg 192
 Val Ala Ala Leu Ala Thr Val Lys Gln Ala Ala Cys Leu Ala Asn Arg
 50 55 60
 gac ctg ggt ctc ctc gac gac cgg cgg gcc gta gcg atc gtg gcc gcg 240
 Asp Leu Gly Leu Leu Asp Asp Arg Arg Ala Val Ala Ile Val Ala Ala
 65 70 75 80
 tgc acg gaa att cgc gcc ggg gca ctg ctc gac cag ttt ccg atc gat 288
 Cys Thr Glu Ile Arg Ala Gly Ala Leu Leu Asp Gln Phe Pro Ile Asp
 85 90 95
 ccg atc cag ggc gga gcg ggc act tcg tcg aac atg aac gtc aac gag 336
 Pro Ile Gln Gly Gly Ala Gly Thr Ser Ser Asn Met Asn Val Asn Glu
 100 105 110
 gtc atc gcg aac cgc gca ctc gag atc ctc ggg ttc ggg cgc ggc gcc 384
 Val Ile Ala Asn Arg Ala Leu Glu Ile Leu Gly Phe Gly Arg Gly Ala
 115 120 125
 tac acc gaa ctc gac cct ctc gct cac gtg aac ctg ggg cag tcc acc 432
 Tyr Thr Glu Leu Asp Pro Leu Ala His Val Asn Leu Gly Gln Ser Thr
 130 135 140
 aac gat gtg tac ccg acc gcg atc aag ctc gcg ctg gtc gag cac ctc 480
 Asn Asp Val Tyr Pro Thr Ala Ile Lys Leu Ala Leu Val Glu His Leu
 145 150 155 160
 cga atg ttg atc gcg tcg ctc ggt cgg ctc gcg gag tcg ttc gag cgc 528
 Arg Met Leu Ile Ala Ser Leu Gly Arg Ala Glu Ser Phe Glu Arg
 165 170 175
 aag tcg atc gaa ttc gac gac atc gtc aag atg ggt cgc acc cag ctg 576
 Lys Ser Ile Glu Phe Asp Asp Ile Val Lys Met Gly Arg Thr Gln Leu
 180 185 190
 cag gac gcg gta ccg atg acc ctc ggg cag gag ttc gcc gcc tac tcg 624
 Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Ala Ala Tyr Ser
 195 200 205
 atc atg ctg aac gag gac tgc gcc cgg ctc tcc gag gga gcg ctt ctg 672
 Ile Met Leu Asn Glu Asp Cys Ala Arg Leu Ser Glu Gly Ala Leu Leu
 210 215 220
 ctg ctg gaa tcg aac ctc ggc ggc acc gcc atc ggc acg ggg atc aac 720
 Leu Leu Glu Ser Asn Leu Gly Gly Thr Ala Ile Gly Thr Gly Ile Asn
 225 230 235 240
 gga cat ccc gag tac tcc gcg ctc gcc tgc gac tac ttg cgc gag ctg 768
 Gly His Pro Glu Tyr Ser Ala Leu Ala Cys Asp Tyr Leu Arg Glu Leu
 245 250 255
 acc ggt gaa ccg gtc gtc ccg gcc ggc aat ctg atc gag gca acc cag 816
 Thr Gly Glu Pro Val Val Pro Ala Gly Asn Leu Ile Glu Ala Thr Gln
 260 265 270

PF59083SeqList PF59083.txt

gac tgc gga gca ttc gtg	cag gtc tcc gga atc ctc aaa cgt gtc gcc	864
Asp Cys Gly Ala Phe Val	Gln Val Ser Gly Ile Leu Lys Arg Val Ala	
	275 280 285	
gtg aaa ctg tcc aag acg tgc aac gat ctg cgg ctc acc tcc tcc ggg	912	
Val Lys Leu Ser Lys Thr Cys Asn Asp Leu Arg Leu Thr Ser Ser Gly		
	290 300	
ccg acc gcc ggg ctc ggt gag atc aat ctg cct ccg gcc caa gcc ggt	960	
Pro Thr Ala Gly Leu Gly Glu Ile Asn Leu Pro Pro Ala Gln Ala Gly		
	305 310 315 320	
tcg tcg atc atg ccc ggc aag gtc aac ccg gtc atc ccc gaa atg gtg	1008	
Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Met Val		
	325 330 335	
aac cag gtc gcg ttc gag gtg atc ggc aac gat ctg acg gtc acg atg	1056	
Asn Gln Val Ala Phe Glu Val Ile Gly Asn Asp Leu Thr Val Thr Met		
	340 345 350	
gcc gcc gag ggt ggg caa ctc cag ctc aac gcg ttc gaa ccc gtg atc	1104	
Ala Ala Glu Gly Gly Gln Leu Gln Leu Asn Ala Phe Glu Pro Val Ile		
	355 360 365	
gtc tac agc ctg ctg cgc tcg acg acg cac ctg gcc gcg gca tcg gac	1152	
Val Tyr Ser Leu Leu Arg Ser Thr Thr His Leu Ala Ala Ser Asp		
	370 375 380	
acc ctg gcg gtg aag tgc gtc gac ggg atc acc gcc aac cgc gac cat	1200	
Thr Leu Ala Val Lys Cys Val Asp Gly Ile Thr Ala Asn Arg Asp His		
	385 390 395 400	
ctc gag cgg ggt gtt cgg cgc tcg atc ggc gtc acc gcg ctc tcg	1248	
Leu Glu Arg Gly Val Arg Arg Ser Ile Gly Ile Val Thr Ala Leu Ser		
	405 410 415	
ccg ttc atc ggc tat gcg gcc agc gcg gat atc gcc aag agg gcc ctg	1296	
Pro Phe Ile Gly Tyr Ala Ala Ser Ala Asp Ile Ala Lys Arg Ala Leu		
	420 425 430	
gcg acc ggc gct tac gtc ggc gac ctc gcc gtc gac gac ggt ctg ctc	1344	
Ala Thr Gly Ala Tyr Val Gly Asp Leu Ala Val Asp Asp Gly Leu Leu		
	435 440 445	
act cgc gcg cag gtc gat gac atc ctg tcc ccc cgg cga ctc gcc ggt	1392	
Thr Arg Ala Gln Val Asp Asp Ile Leu Ser Pro Arg Arg Leu Ala Gly		
	450 455 460	
ctg ctc acc gcg ccc acc gtg gac agc gaa ttc tcc gca ctc gac cat	1440	
Leu Leu Thr Ala Pro Thr Val Asp Ser Glu Phe Ser Ala Leu Asp His		
	465 470 475 480	
ctc acc ggt gtc gcc gcg cac tga	1464	
Leu Thr Gly Val Ala Ala His		
	485	

<210> 9710

<211> 487

<212> PRT

<213> Rhodococcus sp. RHA1

<400> 9710

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

PF59083SeqList PF59083.txt

Arg Met Leu Ile Ala Ser Leu Gly Arg Leu Ala Glu Ser Phe Glu Arg
 165 170 175
 Lys Ser Ile Glu Phe Asp Asp Ile Val Lys Met Gly Arg Thr Gln Leu
 180 185 190
 Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Ala Tyr Ser
 195 200 205
 Ile Met Leu Asn Glu Asp Cys Ala Arg Leu Ser Glu Gly Ala Leu Leu
 210 215 220
 Leu Leu Glu Ser Asn Leu Gly Gly Thr Ala Ile Gly Thr Gly Ile Asn
 225 230 235
 Gly His Pro Glu Tyr Ser Ala Leu Ala Cys Asp Tyr Leu Arg Glu Leu
 245 250 255
 Thr Gly Glu Pro Val Val Pro Ala Gly Asn Leu Ile Glu Ala Thr Gln
 260 265 270
 Asp Cys Gly Ala Phe Val Gln Val Ser Gly Ile Leu Lys Arg Val Ala
 275 280 285
 Val Lys Leu Ser Lys Thr Cys Asn Asp Leu Arg Leu Thr Ser Ser Gly
 290 295 300
 Pro Thr Ala Gly Leu Gly Glu Ile Asn Leu Pro Pro Ala Gln Ala Gly
 305 310 315
 Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Met Val
 325 330 335
 Asn Gln Val Ala Phe Glu Val Ile Gly Asn Asp Leu Thr Val Thr Met
 340 345 350
 Ala Ala Glu Gly Gly Gln Leu Gln Leu Asn Ala Phe Glu Pro Val Ile
 355 360 365
 Val Tyr Ser Leu Leu Arg Ser Thr Thr His Leu Ala Ala Ala Ser Asp
 370 375 380
 Thr Leu Ala Val Lys Cys Val Asp Gly Ile Thr Ala Asn Arg Asp His
 385 390 395
 Leu Glu Arg Gly Val Arg Arg Ser Ile Gly Ile Val Thr Ala Leu Ser
 405 410 415
 Pro Phe Ile Gly Tyr Ala Ala Ser Ala Asp Ile Ala Lys Arg Ala Leu
 420 425 430
 Ala Thr Gly Ala Tyr Val Gly Asp Leu Ala Val Asp Asp Gly Leu Leu
 435 440 445
 Thr Arg Ala Gln Val Asp Asp Ile Leu Ser Pro Arg Arg Leu Ala Gly
 450 455 460
 Leu Leu Thr Ala Pro Thr Val Asp Ser Glu Phe Ser Ala Leu Asp His
 465 470 475 480
 Leu Thr Gly Val Ala Ala His
 485

<210> 9711

<211> 1401

<212> DNA

<213> Hyphomonas neptunium ATCC 15444

<220>

<221> CDS

<222> (1)..(1401)

<223> transl_table=11

<400> 9711

atg gcc aag acc ccc aca cgc aca gaa tcg gac act ttc ggc cct atc	48
Met Ala Lys Thr Pro Thr Arg Thr Glu Ser Asp Thr Phe Gly Pro Ile	
1 5 10 15	
gag gtt gag gcg gac aag tat tgg ggc gcg cag gcg cag cgc tcg ctg	96
Glu Val Glu Ala Asp Lys Tyr Trp Gly Ala Gln Ala Gln Arg Ser Leu	
20 25 30	
ggc aac ttc aag ata ggc tgg gag aaa cag ccc cag ccc atc gtg cgc	144
Gly Asn Phe Lys Ile Gly Trp Glu Lys Gln Pro Gln Pro Ile Val Arg	
35 40 45	
gcg ctc ggc atc gtc aag aaa gcc gcc gcc gaa gtg aac atg gcg atg	192
Ala Leu Gly Ile Val Lys Lys Ala Ala Ala Glu Val Asn Met Ala Met	
50 55 60	
gag aaa atg gac cgt ctg gtc ggc cgc gcc atc gtt cag gcc gcc gat	240
Glu Lys Met Asp Arg Leu Val Gly Arg Ala Ile Val Gln Ala Ala Asp	
65 70 75 80	

PF59083SeqList PF59083.txt																
gaa	gtc	atc	gag	ggc	aag	ctc	gac	gcg	cat	ttc	ccg	ctg	gtc	gtc	tgg	288
Glu	Val	Ile	Glu	Gly	Lys	Leu	Asp	Ala	His	Phe	Pro	Leu	Val	Val	Trp	
				85					90					95		
cag	acc	ggc	tcg	ggc	acc	cag	tcg	aac	atg	aac	gcc	aat	gag	gtg	atc	336
Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	
			100					105					110			
tcc	aac	cg	gcc	atc	gag	atc	ctg	aac	ggc	aag	gtc	ggc	tcc	aag	gcg	384
Ser	Asn	Arg	Ala	Ile	Glu	Ile	Leu	Asn	Gly	Lys	Val	Gly	Ser	Lys	Ala	
		115					120					125				
ccg	gtt	cac	ccg	aac	gat	cat	gtg	aac	atg	tcc	cag	tcg	tcc	aac	gac	432
Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	Met	Ser	Gln	Ser	Ser	Asn	Asp	
	130					135					140					
acc	ttc	ccg	acc	ggc	atg	cac	atc	gcc	tgc	gcc	gag	cag	gtc	gtg	cac	480
Thr	Phe	Pro	Thr	Ala	Met	His	Ile	Ala	Cys	Ala	Glu	Gln	Val	Val	His	
145					150					155					160	
aag	ctg	gtc	ccc	ggc	ctg	caa	cag	ctc	cag	aac	gct	ctg	aac	gac	aag	528
Lys	Leu	Val	Pro	Ala	Leu	Gln	Gln	Leu	Gln	Asn	Ala	Leu	Asn	Asp	Lys	
				165				170						175		
gca	cag	gcc	tgg	aag	gac	atc	atc	aag	atc	ggg	cg	acg	cat	acg	cag	576
Ala	Gln	Ala	Trp	Lys	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	
			180					185					190			
gat	gcc	acc	ccg	gtc	acc	ctc	gga	cag	gaa	ttc	tcc	ggc	tac	gcc	aaa	624
Asp	Ala	Thr	Pro	Val	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Ala	Lys	
		195					200					205				
cag	ctc	gaa	aac	ggc	atc	aag	cg	atc	gag	atg	acc	ctg	ccg	atg	ctg	672
Gln	Leu	Glu	Asn	Gly	Ile	Lys	Arg	Ile	Glu	Met	Thr	Leu	Pro	Met	Leu	
	210					215					220					
atg	gaa	ctc	ggc	cag	ggc	ggc	acg	gcg	gtg	ggc	acc	ggc	ctt	gcc	tcg	720
Met	Glu	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Ala	Ser	
225				230						235					240	
ccg	gag	ggc	ttt	ggc	gag	ctg	gtg	gcc	gac	aag	atc	gcc	cag	atc	acc	768
Pro	Glu	Gly	Phe	Ala	Glu	Leu	Val	Ala	Asp	Lys	Ile	Ala	Gln	Ile	Thr	
				245				250						255		
ggc	ctg	aac	ttc	acc	tcc	gcg	ccc	aac	aag	ttc	gag	gcg	ctt	gcc	gcc	816
Gly	Leu	Asn	Phe	Thr	Ser	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	
			260					265					270			
cat	gac	gcg	atg	gtg	atg	acc	cac	ggc	gcc	atc	acg	acc	gtg	gcg	atg	864
His	Asp	Ala	Met	Val	Met	Thr	His	Gly	Ala	Ile	Thr	Thr	Val	Ala	Met	
		275					280					285				
agc	tgc	ttc	aag	atc	ggc	aac	gac	atc	cgt	ttc	ctc	ggc	tct	ggc	ccg	912
Ser	Cys	Phe	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	
	290					295					300					
cg	tcg	ggc	ctt	ggc	gag	ctg	gcc	ctg	ccg	gag	aac	gag	ccg	ggc	tcc	960
Arg	Ser	Gly	Leu	Gly	Glu	Leu	Ala	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	
305				310						315					320	
tcg	atc	atg	ccg	ggt	aag	gtg	aac	ccg	acc	cag	tgc	gaa	gcc	ctc	acc	1008
Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	
				325				330						335		
cag	gtc	tgc	gcg	cat	att	cac	ggc	aac	aac	gcc	gcc	atc	ggc	ttt	gcc	1056
Gln	Val	Cys	Ala	His	Ile	His	Gly	Asn	Asn	Ala	Ala	Ile	Gly	Phe	Ala	
			340				345						350			
ggc	agc	cag	ggt	cat	ttc	gag	ctg	aac	gtg	ttc	aac	ccg	atg	atg	gcc	1104
Gly	Ser	Gln	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	Asn	Pro	Met	Met	Ala	
		355				360						365				
tac	aac	ttc	ctg	caa	tct	gtc	cag	ctg	ctg	gca	gat	gcg	gcc	gtg	tcc	1152
Tyr	Asn	Phe	Leu	Gln	Ser	Val	Gln	Leu	Leu	Ala	Asp	Ala	Ala	Val	Ser	
		370				375					380					
ttc	acc	gag	aac	tgc	gtt	gtc	ggc	atc	gag	ccg	cg	ctc	gac	aat	atc	1200
Phe	Thr	Glu	Asn	Cys	Val	Val	Gly	Ile	Glu	Pro	Arg	Leu	Asp	Asn	Ile	
385				390						395					400	
cag	cg	ggc	ctt	gaa	aat	tcg	ctg	atg	ctg	gtg	acg	ccg	ctg	aag	gaa	1248
Gln	Arg	Gly	Leu	Glu	Asn	Ser	Leu	Met	Leu	Val	Thr	Pro	Leu	Lys	Glu	
				405				410						415		
aag	tat	ggc	tac	gat	ctg	gcc	gca	aaa	gta	gcc	aag	acc	gcg	cac	aag	1296
Lys	Tyr	Gly	Tyr	Asp	Leu	Ala	Ala	Lys	Val	Ala	Lys	Thr	Ala	His	Lys	
			420				425						430			
aat	ggc	acc	aca	ctg	aag	gtc	gaa	gcc	ctg	gcg	ctc	ggc	att	tcg	gag	1344
Asn	Gly	Thr	Thr	Leu	Lys	Val	Glu	Ala	Leu	Ala	Leu	Gly	Ile	Ser	Glu	
			435				440					445				

PF59083SeqList PF59083.txt

gaa	gat	ttc	gac	gcc	atc	gtg	cgg	cct	gag	aaa	atg	atc	gga	ccg	gac	1392
Glu	Asp	Phe	Asp	Ala	Ile	Val	Arg	Pro	Glu	Lys	Met	Ile	Gly	Pro	Asp	
	450					455					460					
ccg	gca	taa														1401
Pro	Ala															
465																

<210> 9712
 <211> 466
 <212> PRT
 <213> Hyphomonas neptunium ATCC 15444

<400> 9712

Met	Ala	Lys	Thr	Pro	Thr	Arg	Thr	Glu	Ser	Asp	Thr	Phe	Gly	Pro	Ile	
1				5					10					15		
Glu	Val	Glu	Ala	Asp	Lys	Tyr	Trp	Gly	Ala	Gln	Ala	Gln	Arg	Ser	Leu	
			20					25					30			
Gly	Asn	Phe	Lys	Ile	Gly	Trp	Glu	Lys	Gln	Pro	Gln	Pro	Ile	Val	Arg	
		35					40					45				
Ala	Leu	Gly	Ile	Val	Lys	Lys	Ala	Ala	Ala	Glu	Val	Asn	Met	Ala	Met	
	50					55					60					
Glu	Lys	Met	Asp	Arg	Leu	Val	Gly	Arg	Ala	Ile	Val	Gln	Ala	Ala	Asp	
65					70					75					80	
Glu	Val	Ile	Glu	Gly	Lys	Leu	Asp	Ala	His	Phe	Pro	Leu	Val	Val	Trp	
				85					90					95		
Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	
			100					105					110			
Ser	Asn	Arg	Ala	Ile	Glu	Ile	Leu	Asn	Gly	Lys	Val	Gly	Ser	Lys	Ala	
		115					120					125				
Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	Met	Ser	Gln	Ser	Ser	Asn	Asp	
	130					135					140					
Thr	Phe	Pro	Thr	Ala	Met	His	Ile	Ala	Cys	Ala	Glu	Gln	Val	Val	His	
145					150				155						160	
Lys	Leu	Val	Pro	Ala	Leu	Gln	Gln	Leu	Gln	Asn	Ala	Leu	Asn	Asp	Lys	
				165					170					175		
Ala	Gln	Ala	Trp	Lys	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	
			180					185					190			
Asp	Ala	Thr	Pro	Val	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Ala	Lys	
		195					200					205				
Gln	Leu	Glu	Asn	Gly	Ile	Lys	Arg	Ile	Glu	Met	Thr	Leu	Pro	Met	Leu	
	210					215					220					
Met	Glu	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Ala	Ser	
225					230					235					240	
Pro	Glu	Gly	Phe	Ala	Glu	Leu	Val	Ala	Asp	Lys	Ile	Ala	Gln	Ile	Thr	
				245					250					255		
Gly	Leu	Asn	Phe	Thr	Ser	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	
			260					265					270			
His	Asp	Ala	Met	Val	Met	Thr	His	Gly	Ala	Ile	Thr	Thr	Val	Ala	Met	
		275					280					285				
Ser	Cys	Phe	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	
	290					295					300					
Arg	Ser	Gly	Leu	Gly	Glu	Leu	Ala	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	
305					310					315					320	
Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	
				325					330					335		
Gln	Val	Cys	Ala	His	Ile	His	Gly	Asn	Asn	Ala	Ala	Ile	Gly	Phe	Ala	
			340					345					350			
Gly	Ser	Gln	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	Asn	Pro	Met	Met	Ala	
		355					360					365				
Tyr	Asn	Phe	Leu	Gln	Ser	Val	Gln	Leu	Leu	Ala	Asp	Ala	Ala	Val	Ser	
	370					375					380					
Phe	Thr	Glu	Asn	Cys	Val	Val	Gly	Ile	Glu	Pro	Arg	Leu	Asp	Asn	Ile	
385					390					395					400	
Gln	Arg	Gly	Leu	Glu	Asn	Ser	Leu	Met	Leu	Val	Thr	Pro	Leu	Lys	Glu	
				405					410					415		
Lys	Tyr	Gly	Tyr	Asp	Leu	Ala	Ala	Lys	Val	Ala	Lys	Thr	Ala	His	Lys	
			420					425					430			
Asn	Gly	Thr	Thr	Leu	Lys	Val	Glu	Ala	Leu	Ala	Leu	Gly	Ile	Ser	Glu	
		435					440					445				

PF59083SeqList PF59083.txt

Glu Asp Phe Asp Ala Ile Val Arg Pro Glu Lys Met Ile Gly Pro Asp
 450 455 460
 Pro Ala
 465

<210> 9713

<211> 1431

<212> DNA

<213> Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293

<220>

<221> CDS

<222> (1)..(1431)

<223> transl_table=11

<400> 9713

atg cgc aca gaa tca gat tca ctc ggc caa atc aac gta ccc aaa gat	48
Met Arg Thr Glu Ser Asp Ser Leu Gly Gln Ile Asn Val Pro Lys Asp	
1 5 10 15	
gtc tac tac ggg gca cac act caa cgt gcg cta aat aat ttt cca att	96
Val Tyr Tyr Gly Ala His Thr Gln Arg Ala Leu Asn Asn Phe Pro Ile	
20 25 30	
tca aaa gaa aca acc cat cca gaa atc att cga gcc ttt tta gaa att	144
Ser Lys Glu Thr Thr His Pro Glu Ile Ile Arg Ala Phe Leu Glu Ile	
35 40 45	
aaa cag gct gcg gca caa aca aat gct aca tct ggt aat cta gat cga	192
Lys Gln Ala Ala Ala Gln Thr Asn Ala Thr Ser Gly Asn Leu Asp Arg	
50 55 60	
gct gtt gct aaa cat att gtt gat gca aca aaa att ttg tta agt cag	240
Ala Val Ala Lys His Ile Val Asp Ala Thr Lys Ile Leu Leu Ser Gln	
65 70 75 80	
cca atc gat ctt aca atg ttt cca att agt gac gtt caa ggt ggt gct	288
Pro Ile Asp Leu Thr Met Phe Pro Ile Ser Asp Val Gln Gly Gly Ala	
85 90 95	
ggt aca agt acc aat atg aac gtc aat gaa gtt gtt gct aat aca gct	336
Gly Thr Ser Thr Asn Met Asn Val Asn Glu Val Val Ala Asn Thr Ala	
100 105 110	
ctt gag cag gta ggc cgt gca cgt ggt gaa tat ggc tac gtt aac cca	384
Leu Glu Gln Val Gly Arg Ala Arg Gly Glu Tyr Gly Tyr Val Asn Pro	
115 120 125	
aat gac cac gtt aat atg ggt cag agt acc aat gat act tat cct agc	432
Asn Asp His Val Asn Met Gly Gln Ser Thr Asn Asp Thr Tyr Pro Ser	
130 135 140	
gca gga aaa att gct ctt atc cga cta ctc gaa cca ctt ttt tca gaa	480
Ala Gly Lys Ile Ala Leu Ile Arg Leu Leu Glu Pro Leu Phe Ser Glu	
145 150 155 160	
tta aca tta ttg gta gac gct ctt ggt aac aaa gcc gac gaa ttt tca	528
Leu Thr Leu Leu Val Asp Ala Leu Gly Asn Lys Ala Asp Glu Phe Ser	
165 170 175	
aca act tac aaa atg ggt cgt aca cag cta caa gat gct gtg ccc atg	576
Thr Thr Tyr Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met	
180 185 190	
acc tta gga aat acc ttt cat gct tgg tta aaa cca ctt cgt cga gac	624
Thr Leu Gly Asn Thr Phe His Ala Trp Leu Lys Pro Leu Arg Arg Asp	
195 200 205	
ttt aaa cgt atc gaa gcc gca cgc aat gag cta tat aca tta aat ctg	672
Phe Lys Arg Ile Glu Ala Ala Arg Asn Glu Leu Tyr Thr Leu Asn Leu	
210 215 220	
ggc gga tca gct att ggt tcc ggt att aac gta agt tat cat tac caa	720
Gly Gly Ser Ala Ile Gly Ser Gly Ile Asn Val Ser Tyr His Tyr Gln	
225 230 235 240	
gtg cac atc gtt cct aac cta gct agc ata act ggg ctt cca ctt gag	768
Val His Ile Val Pro Asn Leu Ala Ser Ile Thr Gly Leu Pro Leu Glu	
245 250 255	
caa gcc cat gat tta ttt gat gca act tca aac tta gac tcc tat gtt	816
Gln Ala His Asp Leu Phe Asp Ala Thr Ser Asn Leu Asp Ser Tyr Val	
260 265 270	
gcc ctg tct ggt tca tta aaa aat tta gca gtt aat cta tct aaa atg	864
Ala Leu Ser Gly Ser Leu Lys Asn Leu Ala Val Asn Leu Ser Lys Met	

PF59083SeqList PF59083.txt

275	280	285	
tct aat gat cta cgc tta ctc agt tct ggc cca cgt tcg gga tta cat			912
Ser Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Ser Gly Leu His			
290	295	300	
gaa att aac tta cct tca aaa caa gca ggt tca atc atg cct ggt			960
Glu Ile Asn Leu Pro Ser Lys Gln Ala Gly Ser Ser Ile Met Pro Gly			
305	310	315	
aaa gtt aat cca gtt att cca gaa gtt gtc aat caa gtc gcc ttt gaa			1008
Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Val Ala Phe Glu			
325	330	335	
atg att ggt ttt gat acc acc gtt acg gca agc gaa gct ggt caa			1056
Met Ile Gly Phe Asp Thr Thr Val Thr Ala Ala Ser Glu Ala Gly Gln			
340	345	350	
tta gaa ttg aat gca ttt gaa ccc att atc ttc aaa agc tta atc act			1104
Leu Glu Leu Asn Ala Phe Glu Pro Ile Ile Phe Lys Ser Leu Ile Thr			
355	360	365	
ggc att gaa cat ctc caa caa gct atg aat act cta cgc atc aat gcc			1152
Gly Ile Glu His Leu Gln Gln Ala Met Asn Thr Leu Arg Ile Asn Ala			
370	375	380	
att gac ggc att aca gta aac aaa cat cgc ttg tca caa gac att gat			1200
Ile Asp Gly Ile Thr Val Asn Lys His Arg Leu Ser Gln Asp Ile Asp			
385	390	395	
ttg tcg gtg agc ttt gca acc gcg atg gcg cca ata att ggc tac aaa			1248
Leu Ser Val Ser Phe Ala Thr Ala Met Ala Pro Ile Ile Gly Tyr Lys			
405	410	415	
gaa gcc gct aaa att gct aaa gaa tct ctg cgc act gga aaa tct ttg			1296
Glu Ala Ala Lys Ile Ala Lys Glu Ser Leu Arg Thr Gly Lys Ser Leu			
420	425	430	
cgt gaa atc gct gaa aag aaa aat aga ttt act gaa agt gaa ttg gca			1344
Arg Glu Ile Ala Glu Lys Lys Asn Arg Phe Thr Glu Ser Glu Leu Ala			
435	440	445	
cat att ttc aag gtt gaa gat atc gtt att aat gct cga aca cca gag			1392
His Ile Phe Lys Val Glu Asp Ile Val Ile Asn Ala Arg Thr Pro Glu			
450	455	460	
cat ggt cta gta ctg cac gcg cca aaa aca aca gta taa			1431
His Gly Leu Val Leu His Ala Pro Lys Thr Thr Val			
465	470	475	

<210> 9714

<211> 476

<212> PRT

<213> Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293

<400> 9714

Met Arg Thr Glu Ser Asp Ser Leu Gly Gln Ile Asn Val Pro Lys Asp	
1 5 10 15	
Val Tyr Tyr Gly Ala His Thr Gln Arg Ala Leu Asn Asn Phe Pro Ile	
20 25 30	
Ser Lys Glu Thr Thr His Pro Glu Ile Ile Arg Ala Phe Leu Glu Ile	
35 40 45	
Lys Gln Ala Ala Ala Gln Thr Asn Ala Thr Ser Gly Asn Leu Asp Arg	
50 55 60	
Ala Val Ala Lys His Ile Val Asp Ala Thr Lys Ile Leu Leu Ser Gln	
65 70 75 80	
Pro Ile Asp Leu Thr Met Phe Pro Ile Ser Asp Val Gln Gly Gly Ala	
85 90 95	
Gly Thr Ser Thr Asn Met Asn Val Asn Glu Val Val Ala Asn Thr Ala	
100 105 110	
Leu Glu Gln Val Gly Arg Ala Arg Gly Glu Tyr Gly Tyr Val Asn Pro	
115 120 125	
Asn Asp His Val Asn Met Gly Gln Ser Thr Asn Asp Thr Tyr Pro Ser	
130 135 140	
Ala Gly Lys Ile Ala Leu Ile Arg Leu Leu Glu Pro Leu Phe Ser Glu	
145 150 155 160	
Leu Thr Leu Leu Val Asp Ala Leu Gly Asn Lys Ala Asp Glu Phe Ser	
165 170 175	
Thr Thr Tyr Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met	
180 185 190	
Thr Leu Gly Asn Thr Phe His Ala Trp Leu Lys Pro Leu Arg Arg Asp	

PF59083SeqList PF59083.txt

	195					200				205					
Phe	Lys	Arg	Ile	Glu	Ala	Ala	Arg	Asn	Glu	Leu	Tyr	Thr	Leu	Asn	Leu
	210					215					220				
Gly	Gly	Ser	Ala	Ile	Gly	Ser	Gly	Ile	Asn	Val	Ser	Tyr	His	Tyr	Gln
225					230					235					240
Val	His	Ile	Val	Pro	Asn	Leu	Ala	Ser	Ile	Thr	Gly	Leu	Pro	Leu	Glu
				245					250					255	
Gln	Ala	His	Asp	Leu	Phe	Asp	Ala	Thr	Ser	Asn	Leu	Asp	Ser	Tyr	Val
			260					265					270		
Ala	Leu	Ser	Gly	Ser	Leu	Lys	Asn	Leu	Ala	Val	Asn	Leu	Ser	Lys	Met
			275				280					285			
Ser	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Ser	Gly	Leu	His
	290					295					300				
Glu	Ile	Asn	Leu	Pro	Ser	Lys	Gln	Ala	Gly	Ser	Ser	Ile	Met	Pro	Gly
305					310					315					320
Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln	Val	Ala	Phe	Glu
				325					330					335	
Met	Ile	Gly	Phe	Asp	Thr	Thr	Val	Thr	Ala	Ala	Ser	Glu	Ala	Gly	Gln
			340					345					350		
Leu	Glu	Leu	Asn	Ala	Phe	Glu	Pro	Ile	Ile	Phe	Lys	Ser	Leu	Ile	Thr
		355					360					365			
Gly	Ile	Glu	His	Leu	Gln	Gln	Ala	Met	Asn	Thr	Leu	Arg	Ile	Asn	Ala
	370					375					380				
Ile	Asp	Gly	Ile	Thr	Val	Asn	Lys	His	Arg	Leu	Ser	Gln	Asp	Ile	Asp
385					390					395					400
Leu	Ser	Val	Ser	Phe	Ala	Thr	Ala	Met	Ala	Pro	Ile	Ile	Gly	Tyr	Lys
				405					410					415	
Glu	Ala	Ala	Lys	Ile	Ala	Lys	Glu	Ser	Leu	Arg	Thr	Gly	Lys	Ser	Leu
			420					425					430		
Arg	Glu	Ile	Ala	Glu	Lys	Lys	Asn	Arg	Phe	Thr	Glu	Ser	Glu	Leu	Ala
		435					440					445			
His	Ile	Phe	Lys	Val	Glu	Asp	Ile	Val	Ile	Asn	Ala	Arg	Thr	Pro	Glu
	450					455					460				
His	Gly	Leu	Val	Leu	His	Ala	Pro	Lys	Thr	Thr	Val				
465					470					475					

<210> 9715
 <211> 1422
 <212> DNA
 <213> Mycobacterium smegmatis str. MC2 155

<220>
 <221> CDS
 <222> (1)..(1422)
 <223> transl_table=11

<400> 9715	
gtg acg ccg gtg cag tca ttc cgt acc gaa cac gat ctg ctc ggt gac	48
Met Thr Pro Val Gln Ser Phe Arg Thr Glu His Asp Leu Leu Gly Asp	
1 5 10 15	
ctc gag gta ccg gcc gat gtc tac tac ggc gtg cac acc gcg cgc gca	96
Leu Glu Val Pro Ala Asp Val Tyr Tyr Gly Val His Thr Ala Arg Ala	
20 25 30	
ctg ctg aac ttt ccg atc agc gga atg ccc ata tcg cgc cat cct gac	144
Leu Leu Asn Phe Pro Ile Ser Gly Met Pro Ile Ser Arg His Pro Asp	
35 40 45	
ctg gtg gtc gcg ctc gcc tcg gtg aaa cag gcg gca gcc gaa gcg aat	192
Leu Val Val Ala Leu Ala Ser Val Lys Gln Ala Ala Ala Glu Ala Asn	
50 55 60	
cgt caa ctc ggc cag ctc gac tcc act atc gcc ggc gcg atc atc acc	240
Arg Gln Leu Gly Gln Leu Asp Ser Thr Ile Ala Gly Ala Ile Ile Thr	
65 70 75 80	
gcc tgc acc gag att cgc gac ggg gcc ctg cgc gag cag ttc gtc gtc	288
Ala Cys Thr Glu Ile Arg Asp Gly Ala Leu Arg Glu Gln Phe Val Val	
85 90 95	
gac cag att cag ggc ggg gca ggc acg tcg acc aac atg aac gcc aac	336
Asp Gln Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn	
100 105 110	
gag gtg atc gcc aac cgt gcc tgc gag ctc ctc gga cat cag cgc ggc	384

PF59083SeqList PF59083.txt																
Glu	Val	Ile	Ala	Asn	Arg	Ala	Cys	Glu	Leu	Leu	Gly	His	Gln	Arg	Gly	
tcc	tac	gac	gtc	gta	cat	ccc	ctt	gag	cac	gtc	aac	ctc	gga	cag	agc	432
Ser	Tyr	Asp	Val	Val	His	Pro	Leu	Glu	His	Val	Asn	Leu	Gly	Gln	Ser	
130						135					140					
acc	aac	gac	gtc	tac	ccg	acg	gcg	ctc	aag	atc	gca	ctc	gga	act	gcg	480
Thr	Asn	Asp	Val	Tyr	Pro	Thr	Ala	Leu	Lys	Ile	Ala	Leu	Gly	Thr	Ala	
145					150					155					160	
acc	cg	acg	ctc	gaa	cag	gcc	ttg	cg	cg	ctc	gcc	gat	cac	tgc	agc	528
Thr	Arg	Thr	Leu	Glu	Gln	Ala	Leu	Arg	Arg	Leu	Ala	Asp	His	Cys	Ser	
				165					170					175		
acc	aag	tcg	ctc	gaa	ttc	gcc	gac	atg	ctc	aaa	ctc	ggc	cgt	acg	cag	576
Thr	Lys	Ser	Leu	Glu	Phe	Ala	Asp	Met	Leu	Lys	Leu	Gly	Arg	Thr	Gln	
			180					185					190			
ttg	cag	gac	gcg	gtt	ccg	atg	aca	ctc	gg	cag	gaa	ttc	ggg	gcc	ttc	624
Leu	Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Gly	Ala	Phe	
						200						205				
gcg	gtg	acc	att	ctc	gaa	gac	gcc	gac	cg	ctc	gg	gaa	gtg	tca	gcg	672
Ala	Val	Thr	Ile	Leu	Glu	Asp	Ala	Asp	Arg	Leu	Gly	Glu	Val	Ser	Ala	
	210					215					220					
ctc	atc	gcc	gag	atc	aac	ctc	ggc	ggg	acc	gcc	atc	ggc	acg	gga	ctc	720
Leu	Ile	Ala	Glu	Ile	Asn	Leu	Gly	Gly	Thr	Ala	Ile	Gly	Thr	Gly	Leu	
225					230					235					240	
aac	acc	cat	ccg	gaa	tat	gcg	gca	ctg	gtg	tgc	gat	cac	ctg	cg	gcc	768
Asn	Thr	His	Pro	Glu	Tyr	Ala	Ala	Leu	Val	Cys	Asp	His	Leu	Arg	Ala	
				245					250					255		
gtc	acc	ggc	ctg	ccg	ctc	acc	acc	gcg	ggc	aac	ctc	gtg	gag	gcg	acc	816
Val	Thr	Gly	Leu	Pro	Leu	Thr	Thr	Ala	Gly	Asn	Leu	Val	Glu	Ala	Thr	
			260					265					270			
tcc	gac	gtc	ggc	gcg	ttc	gtc	caa	ctg	tcc	gg	gtc	gcg	aaa	cg	agc	864
Ser	Asp	Val	Gly	Ala	Phe	Val	Gln	Leu	Ser	Gly	Val	Ala	Lys	Arg	Ser	
			275				280					285				
gcg	gtg	aaa	ctg	tcg	aag	atc	tgc	aat	gac	cta	cg	ctg	ctc	tcg	tcg	912
Ala	Val	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	
						295				300						
ggc	cca	cg	gcc	gg	ttc	ggc	gag	atc	aac	ctt	ccg	cct	gtg	cag	gcc	960
Gly	Pro	Arg	Ala	Gly	Phe	Gly	Glu	Ile	Asn	Leu	Pro	Pro	Val	Gln	Ala	
305					310					315					320	
ggg	tcg	agc	atc	atg	ccc	ggc	aag	gtg	aat	ccc	gtc	atc	cct	gaa	gtc	1008
Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	
				325					330					335		
gtc	aac	cag	gtc	gcc	ttc	gag	gtg	atc	ggc	aac	gat	ctc	acc	gtc	acc	1056
Val	Asn	Gln	Val	Ala	Phe	Glu	Val	Ile	Gly	Asn	Asp	Leu	Thr	Val	Thr	
			340					345					350			
atg	gcc	gcc	gag	gcc	gga	cag	ttg	cag	ctc	aac	gcg	ttc	gag	ccg	atc	1104
Met	Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Ala	Phe	Glu	Pro	Ile	
			355				360					365				
atc	gcc	cg	gct	ctg	ttg	tca	tcg	atc	aac	cac	ctg	gcc	gcg	gcg	gtc	1152
Ile	Ala	Arg	Ala	Leu	Leu	Ser	Ser	Ile	Asn	His	Leu	Ala	Ala	Ala	Val	
			370			375					380					
aat	gtc	cta	gg	gaa	cg	tgt	atc	gag	ggc	atc	acg	gcc	aac	acc	gat	1200
Asn	Val	Leu	Gly	Glu	Arg	Cys	Ile	Glu	Gly	Ile	Thr	Ala	Asn	Thr	Asp	
385					390					395					400	
cac	atg	cg	gac	gcg	gtt	ctg	aga	tcg	gcg	agt	ctg	gcc	acc	gcg	ctc	1248
His	Met	Arg	Asp	Ala	Val	Leu	Arg	Ser	Ala	Ser	Leu	Ala	Thr	Ala	Leu	
				405					410					415		
aac	ccc	gtg	ctc	gg	tac	gag	gcg	gcg	acc	gca	ttg	gtc	gcc	gaa	gcc	1296
Asn	Pro	Val	Leu	Gly	Tyr	Glu	Ala	Ala	Thr	Ala	Leu	Val	Ala	Glu	Ala	
			420					425					430			
atc	gcg	acc	ggc	gaa	tcg	atc	ccc	gag	atg	gtg	ctg	cg	tgc	gca	ctg	1344
Ile	Ala	Thr	Gly	Glu	Ser	Ile	Pro	Glu	Met	Val	Leu	Arg	Cys	Ala	Leu	
			435				440					445				
gtg	gac	gag	gcg	gtg	ctc	gcc	cg	gtg	ctg	agc	ccg	gag	aac	ctg	tgc	1392
Val	Asp	Glu	Ala	Val	Leu	Ala	Arg	Val	Leu	Ser	Pro	Glu	Asn	Leu	Cys	
			450			455					460					
gga	ctc	agc	ggg	tcc	gag	agg	gct	agg	tag							1422
Gly	Leu	Ser	Gly	Ser	Glu	Arg	Ala	Arg								
465					470											

PF59083SeqList PF59083.txt

<210> 9716

<211> 473

<212> PRT

<213> Mycobacterium smegmatis str. MC2 155

<400> 9716

```

Met Thr Pro Val Gln Ser Phe Arg Thr Glu His Asp Leu Leu Gly Asp
1      5      10      15
Leu Glu Val Pro Ala Asp Val Tyr Tyr Gly Val His Thr Ala Arg Ala
      20      25      30
Leu Leu Asn Phe Pro Ile Ser Gly Met Pro Ile Ser Arg His Pro Asp
      35      40      45
Leu Val Val Ala Leu Ala Ser Val Lys Gln Ala Ala Ala Glu Ala Asn
      50      55      60
Arg Gln Leu Gly Gln Leu Asp Ser Thr Ile Ala Gly Ala Ile Ile Thr
65      70      75      80
Ala Cys Thr Glu Ile Arg Asp Gly Ala Leu Arg Glu Gln Phe Val Val
      85      90      95
Asp Gln Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn
      100      105      110
Glu Val Ile Ala Asn Arg Ala Cys Glu Leu Leu Gly His Gln Arg Gly
      115      120      125
Ser Tyr Asp Val Val His Pro Leu Glu His Val Asn Leu Gly Gln Ser
130      135      140
Thr Asn Asp Val Tyr Pro Thr Ala Leu Lys Ile Ala Leu Gly Thr Ala
145      150      155      160
Thr Arg Thr Leu Glu Gln Ala Leu Arg Arg Leu Ala Asp His Cys Ser
      165      170      175
Thr Lys Ser Leu Glu Phe Ala Asp Met Leu Lys Leu Gly Arg Thr Gln
      180      185      190
Leu Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Gly Ala Phe
      195      200      205
Ala Val Thr Ile Leu Glu Asp Ala Asp Arg Leu Gly Glu Val Ser Ala
210      215      220
Leu Ile Ala Glu Ile Asn Leu Gly Gly Thr Ala Ile Gly Thr Gly Leu
225      230      235      240
Asn Thr His Pro Glu Tyr Ala Ala Leu Val Cys Asp His Leu Arg Ala
      245      250      255
Val Thr Gly Leu Pro Leu Thr Thr Ala Gly Asn Leu Val Glu Ala Thr
      260      265      270
Ser Asp Val Gly Ala Phe Val Gln Leu Ser Gly Val Ala Lys Arg Ser
      275      280      285
Ala Val Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser
290      295      300
Gly Pro Arg Ala Gly Phe Gly Glu Ile Asn Leu Pro Pro Val Gln Ala
305      310      315      320
Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Val
      325      330      335
Val Asn Gln Val Ala Phe Glu Val Ile Gly Asn Asp Leu Thr Val Thr
      340      345      350
Met Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Ala Phe Glu Pro Ile
      355      360      365
Ile Ala Arg Ala Leu Leu Ser Ser Ile Asn His Leu Ala Ala Ala Val
370      375      380
Asn Val Leu Gly Glu Arg Cys Ile Glu Gly Ile Thr Ala Asn Thr Asp
385      390      395      400
His Met Arg Asp Ala Val Leu Arg Ser Ala Ser Leu Ala Thr Ala Leu
      405      410      415
Asn Pro Val Leu Gly Tyr Glu Ala Ala Thr Ala Leu Val Ala Glu Ala
      420      425      430
Ile Ala Thr Gly Glu Ser Ile Pro Glu Met Val Leu Arg Cys Ala Leu
      435      440      445
Val Asp Glu Ala Val Leu Ala Arg Val Leu Ser Pro Glu Asn Leu Cys
450      455      460
Gly Leu Ser Gly Ser Glu Arg Ala Arg
465      470

```

<210> 9717

<211> 1422

PF59083SeqList PF59083.txt

<212> DNA

<213> Nostoc punctiforme PCC 73102

<220>

<221> CDS

<222> (1)..(1422)

<223> transl_table=11

<400> 9717

atg act gaa cac aca gac tct caa ttc cgc atc gaa cgc gat tcg atg	48
Met Thr Glu His Thr Asp Ser Gln Phe Arg Ile Glu Arg Asp Ser Met	
1 5 10 15	
ggc gat cgc caa att gct agt agc ttt tat tac ggc att caa acg cta	96
Gly Asp Arg Gln Ile Ala Ser Ser Phe Tyr Tyr Gly Ile Gln Thr Leu	
20 25 30	
cgg gcg atc gaa aac ttt cct att agt ggc att aag cct tta gct act	144
Arg Ala Ile Glu Asn Phe Pro Ile Ser Gly Ile Lys Pro Leu Ala Thr	
35 40 45	
tac gta gat gct gga tta atc att aaa aaa gct aca gca att gtc aat	192
Tyr Val Asp Ala Gly Leu Ile Ile Lys Lys Ala Thr Ala Ile Val Asn	
50 55 60	
gga gaa ctg aat tgt att ccc gaa gat att agt cag gcg att gtc caa	240
Gly Glu Leu Asn Cys Ile Pro Glu Asp Ile Ser Gln Ala Ile Val Gln	
65 70 75 80	
gca act gat gaa atc ctg gct ggg aag ttc cgg gat cag ttt gtc gtg	288
Ala Thr Asp Glu Ile Leu Ala Gly Lys Phe Arg Asp Gln Phe Val Val	
85 90 95	
gat gtt tat cag gca ggt gct gga aca tcc cac cac atg aat gtc aac	336
Asp Val Tyr Gln Ala Gly Ala Gly Thr Ser His His Met Asn Val Asn	
100 105 110	
gaa gtt ctg gca aat cgc gcc tta gaa att ctg ggt gaa gaa aag ggc	384
Glu Val Leu Ala Asn Arg Ala Leu Glu Ile Leu Gly Glu Glu Lys Gly	
115 120 125	
aat tac aaa cgt gtt agt cct aac gat cac gtt aac tat ggg cag tct	432
Asn Tyr Lys Arg Val Ser Pro Asn Asp His Val Asn Tyr Gly Gln Ser	
130 135 140	
acc aat gat gtg att cct act gcc att cgg att ggt ggt tta ttg gca	480
Thr Asn Asp Val Ile Pro Thr Ala Ile Arg Ile Gly Gly Leu Leu Ala	
145 150 155 160	
tta tcc aag aca tta cca gca ata gaa ggt gcg atc gca tcc tta	528
Leu Ser Lys Thr Leu His Pro Ala Ile Glu Gly Ala Ile Ala Ser Leu	
165 170 175	
gaa aac aaa gct gta gaa ttt caa gat att gtc aaa tct ggc aga acc	576
Glu Asn Lys Ala Val Glu Phe Gln Asp Ile Val Lys Ser Gly Arg Thr	
180 185 190	
cac tta caa gac gct gta ccc gtg cgt ttg ggt gaa aat ttt cgc gct	624
His Leu Gln Asp Ala Val Pro Val Arg Leu Gly Glu Asn Phe Arg Ala	
195 200 205	
tgg gcg cac att ctt aca gaa cac caa aac cgg att tac acc gcc tct	672
Trp Ala His Ile Leu Thr Glu His Gln Asn Arg Ile Tyr Thr Ala Ser	
210 215 220	
gga gat ttg atg gtg ctg ggt ttg gga ggt agt gca gca gga acc ggt	720
Gly Asp Leu Met Val Leu Gly Leu Gly Gly Ser Ala Ala Gly Thr Gly	
225 230 235 240	
tta aat act cat cct cta tat cgc gcc cgt gta gaa gtt ctt tca	768
Leu Asn Thr His Pro Leu Tyr Arg Ala Arg Val Val Glu Val Leu Ser	
245 250 255	
gaa ttg att gat aca cct tta gaa cct gcg ccc cat ctc atg gca gct	816
Glu Leu Ile Asp Thr Pro Leu Glu Pro Ala Pro His Leu Met Ala Ala	
260 265 270	
atg cag agt atg gct cca ttt gta aat gtt tcc ggt gct tta cgc aat	864
Met Gln Ser Met Ala Pro Phe Val Asn Val Ser Gly Ala Leu Arg Asn	
275 280 285	
tta gcg cag gat tta gtc aaa ata tct cat gac ttg cgg ctg atg gat	912
Leu Ala Gln Asp Leu Val Lys Ile Ser His Asp Leu Arg Leu Met Asp	
290 295 300 305	
tcg gga cca aaa act ggt ttg aaa gaa atc caa ctt ccc cca gtg caa	960
Ser Gly Pro Lys Thr Gly Leu Lys Glu Ile Gln Leu Pro Pro Val Gln	
310 315 320	

PF59083SeqList PF59083.txt

ccc	ggt	tcc	tcg	att	atg	cca	ggg	aaa	tat	aac	cca	gtc	atg	gca	gag	1008
Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Tyr	Asn	Pro	Val	Met	Ala	Glu	
				325					330					335		
atg	aca	tca	atg	gtg	tgt	ttt	cag	gtg	atg	ggt	tat	gac	agt	gcg	atc	1056
Met	Thr	Ser	Met	Val	Cys	Phe	Gln	Val	Met	Gly	Tyr	Asp	Ser	Ala	Ile	
			340					345					350			
aca	tta	gcc	gca	caa	gcc	gga	caa	tta	gaa	tta	aat	gtg	atg	atg	ccg	1104
Thr	Leu	Ala	Ala	Gln	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Met	Pro	
		355				360					365					
cta	att	gcc	tat	aac	ttg	att	cac	agt	atc	gaa	att	ctc	ggc	aat	acc	1152
Leu	Ile	Ala	Tyr	Asn	Leu	Ile	His	Ser	Ile	Glu	Ile	Leu	Gly	Asn	Thr	
	370				375						380					
atc	gct	gca	ctc	acc	gaa	cgc	tgc	atc	gag	gga	att	act	gca	aat	caa	1200
Ile	Ala	Ala	Leu	Thr	Glu	Arg	Cys	Ile	Glu	Gly	Ile	Thr	Ala	Asn	Gln	
	385				390					395					400	
gaa	cgt	tgt	tta	gct	tat	gcc	gaa	ggc	agt	tta	gct	tta	gta	acc	gca	1248
Glu	Arg	Cys	Leu	Ala	Tyr	Ala	Glu	Gly	Ser	Leu	Ala	Leu	Val	Thr	Ala	
			405					410						415		
cta	aac	acc	cac	att	ggt	tat	tta	aac	gct	gct	gct	gtc	gcc	aaa	gaa	1296
Leu	Asn	Thr	His	Ile	Gly	Tyr	Leu	Asn	Ala	Ala	Ala	Val	Ala	Lys	Glu	
			420				425						430			
tct	tta	gaa	act	ggt	aaa	tcc	ctg	cgg	caa	att	gtt	cta	gaa	cgg	gga	1344
Ser	Leu	Glu	Thr	Gly	Lys	Ser	Leu	Arg	Gln	Ile	Val	Leu	Glu	Arg	Gly	
		435				440					445					
tta	atg	agt	gaa	aca	gac	tta	gcc	aca	gtg	tta	aat	cta	gaa	cac	atg	1392
Leu	Met	Ser	Glu	Thr	Asp	Leu	Ala	Thr	Val	Leu	Asn	Leu	Glu	His	Met	
	450					455					460					
agt	ggt	atc	tta	ccg	ctc	aaa	aca	gaa	taa							1422
Ser	Gly	Ile	Leu	Pro	Leu	Lys	Thr	Glu								
465					470											

<210> 9718

<211> 473

<212> PRT

<213> Nostoc punctiforme PCC 73102

<400> 9718

Met	Thr	Glu	His	Thr	Asp	Ser	Gln	Phe	Arg	Ile	Glu	Arg	Asp	Ser	Met	
1				5					10					15		
Gly	Asp	Arg	Gln	Ile	Ala	Ser	Ser	Phe	Tyr	Tyr	Gly	Ile	Gln	Thr	Leu	
			20					25					30			
Arg	Ala	Ile	Glu	Asn	Phe	Pro	Ile	Ser	Gly	Ile	Lys	Pro	Leu	Ala	Thr	
		35				40						45				
Tyr	Val	Asp	Ala	Gly	Leu	Ile	Ile	Lys	Lys	Ala	Thr	Ala	Ile	Val	Asn	
	50					55					60					
Gly	Glu	Leu	Asn	Cys	Ile	Pro	Glu	Asp	Ile	Ser	Gln	Ala	Ile	Val	Gln	
65					70					75					80	
Ala	Thr	Asp	Glu	Ile	Leu	Ala	Gly	Lys	Phe	Arg	Asp	Gln	Phe	Val	Val	
			85						90					95		
Asp	Val	Tyr	Gln	Ala	Gly	Ala	Gly	Thr	Ser	His	His	Met	Asn	Val	Asn	
			100					105					110			
Glu	Val	Leu	Ala	Asn	Arg	Ala	Leu	Glu	Ile	Leu	Gly	Glu	Glu	Lys	Gly	
		115				120						125				
Asn	Tyr	Lys	Arg	Val	Ser	Pro	Asn	Asp	His	Val	Asn	Tyr	Gly	Gln	Ser	
	130					135					140					
Thr	Asn	Asp	Val	Ile	Pro	Thr	Ala	Ile	Arg	Ile	Gly	Gly	Leu	Leu	Ala	
145					150					155					160	
Leu	Ser	Lys	Thr	Leu	His	Pro	Ala	Ile	Glu	Gly	Ala	Ile	Ala	Ser	Leu	
			165					170						175		
Glu	Asn	Lys	Ala	Val	Glu	Phe	Gln	Asp	Ile	Val	Lys	Ser	Gly	Arg	Thr	
		180						185					190			
His	Leu	Gln	Asp	Ala	Val	Pro	Val	Arg	Leu	Gly	Glu	Asn	Phe	Arg	Ala	
		195				200						205				
Trp	Ala	His	Ile	Leu	Thr	Glu	His	Gln	Asn	Arg	Ile	Tyr	Thr	Ala	Ser	
	210					215					220					
Gly	Asp	Leu	Met	Val	Leu	Gly	Leu	Gly	Gly	Ser	Ala	Ala	Gly	Thr	Gly	
225					230					235					240	
Leu	Asn	Thr	His	Pro	Leu	Tyr	Arg	Ala	Arg	Val	Val	Glu	Val	Leu	Ser	
				245					250					255		

PF59083SeqList PF59083.txt

Glu Leu Ile Asp Thr Pro Leu Glu Pro Ala Pro His Leu Met Ala Ala
 260 265 270
 Met Gln Ser Met Ala Pro Phe Val Asn Val Ser Gly Ala Leu Arg Asn
 275 280 285
 Leu Ala Gln Asp Leu Val Lys Ile Ser His Asp Leu Arg Leu Met Asp
 290 295 300
 Ser Gly Pro Lys Thr Gly Leu Lys Glu Ile Gln Leu Pro Pro Val Gln
 305 310 315 320
 Pro Gly Ser Ser Ile Met Pro Gly Lys Tyr Asn Pro Val Met Ala Glu
 325 330 335
 Met Thr Ser Met Val Cys Phe Gln Val Met Gly Tyr Asp Ser Ala Ile
 340 345 350
 Thr Leu Ala Ala Gln Ala Gly Gln Leu Glu Leu Asn Val Met Met Pro
 355 360 365
 Leu Ile Ala Tyr Asn Leu Ile His Ser Ile Glu Ile Leu Gly Asn Thr
 370 375 380
 Ile Ala Ala Leu Thr Glu Arg Cys Ile Glu Gly Ile Thr Ala Asn Gln
 385 390 395 400
 Glu Arg Cys Leu Ala Tyr Ala Glu Gly Ser Leu Ala Leu Val Thr Ala
 405 410 415
 Leu Asn Thr His Ile Gly Tyr Leu Asn Ala Ala Val Ala Lys Glu
 420 425 430
 Ser Leu Glu Thr Gly Lys Ser Leu Arg Gln Ile Val Leu Glu Arg Gly
 435 440 445
 Leu Met Ser Glu Thr Asp Leu Ala Thr Val Leu Asn Leu Glu His Met
 450 455 460
 Ser Gly Ile Leu Pro Leu Lys Thr Glu
 465 470

<210> 9719

<211> 1434

<212> DNA

<213> Bifidobacterium longum DJ010A

<220>

<221> CDS

<222> (1)..(1434)

<223> transl_table=11

<400> 9719

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

PF59083SeqList PF59083.txt

145		150		155		160	
gcg atc ggg ccg ctc gcc gag tcc acc aag aaa ctc gcc aag gcc ttc	528						
Ala Ile Gly Pro Leu Ala Glu Ser Thr Lys Lys Leu Ala Lys Ala Phe							
		165		170		175	
cac gat ctg gcc gac aaa cat atc aat gac gtg acg att ggc cgc acg	576						
His Asp Leu Ala Asp Lys His Ile Asn Asp Val Thr Ile Gly Arg Thr							
		180		185		190	
cag ctg cag gac gcc gta cca atg acc tat ggt cag gaa ttt cat gcg	624						
Gln Leu Gln Asp Ala Val Pro Met Thr Tyr Gly Gln Glu Phe His Ala							
		195		200		205	
ttt gcc acg ctg ttg aag tct gat ttg gct gca ttc gat cgc gtg gtg	672						
Phe Ala Thr Leu Leu Lys Ser Asp Leu Ala Ala Phe Asp Arg Val Val							
		210		215		220	
ccg ctg ctg gcc cag ctc aac ctc ggt gcc acc gcc atc ggt acc ggc	720						
Pro Leu Leu Ala Gln Leu Asn Leu Gly Ala Thr 235							
		230		235		240	
att tgc gcg gat ctg cga ttc cgc aag tcc gct atc aag cat ctg gcg	768						
Ile Cys Ala Asp Leu Arg Phe Arg Lys Ser Ala Ile Lys His Leu Ala							
		245		250		255	
cag atc acc ggc ttg ccg gtc acc gcc gcg ccc gat ccg gtg gcc gcc	816						
Gln Ile Thr Gly Leu Pro Val Thr Ala Ala Pro Asp Pro Val Ala Ala							
		260		265		270	
atg acg gat atg ggc gcg tac gtg gcc acc tcg gcc gcc atc aag agc	864						
Met Thr Asp Met Gly Ala Tyr Val Ala Thr Ser Ala Ala Ile Lys Ser							
		275		280		285	
ctc gcc gtg cac ctg aag aag gcc gcc gac gat ttg cga ctg ctc aat	912						
Leu Ala Val His Leu Lys Lys Ala Ala Asp Asp Leu Arg Leu Leu Asn							
		290		295		300	
tcc ggg ccg cgc tgc ggt ttc aac gat ctc aac gtg ccg gct cgc cag	960						
Ser Gly Pro Arg Cys Gly Phe Asn Asp Leu Asn Val Pro Ala Arg Gln							
		310		315		320	
gcc gga tcg tcg atc atg ccg gcc aaa gtg aac cct gtg atc ccc gaa	1008						
Ala Gly Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu							
		325		330		335	
tgc gtc aac cag tgc tgc ttc acg att ttc ggc atg gac gtg act gtg	1056						
Cys Val Asn Gln Cys Cys Phe Thr Ile Phe Gly Met Asp Val Thr Val							
		340		345		350	
aac tgg gct gtg gcc gag gga cag ttg cag ctg aac gcc ttc gac ccg	1104						
Asn Trp Ala Val Ala Glu Gly Gln Leu Gln Leu Asn Ala Phe Asp Pro							
		355		360		365	
gtg atg gtg cat gag ctg ctg acc ggc atg gcg ttg ctg acg cac gcc	1152						
Val Met Val His Glu Leu Leu Thr Gly Met Ala Leu Leu Thr His Ala							
		370		375		380	
atg gag acg ttc cgc gtc aac tgc gtg gaa ggc atc gaa atc aat gct	1200						
Met Glu Thr Phe Arg Val Asn Cys Val Glu Gly Ile Glu Ile Asn Ala							
		385		390		395	
gac ctg ggg cgt tca tac gcc cag tcc tca ccg tcg att tcc gcc gcg	1248						
Asp Leu Gly Arg Ser Tyr Ala Gln Ser Ser Pro Ser Ile Ser Ala Ala							
		405		410		415	
ctc aac cac tac atc ggc tac gag cac gcg gcc gac atc gcc gcc gaa	1296						
Leu Asn His Tyr Ile Gly Tyr Glu His Ala Ala Asp Ile Ala Ala Glu							
		420		425		430	
gcc gtg cac acc ggc cgt acc gtg cgc gag gtg gcc ggc gaa cgc acc	1344						
Ala Val His Thr Gly Arg Thr Val Arg Glu Val Ala Gly Glu Arg Thr							
		435		440		445	
gac ctg ccc gcc gag cag ttg gac gag att ctc gat ccg att cga ctg	1392						
Asp Leu Pro Ala Glu Gln Leu Asp Glu Ile Leu Asp Pro Ile Arg Leu							
		450		455		460	
gcc cgc ggc ctc ggc cag acc tgc cgc gag cac cag gag tag	1434						
Ala Arg Gly Leu Gly Gln Thr Cys Arg Glu His Glu Glu							
		465		470		475	

<210> 9720
 <211> 477
 <212> PRT
 <213> Bifidobacterium longum DJ010A

<400> 9720
 Met Ser Glu Thr Ser Asn Lys Thr Arg Leu Glu His Asp Cys Ile Gly
 Seite 10202

PF59083SeqList PF59083.txt

```

1          5          10          15
Gln Met Glu Val Pro Ala Asn Val Tyr Trp Gly Ile His Thr Gln Arg
Ala Ile Gly 20 Asn Phe Pro Val Ser 25 Gly Ile Thr Asp Ser 30 Gln His Pro
Glu Leu 35 Ile Arg Ala Tyr Ala 40 Thr Val Lys Arg Ala 45 Cys Ala Ile Ala
Asn Glu 50 Glu Leu Gly Leu 55 Ile Asp Pro Ala Lys 60 Ala Glu Ala Ile Arg
65 Ala Ala Cys Leu 70 Glu Ile Glu Ala Gly Lys 75 Leu Ala Asp Gln Phe 80 Pro
Val Asp Val 85 Met Gln Gly Gly Ala Gly Thr Ser Ser Asn Met Asn Met
Asn Glu 100 Val Ile Ala Asn Arg Ala 105 Leu Glu Ile Ala Gly Arg Gln Arg
115 Gly Asp Tyr Thr Tyr Ile His 120 Pro Asn Asp Asp Val 125 Asn Lys Ser Gln
130 Ser Thr Asn Asp Thr Tyr 135 Pro Ala Ala Cys Lys 140 Leu Ala Leu Ile Asp
145 Ala Ile Gly Pro Leu 150 Glu Ser Thr Lys 155 Leu Ala Lys Ala Phe
His Asp Leu 165 Ala Asp Lys His Ile Asn Asp Val Thr Ile Gly Arg Thr
Gln Leu 180 Gln Asp Ala Val Pro Met 185 Thr Tyr Gly Gln Glu Phe His Ala
195 Phe Ala 195 Thr Leu Leu Lys Ser 200 Asp Leu Ala Ala Phe 205 Asp Arg Val Val
210 Pro Leu Leu Ala Gln Leu 215 Asn Leu Gly Ala Thr 220 Ala Ile Gly Thr Gly
225 Ile Cys Ala Asp Leu 230 Phe Arg Lys Ser 235 Ala Ile Lys His Leu Ala
245 Gln Ile Thr Gly Leu Pro Val Thr 250 Ala Ala Pro Asp Pro Val Ala Ala
260 Met Thr Asp Met Gly Ala Tyr Val 265 Ala Thr Ser Ala Ala Ile Lys Ser
275 Leu Ala Val His Leu Lys Lys 280 Ala Ala Asp Asp Leu Arg Leu Leu Asn
290 Ser Gly Pro Arg Cys Gly 295 Phe Asn Asp Leu Asn Val Pro Ala Arg Gln
305 Ala Gly Ser Ser Ile 310 Met Pro Ala Lys Val 315 Asn Pro Val Ile Pro Glu
325 Cys Val Asn Gln Cys Cys Phe Thr Ile Phe Gly Met Asp Val Thr Val
340 Asn Trp Ala Val Ala Glu Gly Gln Leu Gln Leu Asn Ala Phe Asp Pro
355 Val Met Val His Glu Leu Leu Thr Gly Met Ala Leu Leu Thr His Ala
370 Met Glu Thr Phe Arg Val 375 Asn Cys Val Glu Gly Ile Glu Ile Asn Ala
385 Asp Leu Gly Arg Ser 390 Tyr Ala Gln Ser Ser 395 Pro Ser Ile Ser Ala Ala
405 Leu Asn His Tyr Ile Gly Tyr Glu His Ala Ala Asp Ile Ala Ala Glu
420 Ala Val His Thr Gly Arg Thr Val 425 Arg Glu Val Ala Gly Glu Arg Thr
435 Asp Leu Pro Ala Glu Gln Leu 440 Asp Glu Ile Leu Asp Pro Ile Arg Leu
450 Ala Arg Gly Leu Gly Gln Thr 455 Cys Arg Glu His 460 Gln Glu
465          470          475

```

<210> 9721
 <211> 1416
 <212> DNA
 <213> Haemophilus somnus 2336

<220>
 <221> CDS
 <222> (1)..(1416)
 <223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 9721
atg ata acg aga aaa gaa att gat ttg ctt ggt gaa cgt gac gtt cca      48
Met Ile Thr Arg Lys 5 Glu Ile Asp Leu Leu 10 Gly Glu Arg Asp Val 15 Pro
1
gct gat gcg tat tgg ggc att cat aca tta aga gcg gta gaa aat ttt      96
Ala Asp Ala Tyr Trp Gly Ile His Thr Leu Arg Ala Val Glu Asn Phe
20
aac att tct aat gta acg att tct gat gta cct gaa ttt gta cgt ggt      144
Asn Ile Ser Asn Val Thr Ile Ser Asp Val Pro Glu Phe Val Arg Gly
35
atg gtc atg gta aaa aaa gca acc gca ctt gca aat gga gaa ttg ggt      192
Met Val Met Val Lys Lys Ala Thr Ala Leu Ala Asn Gly Glu Leu Gly
50
gca att ccg gat aaa att gct cag gcg att gtg aaa gct tgt gat gcg      240
Ala Ile Pro Asp Lys Ile Ala Gln Ala Ile Val Lys Ala Cys Asp Ala
65
att tta att gat ggt aaa tgt atg gat caa ttt cct tca gat gta tat      288
Ile Leu Ile Asp Gly Lys Cys Met Asp Gln Phe Pro Ser Asp Val Tyr
85
caa ggt ggt gct ggt act tcc gta aat atg aat acc aac gaa gtg gtc      336
Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Val
100
gct aat tta gca tta gaa att tta ggt cat aag aaa ggg gaa tat gat      384
Ala Asn Leu Ala Leu Glu Ile Leu Gly His Lys Lys Gly Glu Tyr Asp
115
att tta gat ccg atg gat cat gtt aat gcc agc caa tct aca aat gat      432
Ile Leu Asp Pro Met Asp His Val Asn Ala Ser Gln Ser Thr Asn Asp
130
gct tat ccg aca ggt ttc cgc att gct gtt tat aac agt att atg aaa      480
Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Asn Ser Ile Met Lys
145
ctg gta act aaa gta ctt tat tta caa caa ggt ttt gaa aat aaa gca      528
Leu Val Thr Lys Val Leu Tyr Leu Gln Gln Gly Phe Glu Asn Lys Ala
165
aaa gag ttt tcg aat atc tta aaa atg gga cgt act caa tta caa gat      576
Lys Glu Phe Ser Asn Ile Leu Lys Met Gly Arg Thr Gln Leu Gln Asp
180
gca gtt cct atg act gtg ggg caa gaa ttt aaa gca ttt tct gta tta      624
Ala Val Pro Met Thr Val Gly Gln Glu Phe Lys Ala Phe Ser Val Leu
195
tta gat gaa gaa gtg cgt aat tta acc cgc acg gct gaa tta ctg tta      672
Leu Asp Glu Glu Val Arg Asn Leu Thr Arg Thr Ala Glu Leu Leu Leu
210
gaa gta aat ttg ggt gca aca gct atc ggt acc ggc tta aat act cct      720
Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr Pro
225
caa ggt tat tca gaa tta gtt gtt aag cgt tta tct gag gtt tca ggt      768
Gln Gly Tyr Ser Glu Leu Val Val Lys Arg Leu Ser Glu Val Ser Gly
245
tta cct tgt aca gtt gca cca aac tta att gaa gcc act tca gac tgt      816
Leu Pro Cys Thr Val Ala Pro Asn Leu Ile Glu Ala Thr Ser Asp Cys
260
ggt gct tat gtt atg gta cac ggt gcg tta aaa cgt act gcg gta aaa      864
Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Thr Ala Val Lys
275
tta tct aaa gta tgc aat gat tta cgt tta ctt tca tca ggt cca cgt      912
Leu Ser Lys Val Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg
290
gca ggt tta aat gaa att aat tta cct gag tta cag gct gga tct tca      960
Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly Ser Ser
305
att atg ccg gca aaa gtc aac ccg gtt gta cct gag gta gtc aac caa      1008
Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val Asn Gln
325
gtt tgt ttc aaa gtg att ggt aat gat act acc gta act ttt gca gct      1056
Val Cys Phe Lys Val Ile Gly Asn Asp Thr Thr Val Thr Phe Ala Ala
340
gaa gcg ggg caa ttg cag tta aat gtg atg gaa ccg gta att ggt caa      1104

```

PF59083SeqList PF59083.txt

Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile	Gly	Gln	
		355					360					365				
gcc	atg	ttt	gaa	agt	att	gaa	att	tta	acg	aat	gct	tgc	gtg	aat	tta	1152
Ala	Met	Phe	Glu	Ser	Ile	Glu	Ile	Leu	Thr	Asn	Ala	Cys	Val	Asn	Leu	
	370					375					380					
cgt	gat	aaa	tgt	att	gat	gga	att	act	gca	aat	aaa	gaa	att	tgt	gaa	1200
Arg	Asp	Lys	Cys	Ile	Asp	Gly	Ile	Thr	Ala	Asn	Lys	Glu	Ile	Cys	Glu	
385					390					395					400	
aat	tat	gtc	ttt	aat	tcc	atc	gga	atc	gta	act	tat	ttg	aat	ccg	ttt	1248
Asn	Tyr	Val	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	Pro	Phe	
				405					410					415		
att	ggc	cat	cat	aat	ggc	gat	ata	gta	ggc	aaa	aca	tgt	gct	aaa	aca	1296
Ile	Gly	His	His	Asn	Gly	Asp	Ile	Val	Gly	Lys	Thr	Cys	Ala	Lys	Thr	
			420				425						430			
gga	cgt	gga	gtg	cgt	gaa	gtt	gta	ctg	gaa	atg	ggc	tta	tta	aca	gaa	1344
Gly	Arg	Gly	Val	Arg	Glu	Val	Val	Leu	Glu	Met	Gly	Leu	Leu	Thr	Glu	
		435					440					445				
gag	cag	tta	gat	aat	att	ctt	tct	gtg	gag	aat	tta	atg	aac	cca	acc	1392
Glu	Gln	Leu	Asp	Asn	Ile	Leu	Ser	Val	Glu	Asn	Leu	Met	Asn	Pro	Thr	
	450					455					460					
tac	aaa	gct	aca	tta	cat	aag	taa									1416
Tyr	Lys	Ala	Thr	Leu	His	Lys										
465					470											

<210> 9722

<211> 471

<212> PRT

<213> Haemophilus somnus 2336

<400> 9722

Met	Ile	Thr	Arg	Lys	Glu	Ile	Asp	Leu	Leu	Gly	Glu	Arg	Asp	Val	Pro	
1				5					10					15		
Ala	Asp	Ala	Tyr	Trp	Gly	Ile	His	Thr	Leu	Arg	Ala	Val	Glu	Asn	Phe	
			20					25					30			
Asn	Ile	Ser	Asn	Val	Thr	Ile	Ser	Asp	Val	Pro	Glu	Phe	Val	Arg	Gly	
		35					40					45				
Met	Val	Met	Val	Lys	Lys	Ala	Thr	Ala	Leu	Ala	Asn	Gly	Glu	Leu	Gly	
	50					55					60					
Ala	Ile	Pro	Asp	Lys	Ile	Ala	Gln	Ala	Ile	Val	Lys	Ala	Cys	Asp	Ala	
65					70					75					80	
Ile	Leu	Ile	Asp	Gly	Lys	Cys	Met	Asp	Gln	Phe	Pro	Ser	Asp	Val	Tyr	
			85						90					95		
Gln	Gly	Gly	Ala	Gly	Thr	Ser	Val	Asn	Met	Asn	Thr	Asn	Glu	Val	Val	
			100					105					110			
Ala	Asn	Leu	Ala	Leu	Glu	Ile	Leu	Gly	His	Lys	Lys	Gly	Glu	Tyr	Asp	
		115					120					125				
Ile	Leu	Asp	Pro	Met	Asp	His	Val	Asn	Ala	Ser	Gln	Ser	Thr	Asn	Asp	
	130					135					140					
Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Ile	Ala	Val	Tyr	Asn	Ser	Ile	Met	Lys	
145					150					155					160	
Leu	Val	Thr	Lys	Val	Leu	Tyr	Leu	Gln	Gln	Gly	Phe	Glu	Asn	Lys	Ala	
			165					170						175		
Lys	Glu	Phe	Ser	Asn	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	Asp	
			180					185					190			
Ala	Val	Pro	Met	Thr	Val	Gly	Gln	Glu	Phe	Lys	Ala	Phe	Ser	Val	Leu	
		195					200					205				
Leu	Asp	Glu	Glu	Val	Arg	Asn	Leu	Thr	Arg	Thr	Ala	Glu	Leu	Leu	Leu	
	210					215					220					
Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Leu	Asn	Thr	Pro	
225					230					235					240	
Gln	Gly	Tyr	Ser	Glu	Leu	Val	Val	Lys	Arg	Leu	Ser	Glu	Val	Ser	Gly	
			245					250						255		
Leu	Pro	Cys	Thr	Val	Ala	Pro	Asn	Leu	Ile	Glu	Ala	Thr	Ser	Asp	Cys	
			260					265					270			
Gly	Ala	Tyr	Val	Met	Val	His	Gly	Ala	Leu	Lys	Arg	Thr	Ala	Val	Lys	
		275					280					285				
Leu	Ser	Lys	Val	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	
	290					295					300					
Ala	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	Ala	Gly	Ser	Ser	

PF59083SeqList PF59083.txt

```

305                               310                               315                               320
Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val Asn Gln
Val Cys Phe Lys Val Ile Gly Asn Asp Thr Thr Val Thr Phe Ala Ala
Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Gln
Ala Met Phe Glu Ser Ile Glu Ile Leu Thr Asn Ala Cys Val Asn Leu
Arg Asp Lys Cys Ile Asp Gly Ile Thr Ala Asn Lys Glu Ile Cys Glu
Asn Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro Phe
Ile Gly His His Asn Gly Asp Ile Val Gly Lys Thr Cys Ala Lys Thr
Gly Arg Gly Val Arg Glu Val Val Glu Met Gly Leu Leu Thr Glu
Glu Gln Leu Asp Asn Ile Leu Ser Val Glu Asn Leu Met Asn Pro Thr
Tyr Lys Ala Thr Leu His Lys
465                               470

```

<210> 9723
 <211> 1419
 <212> DNA
 <213> Haemophilus influenzae R2846

<220>
 <221> CDS
 <222> (1)..(1419)
 <223> transl_table=11

```

<400> 9723
atg act caa ttt aga aaa gaa gta gat tta ctc ggc gaa cgt gat gtg      48
Met Thr Gln Phe Arg Lys Glu Val Asp Leu Leu Gly Glu Arg Asp Val
1                               5                               10                               15
cct gca gaa gca tat tgg ggg att cat aca tta aga gcg gta gaa aat      96
Pro Ala Glu Ala Tyr Trp Gly Ile His Thr Leu Arg Ala Val Glu Asn
20                               25                               30
ttt aat att tct aac gta acc att tct gac gta cca gag ttt gta cgt      144
Phe Asn Ile Ser Asn Val Thr Ile Ser Asp Val Pro Glu Phe Val Arg
35                               40                               45
ggt atg gta atg gta aaa aaa gca acg gct tta gcc aat ggc gaa tta      192
Gly Met Val Met Val Lys Lys Ala Thr Ala Leu Ala Asn Gly Glu Leu
50                               55                               60
ggt gca att cca agt gat att gca aaa gcg att gta gca gct tgt gat      240
Gly Ala Ile Pro Ser Asp Ile Ala Lys Ala Ile Val Ala Ala Cys Asp
65                               70                               75                               80
gaa atc ctt acc act gga aaa tgc tta gat caa ttc cca tca gat gta      288
Glu Ile Leu Thr Thr Gly Lys Cys Leu Asp Gln Phe Pro Ser Asp Val
85                               90                               95
tat caa ggt ggt gca ggt acc tca gtg aat atg aat acc aat gaa gtt      336
Tyr Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val
100                               105                               110
gtg gcg aat ttg gcg tta gag tta tta gga cat aag aaa ggg gaa tac      384
Val Ala Asn Leu Ala Leu Glu Leu Leu Gly His Lys Lys Gly Glu Tyr
115                               120                               125
caa tat tta gat cca atg gat cat gtt aac gct agc caa tca acc aac      432
Gln Tyr Leu Asp Pro Met Asp His Val Asn Ala Ser Gln Ser Thr Asn
130                               135                               140
gat gcg tat cct acc ggt ttc cgt att gca gtg tat aac agc atc tta      480
Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Asn Ser Ile Leu
145                               150                               155                               160
aaa ttg atc gat aaa att caa tat tta cac gac ggt ttt gac aat aaa      528
Lys Leu Ile Asp Lys Ile Gln Tyr Leu His Asp Gly Phe Asp Asn Lys
165                               170                               175
gcg aaa gaa ttt acg aat atc tta aaa atg gga cgt acc caa ttg caa      576
Ala Lys Glu Phe Thr Asn Ile Leu Lys Met Gly Arg Thr Gln Leu Gln
180                               185                               190

```

PF59083SeqList PF59083.txt

gat	gcg	gtg	cca	atg	act	gtt	ggg	caa	gaa	ttc	aaa	gct	ttc	gcc	gta	624
Asp	Ala	Val	Pro	Met	Thr	Val	Gly	Gln	Glu	Phe	Lys	Ala	Phe	Ala	Val	
		195					200					205				
tta	ctt	gaa	gaa	gaa	gtg	cgt	aac	tta	aaa	cgt	aca	gca	ggg	tta	tta	672
Leu	Leu	Glu	Glu	Glu	Val	Arg	Asn	Leu	Lys	Arg	Thr	Ala	Gly	Leu	Leu	
		210					215				220					
ctt	gaa	gta	aac	ctt	ggg	gcg	act	gca	atc	ggg	act	ggg	tta	aat	acg	720
Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Leu	Asn	Thr	
		225					230				235					
cca	caa	ggc	tat	aca	gaa	tta	gtt	gta	aaa	cat	ctt	gct	gac	gtg	act	768
Pro	Gln	Gly	Tyr	Thr	Glu	Leu	Val	Val	Lys	His	Leu	Ala	Asp	Val	Thr	
				245					250					255		
gga	tta	gct	tgt	gta	cca	gca	gaa	aac	tta	att	gaa	gca	aca	tct	gac	816
Gly	Leu	Ala	Cys	Val	Pro	Ala	Glu	Asn	Leu	Ile	Glu	Ala	Thr	Ser	Asp	
			260					265					270			
tgt	ggg	gct	tat	gtc	atg	gtt	cac	ggg	gca	tta	aaa	cgt	act	gca	gtg	864
Cys	Gly	Ala	Tyr	Val	Met	Val	His	Gly	Ala	Leu	Lys	Arg	Thr	Ala	Val	
			275					280					285			
aaa	ctt	tct	aaa	gta	tgt	aat	gac	tta	cgt	tta	ctt	tct	tct	ggc	cct	912
Lys	Leu	Ser	Lys	Val	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	
						295					300					
cgt	gca	ggg	tta	aaa	gaa	att	aat	ctt	cct	gaa	tta	caa	gca	ggg	tct	960
Arg	Ala	Gly	Leu	Lys	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	Ala	Gly	Ser	
						310					315					
tct	att	atg	cca	gca	aaa	gta	aac	cca	gtt	gtt	cct	gaa	gtg	gtg	aac	1008
Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Val	Pro	Glu	Val	Val	Asn	
				325					330					335		
caa	gta	tgc	ttt	aaa	gta	att	ggg	aac	gat	acc	act	gtg	act	ttc	gca	1056
Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Thr	Val	Thr	Phe	Ala	
			340					345					350			
tct	gaa	gca	ggg	caa	tta	caa	tta	aac	gta	atg	gaa	ccc	gtg	att	ggg	1104
Ser	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile	Gly	
			355					360					365			
caa	gca	atg	ttt	gaa	tct	atc	gac	atc	tta	acc	aat	gct	tgt	gtg	aac	1152
Gln	Ala	Met	Phe	Glu	Ser	Ile	Asp	Ile	Leu	Thr	Asn	Ala	Cys	Val	Asn	
			370				375					380				
tta	cgc	gat	aaa	tgc	gtg	gat	ggc	atc	act	gta	aac	aaa	gaa	att	tgt	1200
Leu	Arg	Asp	Lys	Cys	Val	Asp	Gly	Ile	Thr	Val	Asn	Lys	Glu	Ile	Cys	
						390					395				400	
gaa	aac	tac	gtg	ttt	aat	tca	att	ggg	att	gtg	act	tac	ttg	aat	cca	1248
Glu	Asn	Tyr	Val	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	Pro	
				405					410					415		
ttt	atc	ggg	cac	cac	aac	ggc	gac	tta	gtg	ggg	aaa	atc	tgt	gca	caa	1296
Phe	Ile	Gly	His	His	Asn	Gly	Asp	Leu	Val	Gly	Lys	Ile	Cys	Ala	Gln	
			420					425					430			
aca	ggc	aaa	ggc	gta	cgt	gaa	gtt	gtg	tta	gaa	aaa	ggg	tta	tta	aca	1344
Thr	Gly	Lys	Gly	Val	Arg	Glu	Val	Val	Leu	Glu	Lys	Gly	Leu	Leu	Thr	
			435				440					445				
gaa	gaa	caa	ttg	gat	gac	att	ctt	tct	gta	gaa	aac	tta	atg	aat	cca	1392
Glu	Glu	Gln	Leu	Asp	Asp	Ile	Leu	Ser	Val	Glu	Asn	Leu	Met	Asn	Pro	
			450				455				460					
act	tac	aaa	gcg	aaa	tta	aat	aaa	taa								1419
Thr	Tyr	Lys	Ala	Lys	Leu	Asn	Lys									
					470											

<210> 9724

<211> 472

<212> PRT

<213> Haemophilus influenzae R2846

<400> 9724

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

PF59083SeqList PF59083.txt

Gly Ala Ile Pro Ser Asp Ile Ala Lys Ala Ile Val Ala Ala Cys Asp
65 70 75 80
Glu Ile Leu Thr Thr Gly Lys Cys Leu Asp Gln Phe Pro Ser Asp Val
85 90 95
Tyr Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val
100 105 110
Val Ala Asn Leu Ala Leu Glu Leu Leu Gly His Lys Lys Gly Glu Tyr
115 120 125
Gln Tyr Leu Asp Pro Met Asp His Val Asn Ala Ser Gln Ser Thr Asn
130 135 140
Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Asn Ser Ile Leu
145 150 155 160
Lys Leu Ile Asp Lys Ile Gln Tyr Leu His Asp Gly Phe Asp Asn Lys
165 170 175
Ala Lys Glu Phe Thr Asn Ile Leu Lys Met Gly Arg Thr Gln Leu Gln
180 185 190
Asp Ala Val Pro Met Thr Val Gly Gln Glu Phe Lys Ala Phe Ala Val
195 200 205
Leu Leu Glu Glu Glu Val Arg Asn Leu Lys Arg Thr Ala Gly Leu Leu
210 215 220
Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr
225 230 235 240
Pro Gln Gly Tyr Thr Glu Leu Val Val Lys His Leu Ala Asp Val Thr
245 250 255
Gly Leu Ala Cys Val Pro Ala Glu Asn Leu Ile Glu Ala Thr Ser Asp
260 265 270
Cys Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Thr Ala Val
275 280 285
Lys Leu Ser Lys Val Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro
290 295 300
Arg Ala Gly Leu Lys Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly Ser
305 310 315 320
Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val Asn
325 330 335
Gln Val Cys Phe Lys Val Ile Gly Asn Asp Thr Thr Val Thr Phe Ala
340 345 350
Ser Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly
355 360 365
Gln Ala Met Phe Glu Ser Ile Asp Ile Leu Thr Asn Ala Cys Val Asn
370 375 380
Leu Arg Asp Lys Cys Val Asp Gly Ile Thr Val Asn Lys Glu Ile Cys
385 390 395 400
Glu Asn Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro
405 410 415
Phe Ile Gly His Asn Gly Asp Leu Val Gly Lys Ile Cys Ala Gln
420 425 430
Thr Gly Lys Gly Val Arg Glu Val Val Leu Glu Lys Gly Leu Leu Thr
435 440 445
Glu Glu Gln Leu Asp Asp Ile Leu Ser Val Glu Asn Leu Met Asn Pro
450 455 460
Thr Tyr Lys Ala Lys Leu Asn Lys
465 470

<210> 9725

<211> 1464

<212> DNA

<213> Photobacterium sp. SKA34

<220>

<221> CDS

<222> (1)..(1464)

<223> transl_table=11

<400> 9725

atg tct cag atg att gat ctt gaa aaa aat aac gaa gca gca ctg aat
Met Ser Gln Met Ile Asp Leu Glu Lys Asn Asn Glu Ala Ala Leu Asn
1 5 10 15
gtt gca act aga atc gaa gaa gat ctt ctt ggt aag cgt cac gtt cca
Val Ala Thr Arg Ile Glu Glu Asp Leu Leu Gly Lys Arg His Val Pro
48 96

PF59083SeqList PF59083.txt

	20	25	30	
aca gac gcg tat tgg ggt att cac act cta cgt gca atc gaa aac ttt	Thr Asp Ala Tyr Trp Gly Ile His Thr Leu Arg Ala Ile Glu Asn Phe	144		
aat atc tct aat acc act atc tca gac gta cct gag ttt gtt cgc ggc	Asn Ile Ser Asn Thr Thr Ile Ser Asp Val Pro Glu Phe Val Arg Gly	192		
atg gtt ttc acc aaa aaa gca gcg gca atg gcg aac aaa gaa ctc ggt	Met Val Phe Thr Lys Lys Ala Ala Ala Met Ala Asn Lys Glu Leu Gly	240		
gcg atc cct tca gat gtc ggt aac tac atc gag caa gcg tgt gat ctt	Ala Ile Pro Ser Asp Val Gly Asn Tyr Ile Glu Gln Ala Cys Asp Leu	288		
att tta gaa aca ggc cgt tgt atg gat caa ttc cct tct gat gta tac	Ile Leu Glu Thr Gly Arg Cys Met Asp Gln Phe Pro Ser Asp Val Tyr	336		
caa ggt ggc gct ggc aca tct gta aat atg aac acc aat gaa gtg att	Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Ile	384		
gca aac ctt gct ctt gag ctt atg ggc aaa gag aaa ggc gaa tat gac	Ala Asn Leu Ala Leu Glu Leu Met Gly Lys Glu Lys Gly Glu Tyr Asp	432		
atc att aac ccg aac gat cac gta aac aag tcc caa tca act aac tgt	Ile Ile Asn Pro Asn Asp His Val Asn Lys Ser Gln Ser Thr Asn Cys	480		
gct tac cct act ggt ttc cgc gtt gcg gta tat aac agc atc att aac	Ala Tyr Pro Thr Gly Phe Arg Val Ala Val Tyr Asn Ser Ile Ile Asn	528		
atg cta gaa gca tta gag tac cta aag aca gcc ttc gat gtg aaa gca	Met Leu Glu Ala Leu Glu Tyr Leu Lys Thr Ala Phe Asp Val Lys Ala	576		
acg gaa ttt gct agc atc tta aaa atg ggc cgt act cag cta caa gac	Thr Glu Phe Ala Ser Ile Leu Lys Met Gly Arg Thr Gln Leu Gln Asp	624		
gca gta cct atg act gta ggc caa gaa ttc cat gct tat agt gta ttg	Ala Val Pro Met Thr Val Gly Gln Glu Phe His Ala Tyr Ser Val Leu	672		
cta aaa gaa gaa atc aaa aac ctg cat tac acc gcg caa tta ctg ctt	Leu Lys Glu Glu Ile Lys Asn Leu His Tyr Thr Ala Gln Leu Leu Leu	720		
gag gtc aac cta ggt gca act gct atc ggt act ggt ttg aat gca gct	Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Ala Ala	768		
acg ggt tac caa cac cta gcg gtt caa cgc cta gct gaa att aca ggc	Thr Gly Tyr Gln His Leu Ala Val Gln Arg Leu Ala Glu Ile Thr Gly	816		
cta cct gtt aca cca gca gaa gac ttg att gaa gca aca tcc gac tgt	Leu Pro Val Thr Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser Asp Cys	864		
ggt gct tac gtt atg gtt cac ggc gcg cta aaa cgt act gca gtg aaa	Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Thr Ala Val Lys	912		
cta tct aaa atc tgt aac gat cta cgt cta ctc tct tct ggt cct cgt	Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg	960		
gcc ggt att aac gaa att aac ctt cct gaa atg cag gca ggc tct tct	Ala Gly Ile Asn Glu Ile Asn Leu Pro Glu Met Gln Ala Gly Ser Ser	1008		
atc atg cca gca aaa gta aat cct gtt atc cca gaa gtg gtt aac caa	Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln	1056		
att tgc ttt aaa gtg atc ggt aac gat aca acc att act ttt gct gca	Ile Cys Phe Lys Val Ile Gly Asn Asp Thr Thr Ile Thr Phe Ala Ala	1104		
gaa gca ggt cag ctt caa ctt aac gta atg gag cct gtg att ggt caa	Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Gln	1152		
gcg ttg ttt gag tca atc agc tta ctg aaa aat gcg tgt gtt aat tta	Ala Leu Phe Glu Ser Ile Ser Leu Leu Lys Asn Ala Cys Val Asn Leu	1200		

PF59083SeqList PF59083.txt

385					390					395					400	
cgt	gag	aaa	tgt	atc	gaa	ggc	atc	aca	gtg	aat	aaa	gat	gta	tgt	gag	1248
Arg	Glu	Lys	Cys	Ile	Glu	Gly	Ile	Thr	Val	Asn	Lys	Asp	Val	Cys	Glu	
				405					410					415		
agc	cac	gta	ttt	aac	tct	atc	ggg	atc	gtg	act	tat	tta	aac	cca	ttc	1296
Ser	His	Val	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	Pro	Phe	
			420						425				430			
att	ggg	cac	cat	gaa	ggc	gat	atc	gta	ggg	aaa	atc	tgt	gca	gaa	aca	1344
Ile	Gly	His	His	Glu	Gly	Asp	Ile	Val	Gly	Lys	Ile	Cys	Ala	Glu	Thr	
		435					440					445				
gga	aag	agc	gta	cgt	gaa	gtt	gtt	cta	gaa	cgc	ggg	ctt	act	gaa		1392
Gly	Lys	Ser	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gly	Leu	Leu	Thr	Glu	
	450					455					460					
gat	caa	tta	aat	gat	atc	ttc	tct	att	gaa	aac	ttg	atg	cac	cct	caa	1440
Asp	Gln	Leu	Asn	Asp	Ile	Phe	Ser	Ile	Glu	Asn	Leu	Met	His	Pro	Gln	
465					470					475					480	
tac	aag	gca	caa	cga	tac	agc	taa									1464
Tyr	Lys	Ala	Gln	Arg	Tyr	Ser										
				485												

<210> 9726

<211> 487

<212> PRT

<213> Photobacterium sp. SKA34

<400> 9726

Met	Ser	Gln	Met	Ile	Asp	Leu	Glu	Lys	Asn	Asn	Glu	Ala	Ala	Leu	Asn
1				5					10					15	
Val	Ala	Thr	Arg	Ile	Glu	Glu	Asp	Leu	Leu	Gly	Lys	Arg	His	Val	Pro
			20					25					30		
Thr	Asp	Ala	Tyr	Trp	Gly	Ile	His	Thr	Leu	Arg	Ala	Ile	Glu	Asn	Phe
		35				40					45				
Asn	Ile	Ser	Asn	Thr	Thr	Ile	Ser	Asp	Val	Pro	Glu	Phe	Val	Arg	Gly
	50				55					60					
Met	Val	Phe	Thr	Lys	Lys	Ala	Ala	Ala	Met	Ala	Asn	Lys	Glu	Leu	Gly
65				70					75					80	
Ala	Ile	Pro	Ser	Asp	Val	Gly	Asn	Tyr	Ile	Glu	Gln	Ala	Cys	Asp	Leu
			85				90						95		
Ile	Leu	Glu	Thr	Gly	Arg	Cys	Met	Asp	Gln	Phe	Pro	Ser	Asp	Val	Tyr
		100					105					110			
Gln	Gly	Gly	Ala	Gly	Thr	Ser	Val	Asn	Met	Asn	Thr	Asn	Glu	Val	Ile
	115					120					125				
Ala	Asn	Leu	Ala	Leu	Glu	Leu	Met	Gly	Lys	Glu	Lys	Gly	Glu	Tyr	Asp
	130					135				140					
Ile	Ile	Asn	Pro	Asn	Asp	His	Val	Asn	Lys	Ser	Gln	Ser	Thr	Asn	Cys
145				150				155						160	
Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Val	Ala	Val	Tyr	Asn	Ser	Ile	Ile	Asn
			165				170						175		
Met	Leu	Glu	Ala	Leu	Glu	Tyr	Leu	Lys	Thr	Ala	Phe	Asp	Val	Lys	Ala
		180					185					190			
Thr	Glu	Phe	Ala	Ser	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	Asp
	195					200					205				
Ala	Val	Pro	Met	Thr	Val	Gly	Gln	Glu	Phe	His	Ala	Tyr	Ser	Val	Leu
	210				215						220				
Leu	Lys	Glu	Glu	Ile	Lys	Asn	Leu	His	Tyr	Thr	Ala	Gln	Leu	Leu	Leu
225				230					235					240	
Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Leu	Asn	Ala	Ala
			245					250					255		
Thr	Gly	Tyr	Gln	His	Leu	Ala	Val	Gln	Arg	Leu	Ala	Glu	Ile	Thr	Gly
		260					265					270			
Leu	Pro	Val	Thr	Pro	Ala	Glu	Asp	Leu	Ile	Glu	Ala	Thr	Ser	Asp	Cys
	275					280					285				
Gly	Ala	Tyr	Val	Met	Val	His	Gly	Ala	Leu	Lys	Arg	Thr	Ala	Val	Lys
	290				295					300					
Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg
305				310					315						320
Ala	Gly	Ile	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Met	Gln	Ala	Gly	Ser	Ser
			325					330					335		
Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln

PF59083SeqList PF59083.txt

```

          340          345          350
Ile Cys Phe Lys Val Ile Gly Asn Asp Thr Thr Ile Thr Phe Ala Ala
          355          360          365
Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Gln
          370          375          380
Ala Leu Phe Glu Ser Ile Ser Leu Leu Lys Asn Ala Cys Val Asn Leu
          385          390          395
Arg Glu Lys Cys Ile Glu Gly Ile Thr Val Asn Lys Asp Val Cys Glu
          405          410          415
Ser His Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro Phe
          420          425          430
Ile Gly His His Glu Gly Asp Ile Val Gly Lys Ile Cys Ala Glu Thr
          435          440          445
Gly Lys Ser Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu Thr Glu
          450          455          460
Asp Gln Leu Asn Asp Ile Phe Ser Ile Glu Asn Leu Met His Pro Gln
          465          470          475
Tyr Lys Ala Gln Arg Tyr Ser
          485

```

<210> 9727
 <211> 1404
 <212> DNA
 <213> Oceanospirillum sp. MED92

<220>
 <221> CDS
 <222> (1)..(1404)
 <223> transl_table=11

```

<400> 9727
atg gtc act cgt atc gaa cac gac atg cta ggt gag atg caa att cct      48
Met Val Thr Arg Ile Glu His Asp Met Leu Gly Glu Met Gln Ile Pro
1      5      10      15
agc gac gtc tgg tac gga gta caa acc ctt cga gca aag gaa aac ttc      96
Ser Asp Val Trp Tyr Gly Val Gln Thr Leu Arg Ala Lys Glu Asn Phe
20      25      30
tcc att aca ggc gtg ccg atc agt cac ttt cct cac tta atc aaa gca      144
Ser Ile Thr Gly Val Pro Ile Ser His Phe Pro His Leu Ile Lys Ala
35      40      45
ctg gca atg gtg aag tgg tcc gcg gca caa acc aat aaa gaa ttg aag      192
Leu Ala Met Val Lys Trp Ser Ala Ala Gln Thr Asn Lys Glu Leu Lys
50      55      60
ctg ctt gaa gaa cat aaa gct gac gcc att atg gcc gcc tgt cgt gac      240
Leu Leu Glu Glu His Lys Ala Asp Ala Ile Met Ala Ala Cys Arg Asp
65      70      75      80
att atc gac gga gca ctg cat cag caa ttt gtc gtc gat ctc att cag      288
Ile Ile Asp Gly Ala Leu His Gln Gln Phe Val Val Asp Leu Ile Gln
85      90      95
ggc ggc gca ggc act tca acc aat atg aat gcc aat gag gtg att gct      336
Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu Val Ile Ala
100      105      110
aac ctg gca ctg agc aag ttg ggc aaa gag aaa ggt gac tac caa cac      384
Asn Leu Ala Leu Ser Lys Leu Gly Lys Glu Lys Gly Asp Tyr Gln His
115      120      125
ctg cat cca aac gat gac gta aac tgc tct caa tcc act aac gac gct      432
Leu His Pro Asn Asp Asp Val Asn Cys Ser Gln Ser Thr Asn Asp Ala
130      135      140
tat cca acc gca gta tgt ttg ggc att caa ttc gcg gct gaa cct ctg      480
Tyr Pro Thr Ala Val Cys Leu Gly Ile Gln Phe Ala Ala Glu Pro Leu
145      150      155      160
acc gag cac ctg gaa agc ttg atc caa gcc ttt aac aac aaa ggc caa      528
Thr Glu His Leu Glu Ser Leu Ile Gln Ala Phe Asn Asn Lys Gly Gln
165      170      175
gaa ttt aac gat gtg gtc aaa atg ggt cgt acc caa cta caa gat gcc      576
Glu Phe Asn Asp Val Val Lys Met Gly Arg Thr Gln Leu Gln Asp Ala
180      185      190
gta ccc atg acg ctg ggg cag gag ttc gaa gcc ttt gca gtc acc cta      624
Val Pro Met Thr Leu Gly Gln Glu Phe Glu Ala Phe Val Thr Leu

```

PF59083SeqList PF59083.txt

195	200	205	
agt gaa gat atc gac cgt ata aag gaa gcc tgc aag ctg ttg tgt gag			672
Ser Glu Asp Ile Asp Arg Ile Lys Glu Ala Cys Lys Leu Leu Cys Glu			
210	215	220	
gtt aac ctc ggt ggc acc gct att ggt acc ggg atc aac acg cac ccg			720
Val Asn Leu Gly Gly Thr Ala Ile Gly Thr Gly Ile Asn Thr His Pro			
225	230	235	
gag tat gca agc cgt gtc gtt aag agg tta gca gaa atc tct ggc aaa			768
Glu Tyr Ala Ser Arg Val Val Lys Arg Leu Ala Glu Ile Ser Gly Lys			
245	250	255	
cct atg att cct gcc agc cac ttg gta gaa gcc acc tca gac ctg ggc			816
Pro Met Ile Pro Ala Ser His Leu Val Glu Ala Thr Ser Asp Leu Gly			
260	265	270	
gca ttt gtt ctg ttc tct ggc att ctt aaa cgt atg gca gtc aag ctc			864
Ala Phe Val Leu Phe Ser Gly Ile Leu Lys Arg Met Ala Val Lys Leu			
275	280	285	
ggg aag ata tgt aat gac ctt cga tta ctt tca agc ggc ccg cgc act			912
Gly Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Thr			
290	295	300	
ggc ttt gct gag atc cat ctt cca ccg atg caa ccc gga tca tct atc			960
Gly Phe Ala Glu Ile His Leu Pro Pro Met Gln Pro Gly Ser Ser Ile			
305	310	315	
atg cct ggc aag gtg aac ccg gtg ata cct gaa gcg gtc aat caa act			1008
Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Ala Val Asn Gln Thr			
325	330	335	
gcc tac cag gtg atc gct aac gac ctg gcc gtc aca ctt gcc gct gaa			1056
Ala Tyr Gln Val Ile Ala Asn Asp Leu Ala Val Thr Leu Ala Ala Glu			
340	345	350	
tca ggt cag ctg cag ctg aat gcg atg gaa ccg ctg atc gtt tat aac			1104
Ser Gly Gln Leu Gln Leu Asn Ala Met Glu Pro Leu Ile Val Tyr Asn			
355	360	365	
ctg ctt agc tcg atg aag atg ctg tgt aac gcc tgt gaa atg ctg gag			1152
Leu Leu Ser Ser Met Lys Met Leu Cys Asn Ala Cys Glu Met Leu Glu			
370	375	380	
gaa cgc tgt gtc agt ggt att aaa gcg aat cgg gaa caa tgc tcg cga			1200
Glu Arg Cys Val Ser Gly Ile Lys Ala Asn Arg Glu Gln Cys Ser Arg			
385	390	395	
cat ctg gat aac agc atc ggt gta atc act gct ctg gta cca cac atc			1248
His Leu Asp Asn Ser Ile Gly Val Ile Thr Ala Leu Val Pro His Ile			
405	410	415	
ggg tat gcc aat gcc tct cgt atc gcc aaa acc gcg tta aat acg ggc			1296
Gly Tyr Ala Asn Ala Ser Arg Ile Ala Lys Thr Ala Leu Asn Thr Gly			
420	425	430	
tcg acg gta cgc gaa ctg gtg att ggt gaa ggt ctg ctg gac agt atc			1344
Ser Thr Val Arg Glu Leu Val Ile Gly Glu Gly Leu Leu Asp Ser Ile			
435	440	445	
cag ctt gat cgc cta ctt agc cct gaa tcg atg cta gcc cct gga gag			1392
Gln Leu Asp Arg Leu Leu Ser Pro Glu Ser Met Leu Ala Pro Gly Glu			
450	455	460	
cga gtt tca tga			1404
Arg Val Ser			
465			

<210> 9728

<211> 467

<212> PRT

<213> Oceanospirillum sp. MED92

<400> 9728

Met Val Thr Arg Ile Glu His Asp Met Leu Gly Glu Met Gln Ile Pro	
1 Ser Asp Val Trp Tyr Gly Val Gln Thr Leu Arg Ala Lys Glu Asn Phe	
20 Ser Ile Thr Gly Val Pro Ile Ser His Phe Pro His Leu Ile Lys Ala	
35 Leu Ala Met Val Lys Trp Ser Ala Ala Gln Thr Asn Lys Glu Leu Lys	
50 Leu Leu Glu Glu His Lys Ala Asp Ala Ile Met Ala Ala Cys Arg Asp	
65 70 75 80	

PF59083SeqList PF59083.txt

Ile Ile Asp Gly Ala Leu His Gln Gln Phe Val Val Asp Leu Ile Gln
 85 90 95
 Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu Val Ile Ala
 100 105 110
 Asn Leu Ala Leu Ser Lys Leu Gly Lys Glu Lys Gly Asp Tyr Gln His
 115 120 125
 Leu His Pro Asn Asp Asp Val Asn Cys Ser Gln Ser Thr Asn Asp Ala
 130 135 140
 Tyr Pro Thr Ala Val Cys Leu Gly Ile Gln Phe Ala Ala Glu Pro Leu
 145 150 155 160
 Thr Glu His Leu Glu Ser Leu Ile Gln Ala Phe Asn Asn Lys Gly Gln
 165 170 175
 Glu Phe Asn Asp Val Val Lys Met Gly Arg Thr Gln Leu Gln Asp Ala
 180 185 190
 Val Pro Met Thr Leu Gly Gln Glu Phe Glu Ala Phe Ala Val Thr Leu
 195 200 205
 Ser Glu Asp Ile Asp Arg Ile Lys Glu Ala Cys Lys Leu Leu Cys Glu
 210 215 220
 Val Asn Leu Gly Gly Thr Ala Ile Gly Thr Gly Ile Asn Thr His Pro
 225 230 235 240
 Glu Tyr Ala Ser Arg Val Val Lys Arg Leu Ala Glu Ile Ser Gly Lys
 245 250 255
 Pro Met Ile Pro Ala Ser His Leu Val Glu Ala Thr Ser Asp Leu Gly
 260 265 270
 Ala Phe Val Leu Phe Ser Gly Ile Leu Lys Arg Met Ala Val Lys Leu
 275 280 285
 Gly Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Thr
 290 295 300
 Gly Phe Ala Glu Ile His Leu Pro Pro Met Gln Pro Gly Ser Ser Ile
 305 310 315 320
 Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu Ala Val Asn Gln Thr
 325 330 335
 Ala Tyr Gln Val Ile Ala Asn Asp Leu Ala Val Thr Leu Ala Ala Glu
 340 345 350
 Ser Gly Gln Leu Gln Leu Asn Ala Met Glu Pro Leu Ile Val Tyr Asn
 355 360 365
 Leu Leu Ser Ser Met Lys Met Leu Cys Asn Ala Cys Glu Met Leu Glu
 370 375 380
 Glu Arg Cys Val Ser Gly Ile Lys Ala Asn Arg Glu Gln Cys Ser Arg
 385 390 395 400
 His Leu Asp Asn Ser Ile Gly Val Ile Thr Ala Leu Val Pro His Ile
 405 410 415
 Gly Tyr Ala Asn Ala Ser Arg Ile Ala Lys Thr Ala Leu Asn Thr Gly
 420 425 430
 Ser Thr Val Arg Glu Leu Val Ile Gly Glu Gly Leu Leu Asp Ser Ile
 435 440 445 450
 Gln Leu Asp Arg Leu Leu Ser Pro Glu Ser Met Leu Ala Pro Gly Glu
 455 460
 Arg Val Ser
 465

<210> 9729

<211> 1383

<212> DNA

<213> Oceanobacter sp. RED65

<220>

<221> CDS

<222> (1)..(1383)

<223> transl_table=11

<400> 9729

atg gac gta cgc act gaa agc gat tca tta ggt aca aaa cag att ggc 48
 Met Asp Val Arg Thr Glu Ser Asp Ser Leu Gly Thr Lys Gln Ile Gly
 1 5 10 15

agt cat cat tat tac ggt att caa act caa aga gcc gta gaa aat ttt 96
 Ser His His Tyr Tyr Gly Ile Gln Thr Gln Arg Ala Val Glu Asn Phe
 20 25 30

tcg atc aca gat att cca ctc agt att gat ccg gaa atg gtg att gct 144
 Seite 10213

PF59083SeqList PF59083.txt

Ser	Ile	Thr	Asp	Ile	Pro	Leu	Ser	Ile	Asp	Pro	Glu	Met	Val	Ile	Ala	
35							40					45				
ttg	gcc	atg	gtg	aaa	aaa	gct	tgc	gcc	tta	acc	aac	tgc	gat	ctt	ggg	192
Leu	Ala	Met	Val	Lys	Lys	Ala	Cys	Ala	Leu	Thr	Asn	Cys	Asp	Leu	Gly	
50						55					60					
gtg	ctt	cct	aaa	gaa	aaa	acc	gat	gcc	atc	gtc	gct	gca	tgc	gat	gaa	240
Val	Leu	Pro	Lys	Glu	Lys	Thr	Asp	Ala	Ile	Val	Ala	Ala	Cys	Asp	Glu	
65					70					75					80	
att	att	gcg	ggg	aag	cac	cat	caa	gag	ttc	gtt	ggt	gat	gtc	att	caa	288
Ile	Ile	Ala	Gly	Lys	His	His	Gln	Glu	Phe	Val	Val	Asp	Val	Ile	Gln	
				85					90					95		
ggg	ggg	gca	ggg	act	tct	gcc	aat	atg	aac	gcc	aat	gaa	gtc	atc	gcc	336
Gly	Gly	Ala	Gly	Thr	Ser	Ala	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	
			100				105					110				
aac	cgt	gcg	ctt	gaa	atc	atg	ggg	tat	agc	aag	ggg	cac	tat	cag	cat	384
Asn	Arg	Ala	Leu	Glu	Ile	Met	Gly	Tyr	Ser	Lys	Gly	His	Tyr	Gln	His	
			115				120					125				
cta	cac	cca	aac	aat	gat	gtt	aat	gcc	tct	caa	tcg	act	aat	gac	gtt	432
Leu	His	Pro	Asn	Asn	Asp	Val	Asn	Ala	Ser	Gln	Ser	Thr	Asn	Asp	Val	
						135					140					
tat	cca	tct	gca	ctt	cg	gct	ctt	tat	aat	aag	tcc	caa	gat	tta		480
Tyr	Pro	Ser	Ala	Leu	Arg	Leu	Ala	Leu	Tyr	Asn	Lys	Ser	Gln	Asp	Leu	
145					150					155					160	
atc	tca	gca	cta	gaa	gaa	tta	gtt	gat	gca	ttt	ggg	gta	aaa	gca	gaa	528
Ile	Ser	Ala	Leu	Glu	Glu	Leu	Val	Asp	Ala	Phe	Gly	Val	Lys	Ala	Glu	
				165					170					175		
gcg	ttt	aaa	gac	gtt	tat	aaa	atc	ggg	cg	acc	cag	ttg	caa	gat	gcg	576
Ala	Phe	Lys	Asp	Val	Tyr	Lys	Ile	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	
			180					185				190				
gtg	cct	atg	acg	ttg	ggc	atg	gaa	ttt	ggg	gct	ttt	gct	acg	gct	att	624
Val	Pro	Met	Thr	Leu	Gly	Met	Glu	Phe	Gly	Ala	Phe	Ala	Thr	Ala	Ile	
			195				200					205				
gca	gaa	gac	att	gtt	caa	ata	aaa	cat	aca	gcg	cat	ctt	tta	ctc	gac	672
Ala	Glu	Asp	Ile	Val	Gln	Ile	Lys	His	Thr	Ala	His	Leu	Leu	Leu	Asp	
			210			215					220					
acc	aac	tta	ggc	gcc	acg	gct	atc	ggg	act	ggc	atc	aat	acg	cct	aaa	720
Thr	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Thr	Pro	Lys	
225					230					235					240	
ggg	tat	agc	aca	aaa	gtg	ata	gag	cat	tta	cgt	gaa	gta	agt	ggg	gta	768
Gly	Tyr	Ser	Thr	Lys	Val	Ile	Glu	His	Leu	Arg	Glu	Val	Ser	Gly	Val	
				245					250					255		
caa	gtg	cga	tca	gcg	gaa	aac	cta	att	gaa	gcc	acc	tgg	gat	act	ggc	816
Gln	Val	Arg	Ser	Ala	Glu	Asn	Leu	Ile	Glu	Ala	Thr	Trp	Asp	Thr	Gly	
			260					265					270			
gac	ttt	gtt	caa	tta	agc	ggg	acc	tta	aaa	cg	tat	gcc	acc	aag	atc	864
Asp	Phe	Val	Gln	Leu	Ser	Gly	Thr	Leu	Lys	Arg	Tyr	Ala	Thr	Lys	Ile	
			275				280					285				
agt	aaa	att	tgc	aat	gat	ttg	cgt	ttg	tta	agt	tca	gga	cca	tta	tgc	912
Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Leu	Cys	
						295					300					
ggc	tta	ggg	gaa	atc	aac	tta	cct	aaa	atg	cag	cca	ggg	tca	tcc	atc	960
Gly	Leu	Gly	Glu	Ile	Asn	Leu	Pro	Lys	Met	Gln	Pro	Gly	Ser	Ser	Ile	
305					310					315					320	
atg	cct	ggc	aaa	gtg	aat	ccc	gtt	att	cct	gaa	gtc	atg	aat	caa	att	1008
Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Met	Asn	Gln	Ile	
				325					330					335		
gct	tat	gac	gtt	atc	ggg	aaa	gac	gtt	act	gtt	tcc	atg	gca	tct	gaa	1056
Ala	Tyr	Asp	Val	Ile	Gly	Lys	Asp	Val	Thr	Val	Ser	Met	Ala	Ser	Glu	
			340					345					350			
ggc	gga	caa	atg	cag	cta	aac	gca	ttt	gaa	cca	gtt	att	gcc	aac	tgc	1104
Gly	Gly	Gln	Met	Gln	Leu	Asn	Ala	Phe	Glu	Pro	Val	Ile	Ala	Asn	Cys	
			355				360					365				
ctc	ttt	tta	tct	tta	ggc	atg	ctt	acc	cgt	ggg	tct	cg	att	tta	cgt	1152
Leu	Phe	Leu	Ser	Leu	Gly	Met	Leu	Thr	Arg	Gly	Ser	Arg	Ile	Leu	Arg	
					375						380					
gaa	aag	tgc	att	caa	ggg	atc	acg	gct	aac	cgt	gag	aaa	tgc	gaa	gaa	1200
Glu	Lys	Cys	Ile	Gln	Gly	Ile	Thr	Ala	Asn	Arg	Glu	Lys	Cys	Glu	Glu	
385					390					395					400	
tat	ttg	gat	aaa	tca	gta	ggg	atc	gta	acc	gca	tta	aac	ccg	att	cta	1248

PF59083SeqList PF59083.txt

Tyr	Leu	Asp	Lys	Ser	Val	Gly	Ile	Val	Thr	Ala	Leu	Asn	Pro	Ile	Leu	
				405					410					415		
ggg	tat	gaa	gtc	aca	tcg	gca	ctt	gct	caa	gaa	gcc	gtc	gca	gaa	ggg	1296
Gly	Tyr	Glu	Val	Thr	Ser	Ala	Leu	Ala	Gln	Glu	Ala	Val	Ala	Glu	Gly	
			420					425					430			
aag	tcc	att	aaa	aaa	tta	gtg	att	gag	aaa	cag	ctt	ttg	cca	gca	gag	1344
Lys	Ser	Ile	Lys	Lys	Leu	Val	Ile	Glu	Lys	Gln	Leu	Leu	Pro	Ala	Glu	
		435					440					445				
cag	gtt	gat	gct	ttg	ctg	caa	agc	gcg	atg	ggg	caa	taa				1383
Gln	Val	Asp	Ala	Leu	Leu	Gln	Ser	Ala	Met	Gly	Gln					
	450					455					460					

<210> 9730

<211> 460

<212> PRT

<213> Oceanobacter sp. RED65

<400> 9730

Met	Asp	Val	Arg	Thr	Glu	Ser	Asp	Ser	Leu	Gly	Thr	Lys	Gln	Ile	Gly	
1				5					10					15		
Ser	His	His	Tyr	Tyr	Gly	Ile	Gln	Thr	Gln	Arg	Ala	Val	Glu	Asn	Phe	
			20					25					30			
Ser	Ile	Thr	Asp	Ile	Pro	Leu	Ser	Ile	Asp	Pro	Glu	Met	Val	Ile	Ala	
		35					40					45				
Leu	Ala	Met	Val	Lys	Lys	Ala	Cys	Ala	Leu	Thr	Asn	Cys	Asp	Leu	Gly	
	50					55					60					
Val	Leu	Pro	Lys	Glu	Lys	Thr	Asp	Ala	Ile	Val	Ala	Ala	Cys	Asp	Glu	
65				70					75						80	
Ile	Ile	Ala	Gly	Lys	His	His	Gln	Glu	Phe	Val	Val	Asp	Val	Ile	Gln	
			85					90						95		
Gly	Gly	Ala	Gly	Thr	Ser	Ala	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	
		100						105					110			
Asn	Arg	Ala	Leu	Glu	Ile	Met	Gly	Tyr	Ser	Lys	Gly	His	Tyr	Gln	His	
		115					120					125				
Leu	His	Pro	Asn	Asn	Asp	Val	Asn	Ala	Ser	Gln	Ser	Thr	Asn	Asp	Val	
	130					135					140					
Tyr	Pro	Ser	Ala	Leu	Arg	Leu	Ala	Leu	Tyr	Asn	Lys	Ser	Gln	Asp	Leu	
145				150						155				160		
Ile	Ser	Ala	Leu	Glu	Leu	Val	Asp	Ala	Phe	Gly	Val	Lys	Ala	Glu		
			165					170					175			
Ala	Phe	Lys	Asp	Val	Tyr	Lys	Ile	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	
			180					185					190			
Val	Pro	Met	Thr	Leu	Gly	Met	Glu	Phe	Gly	Ala	Phe	Ala	Thr	Ala	Ile	
		195					200					205				
Ala	Glu	Asp	Ile	Val	Gln	Ile	Lys	His	Thr	Ala	His	Leu	Leu	Leu	Asp	
	210					215					220					
Thr	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Thr	Pro	Lys	
225				230						235				240		
Gly	Tyr	Ser	Thr	Lys	Val	Ile	Glu	His	Leu	Arg	Glu	Val	Ser	Gly	Val	
			245					250						255		
Gln	Val	Arg	Ser	Ala	Glu	Asn	Leu	Ile	Glu	Ala	Thr	Trp	Asp	Thr	Gly	
			260					265					270			
Asp	Phe	Val	Gln	Leu	Ser	Gly	Thr	Leu	Lys	Arg	Tyr	Ala	Thr	Lys	Ile	
		275					280					285				
Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Leu	Cys	
	290					295					300					
Gly	Leu	Gly	Glu	Ile	Asn	Leu	Pro	Lys	Met	Gln	Pro	Gly	Ser	Ser	Ile	
305					310					315				320		
Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Met	Asn	Gln	Ile	
			325						330					335		
Ala	Tyr	Asp	Val	Ile	Gly	Lys	Asp	Val	Thr	Val	Ser	Met	Ala	Ser	Glu	
			340					345					350			
Gly	Gly	Gln	Met	Gln	Leu	Asn	Ala	Phe	Glu	Pro	Val	Ile	Ala	Asn	Cys	
		355					360					365				
Leu	Phe	Leu	Ser	Leu	Gly	Met	Leu	Thr	Arg	Gly	Ser	Arg	Ile	Leu	Arg	
	370					375					380					
Glu	Lys	Cys	Ile	Gln	Gly	Ile	Thr	Ala	Asn	Arg	Glu	Lys	Cys	Glu	Glu	
385					390					395				400		
Tyr	Leu	Asp	Lys	Ser	Val	Gly	Ile	Val	Thr	Ala	Leu	Asn	Pro	Ile	Leu	

PF59083SeqList PF59083.txt

Gly Tyr Glu Val Thr Ser Ala Leu Ala Gln Glu Ala Val Ala Glu Gly
 Lys Ser Ile Lys Lys Leu Val Ile Glu Lys Gln Leu Leu Pro Ala Glu
 Gln Val Asp Ala Leu Leu Gln Ser Ala Met Gly Gln
 405 410 415
 420 425 430
 435 440 445
 450 455 460

<210> 9731
 <211> 1452
 <212> DNA
 <213> vibrio sp. Ex25

<220>
 <221> CDS
 <222> (1)..(1452)
 <223> transl_table=11

<400> 9731
 atg gct acc cta tct gat gct cca aaa aca gca aac cca gcc act cgt 48
 Met Ala Thr Leu Ser Asp Ala Pro Lys Thr Ala Asn Pro Ala Thr Arg
 1 5 10 15
 att gaa gaa gat cta tta ggt caa cgt cat gtc cct gca gat gcg tac 96
 Ile Glu Glu Asp Leu Leu Gly Gln Arg His Val Pro Ala Asp Ala Tyr
 20 25 30
 tac ggt att cat acg cta cgt gcg atc gag aac ttc aac atc tct aat 144
 Tyr Gly Ile His Thr Leu Arg Ala Ile Glu Asn Phe Asn Ile Ser Asn
 35 40 45
 atg acc atc tct gac gta cca gaa ttt gta cgc ggt atg gta atg acc 192
 Met Thr Ile Ser Asp Val Pro Glu Phe Val Arg Gly Met Val Met Thr
 50 55 60
 aaa aaa gca gcg gcg ttg gca aac aaa gaa ctt ggt gcg att cca aaa 240
 Lys Lys Ala Ala Ala Leu Ala Asn Lys Glu Leu Gly Ala Ile Pro Lys
 65 70 75 80
 gac gtt gca aac tac atc atc gaa gcg tgt gat ttg atc cta gaa act 288
 Asp Val Ala Asn Tyr Ile Ile Glu Ala Cys Asp Leu Ile Leu Glu Thr
 85 90 95
 ggc aag tgc atg gat cag ttc cca tca gac gta ttc caa ggt ggt gcg 336
 Gly Lys Cys Met Asp Gln Phe Pro Ser Asp Val Phe Gln Gly Gly Ala
 100 105 110
 ggc act tcc gtg aac atg aac aca aac gaa gtg atc gca aac gtt gcg 384
 Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Ile Ala Asn Val Ala
 115 120 125
 ctt gag cta atg ggt aaa gag aaa ggt caa tac gaa ttt gtc aac cca 432
 Leu Glu Leu Met Gly Lys Lys Gly Gln Tyr Glu Phe Val Asn Pro
 130 135 140
 aat gac cac gta aac aag agc caa tca acc aac tgt gcg tat cca acg 480
 Asn Asp His Val Asn Lys Ser Gln Ser Thr Asn Cys Ala Tyr Pro Thr
 145 150 155 160
 ggt ttc cgt atc gcg gtt tac aac agc gta cac aaa cta atg gaa gca 528
 Gly Phe Arg Ile Ala Val Tyr Asn Ser Val His Lys Leu Met Glu Ala
 165 170 175
 att gag tac cta aaa ggc gca ttc gaa ctt aaa gca att gag ttt aaa 576
 Ile Glu Tyr Leu Lys Gly Ala Phe Glu Leu Lys Ala Ile Glu Phe Lys
 180 185 190
 gat gta ctg aaa atg ggt cgt act cag cta caa gac gcg gta ccg atg 624
 Asp Val Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met
 195 200 205
 act gta ggt caa gag ttc cac gct tgg gca gta aca cta aac gaa gag 672
 Thr Val Gly Gln Glu Phe His Ala Trp Ala Val Thr Leu Asn Glu Glu
 210 215 220
 att cgt gct cta gat tac acc tct aaa cta ctc cta gaa atc aac cta 720
 Ile Arg Ala Leu Asp Tyr Thr Ser Lys Leu Leu Leu Glu Ile Asn Leu
 225 230 235 240
 ggc gca acc gca atc ggt aca ggt cta aat cca ccg act ggc tac caa 768
 Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr Pro Thr Gly Tyr Gln
 245 250 255
 gcg ctt gca gta aaa cac cta gcg gaa gta aca ggt ctt gac gtt gtt 816
 Ala Leu Ala Val Lys His Leu Ala Glu Val Thr Gly Leu Asp Val Val

PF59083SeqList PF59083.txt

[illegible]

```
<210> 9732
<211> 483
<212> PRT
<213> Vibrio sp. Ex25
```

<400>	9732															
Met	Ala	Thr	Leu	Ser ⁵	Asp	Ala	Pro	Lys	Thr ¹⁰	Ala	Asn	Pro	Ala	Thr	Arg	
Ile	Glu	Glu	Asp ²⁰	Leu	Leu	Gly	Gln	Arg ²⁵	His	Val	Pro	Ala	Asp ³⁰	Ala	Tyr	
Tyr	Gly	Ile ³⁵	His	Thr	Leu	Arg	Ala ⁴⁰	Ile	Glu	Asn	Phe	Asn ⁴⁵	Ile	Ser	Asn	
Met	Thr ⁵⁰	Ile	Ser	Asp	Val	Pro ⁵⁵	Glu	Phe	Val	Arg	Gly ⁶⁰	Met	Val	Met	Thr	
Lys	Lys	Ala	Ala	Ala	Leu ⁷⁰	Ala	Asn	Lys	Glu	Leu ⁷⁵	Gly	Ala	Ile	Pro	Lys ⁸⁰	
Asp	Val	Ala	Asn	Tyr ⁸⁵	Ile	Ile	Glu	Ala	Cys ⁹⁰	Asp	Leu	Ile	Leu	Glu	Thr ⁹⁵	
Gly	Lys	Cys	Met ¹⁰⁰	Asp	Gln	Phe	Pro	Ser ¹⁰⁵	Asp	Val	Phe	Gln	Gly ¹¹⁰	Gly	Ala	
Gly	Thr	Ser ¹¹⁵	Val	Asn	Met	Asn	Thr ¹²⁰	Asn	Glu	Val	Ile	Ala ¹²⁵	Asn	Val	Ala	
Leu	Glu ¹³⁰	Leu	Met	Gly	Lys	Glu ¹³⁵	Lys	Gly	Gln	Tyr	Glu ¹⁴⁰	Phe	Val	Asn	Pro	
Asn	Asp	His	Val	Asn	Lys	Ser	Gln	Ser	Thr	Asn	Cys	Ala	Tyr	Pro	Thr	
Seite 10217																

PF59083SeqList PF59083.txt

```

145      150      155      160
Gly Phe Arg Ile Ala Val Tyr Asn Ser Val His Lys Leu Met Glu Ala
      165      170      175
Ile Glu Tyr Leu Lys Gly Ala Phe Glu Leu Lys Ala Ile Glu Phe Lys
      180      185      190
Asp Val Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met
      195      200      205
Thr Val Gly Gln Glu Phe His Ala Trp Ala Val Thr Leu Asn Glu Glu
      210      215      220
Ile Arg Ala Leu Asp Tyr Thr Ser Lys Leu Leu Glu Ile Asn Leu
      225      230      235
Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr Pro Thr Gly Tyr Gln
      245      250      255
Ala Leu Ala Val Lys His Leu Ala Glu Val Thr Gly Leu Asp Val Val
      260      265      270
Ala Ala Glu Asp Leu Ile Glu Ala Thr Ser Asp Cys Gly Ala Tyr Val
      275      280      285
Met Thr His Ser Ala Leu Lys Arg Leu Ala Val Lys Leu Ser Lys Ile
      290      295      300
Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Ala Gly Leu Asn
      305      310      315
Glu Leu Asn Leu Pro Glu Met Gln Ala Gly Ser Ser Ile Met Pro Ala
      325      330      335
Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln Val Cys Phe Lys
      340      345      350
Val Leu Gly Asn Asp Asn Thr Val Ser Phe Ala Ala Glu Gly Gly Gln
      355      360      365
Leu Gln Leu Asn Val Met Glu Pro Val Ile Ala Gln Ser Met Phe Glu
      370      375      380
Ser Ile Ser Leu Leu His Asn Ala Cys Val Asn Leu Arg Asp Lys Cys
      385      390      395
Ile Asp Gly Ile Thr Val Asn Lys Glu Thr Cys Glu Asn Tyr Val Tyr
      405      410      415
Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro Tyr Ile Gly His His
      420      425      430
Glu Gly Asp Ile Val Gly Lys Ile Cys Ala Glu Thr Gly Lys Ser Val
      435      440      445
Arg Glu Val Val Leu Glu Arg Gly Leu Leu Thr Ala Glu Glu Leu Asp
      450      455      460
Glu Ile Leu Ser Val Glu Asn Phe Met His Pro Thr Tyr Lys Ala Lys
      465      470      475
Arg Tyr Glu

```

<210> 9733
 <211> 1437
 <212> DNA
 <213> Pseudomonas putida GB-1

<220>
 <221> CDS
 <222> (1)..(1437)
 <223> transl_table=11

```

<400> 9733
atg ata tac atc atg tcc tcc gct gca tcg ttc cgc gtc gaa aaa gac      48
Met Ile Tyr Ile Met Ser Ser Ala Ala Ser Phe Arg Val Glu Lys Asp
1      5      10      15
ttg ttg ggt acc ctt gaa gtt cct gca gat gcc tac tac ggc atc cag      96
Leu Leu Gly Thr Leu Glu Val Pro Ala Asp Ala Tyr Tyr Gly Ile Gln
20      25      30
acc ctg cgc gct gcc aac aac ttc cac ctc tcc ggt gtt cca ctg tcg      144
Thr Leu Arg Ala Ala Asn Asn Phe His Leu Ser Gly Val Pro Leu Ser
35      40      45
cac tac ccg aag ctg gtc gtg gcc ctg gcc atg gtc aag cag gcc gct      192
His Tyr Pro Lys Leu Val Val Ala Leu Ala Met Val Lys Gln Ala Ala
50      55      60
gcc gac gcc aac cgt gag ctg ggt cac ctg agc gat gcc aag cac gct      240
Ala Asp Ala Asn Arg Glu Leu Gly His Leu Ser Asp Ala Lys His Ala
Seite 10218

```

PF59083SeqList PF59083.txt

65											70											75											80	
gcc	atc	acc	gca	gcc	tgc	gcc	cgc	ctg	atc	aaa	ggc	gat	tac	cac	gac	288																		
Ala	Ile	Thr	Ala	Ala	Cys	Ala	Arg	Leu	Ile	Lys	Gly	Asp	Tyr	His	Asp																			
				85										95																				
cag	ttc	gtg	gtg	gac	atg	atc	caa	ggc	ggg	gct	ggg	act	tct	acc	aac	336																		
Gln	Phe	Val	Val	Asp	Met	Ile	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Thr	Asn																			
			100					105					110																					
atg	aac	gcc	aac	gaa	gtc	att	gcc	aac	gtt	gca	ctg	gag	gcc	atg	ggc	384																		
Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Val	Ala	Leu	Glu	Ala	Met	Gly																			
		115					120					125																						
cac	cag	aag	ggg	gag	tac	cag	tac	ctg	cac	ccg	aac	aac	gac	gtg	aac	432																		
His	Gln	Lys	Gly	Glu	Tyr	Gln	Tyr	Leu	His	Pro	Asn	Asn	Asp	Val	Asn																			
	130					135				140																								
atg	gcg	cag	tcg	acc	aac	gac	gcc	tac	ccg	acc	gct	atc	cgt	ctg	ggc	480																		
Met	Ala	Gln	Ser	Thr	Asn	Asp	Ala	Tyr	Pro	Thr	Ala	Ile	Arg	Leu	Gly																			
	145				150					155				160																				
ctg	ctg	ctg	ggg	cac	gac	gca	ctg	ctg	gcc	agc	ctc	gac	agc	ctg	att	528																		
Leu	Leu	Leu	Gly	His	Asp	Ala	Leu	Leu	Ala	Ser	Leu	Asp	Ser	Leu	Ile																			
			165					170					175																					
cag	gcc	ttc	gct	gcc	aag	ggg	aaa	gaa	ttc	gac	cac	gta	ctg	aag	atg	576																		
Gln	Ala	Phe	Ala	Ala	Lys	Gly	Lys	Glu	Phe	Asp	His	Val	Leu	Lys	Met																			
			180				185					190																						
ggc	cgt	acc	cag	ctg	cag	gac	gcc	gta	ccg	atg	acc	ctg	ggc	cag	gaa	624																		
Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu																			
	195					200				205																								
ttc	cgc	gcc	ttc	gcc	acc	acc	atg	acc	gaa	gac	ctg	cag	cgc	ctg	cgc	672																		
Phe	Arg	Ala	Phe	Ala	Thr	Thr	Met	Thr	Glu	Asp	Leu	Gln	Arg	Leu	Arg																			
	210				215					220																								
tcg	ctg	gcc	ccg	gaa	ctg	acc	gaa	atc	aac	ctg	ggc	ggg	acc	gcc		720																		
Ser	Leu	Ala	Pro	Glu	Leu	Thr	Glu	Ile	Asn	Leu	Gly	Gly	Thr	Ala																				
	225			230					235					240																				
atc	ggc	acc	ggc	atc	aac	gcc	gac	cct	ggc	tac	cag	gct	ctg	gcc	gta	768																		
Ile	Gly	Thr	Gly	Ile	Asn	Ala	Asp	Pro	Gly	Tyr	Gln	Ala	Leu	Ala	Val																			
			245				250					255																						
cag	cgc	ctg	gcc	gcc	atc	agt	ggc	cag	ccg	ctg	gta	ccg	gct	gcc	gac	816																		
Gln	Arg	Leu	Ala	Ala	Ile	Ser	Gly	Gln	Pro	Leu	Val	Pro	Ala	Ala	Asp																			
		260					265				270																							
ctg	atc	gaa	gcc	act	tcc	gac	atg	ggc	gcc	ttc	gtg	ctg	ttc	tcc	ggc	864																		
Leu	Ile	Glu	Ala	Thr	Ser	Asp	Met	Gly	Ala	Phe	Val	Leu	Phe	Ser	Gly																			
		275				280					285																							
atg	ctc	aag	cgt	acc	gcg	gtc	aag	ctc	tcg	aaa	atc	tgt	aac	gac	ttg	912																		
Met	Leu	Lys	Arg	Thr	Ala	Val	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu																			
	290				295					300																								
cgt	ctg	ctg	tcc	agc	ggc	ccg	cgc	acc	ggc	atc	aac	gag	atc	aac	ctg	960																		
Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Thr	Gly	Ile	Asn	Glu	Ile	Asn	Leu																			
	305				310				315						320																			
cca	gcg	cgt	cag	cca	ggc	agc	tcg	atc	atg	cca	ggc	aag	gtc	aac	ccg	1008																		
Pro	Ala	Arg	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro																			
			325				330						335																					
gtt	atc	ccg	gaa	gcc	gtc	aac	cag	gtg	gcc	ttc	gcc	atc	atg	ggc	aac	1056																		
Val	Ile	Pro	Glu	Ala	Val	Asn	Gln	Val	Ala	Phe	Ala	Ile	Met	Gly	Asn																			
		340					345				350																							
gac	ctg	gcc	ctg	acc	gtc	gcc	gcc	gaa	ggg	ggc	cag	ctg	cag	ctg	aac	1104																		
Asp	Leu	Ala	Leu	Thr	Val	Ala	Ala	Glu	Gly	Gly	Gln	Leu	Gln	Leu	Asn																			
		355				360					365																							
gtg	atg	gag	ccg	ctg	atc	gcc	tac	aag	atc	ttc	gac	tcg	atc	cgc	ctg	1152																		
Val	Met	Glu	Pro	Leu	Ile	Ala	Tyr	Lys	Ile	Phe	Asp	Ser	Ile	Arg	Leu																			
	370				375					380																								
ctg	caa	cgc	gcc	atg	gac	atg	ctg	cgc	gag	cac	tgk	atc	gtc	ggc	atc	1200																		
Leu	Gln	Arg	Ala	Met	Asp	Met	Leu	Arg	Glu	His	Cys	Ile	Val	Gly	Ile																			
	385				390					395				400																				
acc	gcc	aac	gaa	cag	cgc	tgc	cgt	gaa	ctg	gtc	gag	cac	tcg	atc	ggc	1248																		
Thr	Ala	Asn	Glu	Gln	Arg	Cys	Arg	Glu	Leu	Val	Glu	His	Ser	Ile	Gly																			
			405					410					415																					
ctg	gtc	act	gca	ctg	aac	ccg	tac	atc	ggc	tac	gaa	aac	gcc	acc	cgt	1296																		
Leu	Val	Thr	Ala	Leu	Asn	Pro	Tyr	Ile	Gly	Tyr	Glu	Asn	Ala	Thr	Arg																			
		420					425				430																							
atc	gcc	cgc	gtt	gcc	ctg	gaa	agc	ggc	cgc	ggc	gtg	ctg	gaa	ctg	gtg	1344																		
Ile	Ala	Arg	Val	Ala	Leu	Glu	Ser	Gly	Arg	Gly	Val	Leu	Glu	Leu	Val																			

1392

435										440					445				
cgt	gaa	gag	aag	ctg	ctg	gac	gac	gcg	atg	ctc	gac	gac	atc	ctg	cgt				
Arg	Glu	Glu	Lys	Leu	Leu	Asp	Asp	Ala	Met	Leu	Asp	Asp	Ile	Leu	Arg				
450										455					460				
cca	gaa	aac	atg	atc	gcc	ccg	cgc	ctg	gtt	ccg	ctg	aag	tcg	taa					
Pro	Glu	Asn	Met	Ile	Ala	Pro	Arg	Leu	Val	Pro	Leu	Lys	Ser						
465										470					475				

1437

```
<210> 9734
<211> 478
<212> PRT
<213> Pseudomonas putida GB-1
```

<400>	9734																
Met	Ile	Tyr	Ile	Met	Ser	Ser	Ala	Ala	Ser	Phe	Arg	Val	Glu	Lys	Asp		
1				5					10					15			
Leu	Leu	Gly	Thr	Leu	Glu	Val	Pro	Ala	Asp	Ala	Tyr	Tyr	Gly	Ile	Gln		
			20					25					30				
Thr	Leu	Arg	Ala	Ala	Asn	Asn	Phe	His	Leu	Ser	Gly	Val	Pro	Leu	Ser		
		35					40					45					
His	Tyr	Pro	Lys	Leu	Val	Val	Ala	Leu	Ala	Met	Val	Lys	Gln	Ala	Ala		
	50					55					60						
Ala	Asp	Ala	Asn	Arg	Glu	Leu	Gly	His	Leu	Ser	Asp	Ala	Lys	His	Ala		
65					70					75					80		
Ala	Ile	Thr	Ala	Ala	Cys	Ala	Arg	Leu	Ile	Lys	Gly	Asp	Tyr	His	Asp		
			85						90					95			
Gln	Phe	Val	Val	Asp	Met	Ile	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Thr	Asn		
			100					105					110				
Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Val	Ala	Leu	Glu	Ala	Met	Gly		
		115					120					125					
His	Gln	Lys	Gly	Glu	Tyr	Gln	Tyr	Leu	His	Pro	Asn	Asn	Asp	Val	Asn		
	130					135					140						
Met	Ala	Gln	Ser	Thr	Asn	Asp	Ala	Tyr	Pro	Thr	Ala	Ile	Arg	Leu	Gly		
145					150					155					160		
Leu	Leu	Leu	Gly	His	Asp	Ala	Leu	Leu	Ala	Ser	Leu	Asp	Ser	Leu	Ile		
			165						170					175			
Gln	Ala	Phe	Ala	Ala	Lys	Gly	Lys	Glu	Phe	Asp	His	Val	Leu	Lys	Met		
			180					185					190				
Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu		
		195					200					205					
Phe	Arg	Ala	Phe	Ala	Thr	Thr	Met	Thr	Glu	Asp	Leu	Gln	Arg	Leu	Arg		
	210					215					220						
Ser	Leu	Ala	Pro	Glu	Leu	Leu	Thr	Glu	Ile	Asn	Leu	Gly	Gly	Thr	Ala		
225					230					235					240		
Ile	Gly	Thr	Gly	Ile	Asn	Ala	Asp	Pro	Gly	Tyr	Gln	Ala	Leu	Ala	Val		
			245						250					255			
Gln	Arg	Leu	Ala	Ala	Ile	Ser	Gly	Gln	Pro	Leu	Val	Pro	Ala	Ala	Asp		
			260					265					270				
Leu	Ile	Glu	Ala	Thr	Ser	Asp	Met	Gly	Ala	Phe	Val	Leu	Phe	Ser	Gly		
		275					280					285					
Met	Leu	Lys	Arg	Thr	Ala	Val	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu		
	290					295					300						
Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Thr	Gly	Ile	Asn	Glu	Ile	Asn	Leu		
305																	

PF59083SeqList PF59083.txt

435 440 445
 Arg Glu Glu Lys Leu Leu Asp Asp Ala Met Leu Asp Asp Ile Leu Arg
 450 455 460
 Pro Glu Asn Met Ile Ala Pro Arg Leu Val Pro Leu Lys Ser
 465 470 475

<210> 9735
 <211> 1395
 <212> DNA
 <213> Pseudomonas putida GB-1

<220>
 <221> CDS
 <222> (1)..(1395)
 <223> transl_table=11

<400> 9735
 atg agc cgt atc gag aca gac agc ctg ggc ccg gtc gaa gtt ccg gag 48
 Met Ser Arg Ile Glu Thr Asp Ser Leu Gly Pro Val Glu Val Pro Glu
 1 5 10 15
 gac gcc tac tgg ggt gcg cag acc cag cgt tcg ctg atc aac ttc gcc 96
 Asp Ala Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Ile Asn Phe Ala
 20 25 30
 att ggc aag gaa cgc atg ccc ctc gcg gtg ctg cac gcc ctg gca ctg 144
 Ile Gly Lys Glu Arg Met Pro Leu Ala Val Leu His Ala Leu
 35 40 45
 atc aag aag gcc gcg gcg cgc gtc aac gac cgc aat ggc gac ttg ccg 192
 Ile Lys Lys Ala Ala Ala Arg Val Asn Asp Arg Asn Gly Asp Leu Pro
 50 55 60
 gcc gac atc gcc cgg ttg atc gaa cag gcc gcc gat gaa gtg ctg gat 240
 Ala Asp Ile Ala Arg Leu Ile Glu Gln Ala Ala Asp Glu Val Leu Asp
 65 70 75 80
 ggc aag cac gat gac cag ttc ccg ctc gtc gtc tgg caa acg ggc agc 288
 Gly Lys His Asp Asp Gln Phe Pro Leu Val Val Trp Gln Thr Gly Ser
 85 90 95
 ggc acc cag agc aac atg aac gtc aac gag gtt att gcc ggg cgc gcc 336
 Gly Thr Gln Ser Asn Met Asn Val Asn Glu Val Ile Ala Gly Arg Ala
 100 105 110
 aac gag ctg gcc ggc aaa ggc cgt ggc ggc aag gcg cca gta cac ccc 384
 Asn Glu Leu Ala Gly Lys Gly Arg Gly Gly Lys Ala Pro Val His Pro
 115 120 125
 aac gac cac gtc aac cgc tcg caa agc tcc aac gac tgc ttc ccc acg 432
 Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp Cys Phe Pro Thr
 130 135 140
 gcc atg cac att gct gct gcg cag gca gtg cat gaa cag ctg ctg cca 480
 Ala Met His Ile Ala Ala Ala Gln Ala Val His Glu Gln Leu Leu Pro
 145 150 155 160
 gcg atc gcc gag ctg tcg tca ggg ctg gcc gag ttg tcg gcg cgc cac 528
 Ala Ile Ala Glu Leu Ser Ser Gly Leu Ala Glu Leu Ser Ala Arg His
 165 170 175
 aac aag ctg gtg aaa acc ggc cgc acg cac atg atg gac gcc aca ccg 576
 Asn Lys Leu Val Lys Thr Gly Arg Thr His Met Met Asp Ala Thr Pro
 180 185 190
 atc acc ttc ggc cag gag gtt tcg gcc ttc gtc gcg caa ctc gac tac 624
 Ile Thr Phe Gly Gln Glu Val Ser Ala Phe Val Ala Gln Leu Asp Tyr
 195 200 205
 gcc cag cgc gcc atc cgc gcc acc ctg ccg gcg gtg tgt gaa ctg gcc 672
 Ala Gln Arg Ala Ile Arg Ala Thr Leu Pro Ala Val Cys Glu Leu Ala
 210 215 220
 cag ggc ggt acc gcc gtg ggt acc ggg ctc aac gcc ccg cat ggt ttt 720
 Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Ala Pro His Gly Phe
 225 230 235 240
 gcc gaa gcc atc gct gcc gag ttg gcg gcg gag tcc ggg ctg cca ttc 768
 Ala Glu Ala Ile Ala Ala Glu Leu Ala Ala Glu Ser Gly Leu Pro Phe
 245 250 255
 gtc acc gcg ccc aac aag ttt gcc gcc ctc gct ggc cac gaa ccg ctg 816
 Val Thr Ala Pro Asn Lys Phe Ala Ala Leu Ala Gly His Glu Pro Leu
 260 265 270
 acc agc ctg gcc ggg gcc ctg aag acc ctg gct gta gcc ctg atg aaa 864

PF59083SeqList PF59083.txt

Thr	Ser	Leu	Ala	Gly	Ala	Leu	Lys	Thr	Leu	Ala	Val	Ala	Leu	Met	Lys	
		275					280					285				
atc	gcc	aac	gac	ctg	cg	ctg	ctg	ggc	tct	ggc	ccg	cg	gcg	gga	ctg	912
Ile	Ala	Asn	Asp	Leu	Arg	Leu	Leu	Gly	Ser	Gly	Pro	Arg	Ala	Gly	Leu	
	290					295					300					
gcc	gag	gtg	cg	ctg	ccg	gcc	aac	gag	ccg	ggc	agt	tcg	atc	atg	ccg	960
Ala	Glu	Val	Arg	Leu	Pro	Ala	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
305					310					315					320	
ggc	aag	gtc	aac	ccg	acc	cag	tgc	gag	gca	ctg	tcg	atg	ctg	gcc	tgc	1008
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Ser	Met	Leu	Ala	Cys	
				325				330						335		
cag	gtg	ctg	ggc	aat	gac	gcg	gcg	att	ggg	ttt	gcc	gcc	agc	cag	ggg	1056
Gln	Val	Leu	Gly	Asn	Asp	Ala	Ala	Ile	Gly	Phe	Ala	Ala	Ser	Gln	Gly	
			340					345					350			
cat	ttg	cag	ttg	aac	gta	ttc	aag	ccg	gta	atc	att	cat	aac	ctg	ctg	1104
His	Leu	Gln	Leu	Asn	Val	Phe	Lys	Pro	Val	Ile	Ile	His	Asn	Leu	Leu	
			355				360					365				
caa	tcg	gtc	gaa	ttg	ctg	gcc	gat	ggg	tgc	cg	aat	ttc	cag	ctg	cat	1152
Gln	Ser	Val	Glu	Leu	Leu	Ala	Asp	Gly	Cys	Arg	Asn	Phe	Gln	Leu	His	
	370					375					380					
tgc	gtg	gcg	ggg	atc	gaa	ccg	gat	gcc	cag	cag	atg	gct	gcg	cac	ctg	1200
Cys	Val	Ala	Gly	Ile	Glu	Pro	Asp	Ala	Gln	Gln	Met	Ala	Ala	His	Leu	
385					390					395					400	
gaa	cg	ggg	ttg	atg	ctg	gtg	acc	gcg	ctc	aac	ccg	cac	att	ggc	tat	1248
Glu	Arg	Gly	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	
				405				410						415		
gac	aag	gca	gcg	gaa	att	gcc	aag	aag	gct	tac	agc	gaa	ggc	aag	acc	1296
Asp	Lys	Ala	Ala	Glu	Ile	Ala	Lys	Lys	Ala	Tyr	Ser	Glu	Gly	Lys	Thr	
				420				425					430			
ttg	agg	gag	gcg	gca	ttg	gag	ttg	aag	tat	ctg	acc	aat	gag	cag	ttc	1344
Leu	Arg	Glu	Ala	Ala	Leu	Glu	Leu	Lys	Tyr	Leu	Thr	Asn	Glu	Gln	Phe	
				435			440					445				
gac	cag	tgg	gtg	cg	cca	gag	aac	atg	ctg	gcc	cca	ggg	ggg	cat	ggc	1392
Asp	Gln	Trp	Val	Arg	Pro	Glu	Asn	Met	Leu	Ala	Pro	Gly	Gly	His	Gly	
	450					455					460					
taa																1395

<210> 9736
 <211> 464
 <212> PRT
 <213> Pseudomonas putida GB-1

<400> 9736
 Met Ser Arg Ile Glu Thr Asp Ser Leu Gly Pro Val Glu Val Pro Glu
 1 5 10 15
 Asp Ala Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Ile Asn Phe Ala
 20 25 30
 Ile Gly Lys Glu Arg Met Pro Leu Val Leu His Ala Leu Ala Leu
 35 40 45
 Ile Lys Lys Ala Ala Ala Arg Val Asn Asp Arg Asn Gly Asp Leu Pro
 50 55 60
 Ala Asp Ile Ala Arg Leu Ile Glu Gln Ala Ala Asp Glu Val Leu Asp
 65 70 75 80
 Gly Lys His Asp Asp Gln Phe Pro Leu Val Val Trp Gln Thr Gly Ser
 85 90 95
 Gly Thr Gln Ser Asn Met Asn Val Asn Glu Val Ile Ala Gly Arg Ala
 100 105 110
 Asn Glu Leu Ala Gly Lys Gly Arg Gly Lys Ala Pro Val His Pro
 115 120 125
 Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp Cys Phe Pro Thr
 130 135 140
 Ala Met His Ile Ala Ala Gln Ala Val His Glu Gln Leu Leu Pro
 145 150 155 160
 Ala Ile Ala Glu Leu Ser Ser Gly Leu Ala Glu Leu Ser Ala Arg His
 165 170 175
 Asn Lys Leu Val Lys Thr Gly Arg Thr His Met Met Asp Ala Thr Pro
 180 185 190

PF59083SeqList PF59083.txt

Ile Thr Phe Gly Gln Glu Val Ser Ala Phe Val Ala Gln Leu Asp Tyr
 195 200 205
 Ala Gln Arg Ala Ile Arg Ala Thr Leu Pro Ala Val Cys Glu Leu Ala
 210 215 220
 Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Ala Pro His Gly Phe
 225 230 235 240
 Ala Glu Ala Ile Ala Ala Glu Leu Ala Ala Glu Ser Gly Leu Pro Phe
 245 250 255
 Val Thr Ala Pro Asn Lys Phe Ala Ala Leu Ala Gly His Glu Pro Leu
 260 265 270
 Thr Ser Leu Ala Gly Ala Leu Lys Thr Leu Ala Val Ala Leu Met Lys
 275 280 285
 Ile Ala Asn Asp Leu Arg Leu Leu Gly Ser Gly Pro Arg Ala Gly Leu
 290 295 300
 Ala Glu Val Arg Leu Pro Ala Asn Glu Pro Gly Ser Ser Ile Met Pro
 305 310 315 320
 Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Ser Met Leu Ala Cys
 325 330 335
 Gln Val Leu Gly Asn Asp Ala Ala Ile Gly Phe Ala Ala Ser Gln Gly
 340 345 350
 His Leu Gln Leu Asn Val Phe Lys Pro Val Ile Ile His Asn Leu Leu
 355 360 365
 Gln Ser Val Glu Leu Leu Ala Asp Gly Cys Arg Asn Phe Gln Leu His
 370 375 380
 Cys Val Ala Gly Ile Glu Pro Asp Ala Gln Gln Met Ala Ala His Leu
 385 390 395 400
 Glu Arg Gly Leu Met Leu Val Thr Ala Leu Asn Pro His Ile Gly Tyr
 405 410 415
 Asp Lys Ala Ala Glu Ile Ala Lys Lys Ala Tyr Ser Glu Gly Lys Thr
 420 425 430
 Leu Arg Glu Ala Ala Leu Glu Leu Lys Tyr Leu Thr Asn Glu Gln Phe
 435 440 445
 Asp Gln Trp Val Arg Pro Glu Asn Met Leu Ala Pro Gly Gly His Gly
 450 455 460

<210> 9737

<211> 1380

<212> DNA

<213> Pseudomonas putida GB-1

<220>

<221> CDS

<222> (1)..(1380)

<223> transl_table=11

<400> 9737

atg atg agt gat acc cgt atc gag cgt gac agc atg ggt gaa ctg cag	48
Met Met Ser Asp Thr Arg Ile Glu Arg Asp Ser Met Gly Glu Leu Gln	
1 5 10 15	
gtg cct gcc cag gcc ctg tac ggc gcc cag acc caa cgc gcg gtc gac	96
Val Pro Ala Gln Ala Leu Tyr Gly Ala Gln Thr Gln Arg Ala Val Asp	
20 25 30	
aac ttc ccg atc agc ggc cag cgc atg ccg gcc cag ttc att cgt gct	144
Asn Phe Pro Ile Ser Gly Gln Arg Met Pro Ala Gln Phe Ile Arg Ala	
35 40 45	
ctg ctg ctg gcc aag gca gcc gcg gcc aag gcc aac atc gag ctg gaa	192
Leu Leu Leu Ala Lys Ala Ala Ala Lys Ala Asn Ile Glu Leu Glu	
50 55 60	
caa ctg tcc gcc gcg cag ggc caa gcc atc gtc aag gct gtc gag caa	240
Gln Leu Ser Ala Ala Gln Gly Gln Ala Ile Val Lys Ala Val Glu Gln	
65 70 75 80	
ctg ttg gcc gaa gac ttc atc cag cat ttc ccg gtc gat gtg ttc cag	288
Leu Leu Ala Glu Asp Phe Ile Gln His Phe Pro Val Asp Val Phe Gln	
85 90 95	
acc ggc tcc ggc acc agc tcg aac atg aac gcc aac gaa gtg atc gcg	336
Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Ala Asn Glu Val Ile Ala	
100 105 110	
acc ttg gcc agc cgc gta ctg ggt gag gca gtc aat gcc aat gat cac	384
Thr Leu Ala Ser Arg Val Leu Gly Glu Ala Val Asn Ala Asn Asp His	

PF59083SeqList PF59083.txt

gtc	aac	tgt	ggc	cag	agc	agc	aat	gac	atc	atc	ccg	acc	act	atc	cac	432
Val	Asn	Cys	Gly	Gln	Ser	Ser	Asn	Asp	Ile	Ile	Pro	Thr	Thr	Ile	His	
130						135					140					
gtc	agt	gcc	gcg	ctg	gcc	ctg	cac	gaa	cag	ttg	ctg	cca	gcc	ttg	gcg	480
Val	Ser	Ala	Ala	Leu	Ala	Leu	His	Glu	Gln	Leu	Leu	Pro	Ala	Leu	Ala	
145					150					155					160	
cac	ctg	gta	cag	gtg	atc	gag	gcc	aag	tcg	gcg	caa	gtg	cat	cag	tat	528
His	Leu	Val	Gln	Val	Ile	Glu	Ala	Lys	Ser	Ala	Gln	Val	His	Gln	Tyr	
			165			170								175		
gtg	aaa	acg	ggc	cgc	acc	cac	ctg	atg	gac	gcc	atg	ccg	gtg	cgc	atg	576
Val	Lys	Thr	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Met	Pro	Val	Arg	Met	
			180					185						190		
agc	cag	gtg	ctg	gat	ggc	tgg	gcg	gca	cag	atc	aac	ggc	gcc	aag	gca	624
Ser	Gln	Val	Leu	Asp	Gly	Trp	Ala	Ala	Gln	Ile	Asn	Gly	Ala	Lys	Ala	
			195			200						205				
cac	ctc	gaa	gcc	acc	ttg	ctg	agc	ctg	cag	gcg	ctg	gcc	cag	ggc	ggc	672
His	Leu	Glu	Ala	Thr	Leu	Leu	Ser	Leu	Gln	Ala	Leu	Ala	Gln	Gly	Gly	
			210			215					220					
acc	gcc	gtg	ggt	acc	ggc	atc	aat	gcc	cac	ccc	cgg	ttc	gct	ggc	gtg	720
Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Ala	His	Pro	Arg	Phe	Ala	Gly	Val	
225					230					235					240	
ttt	gcc	cgc	caa	ctc	agt	ggc	ctg	acc	caa	gtc	gag	ttc	acc	cca	ggg	768
Phe	Ala	Arg	Gln	Leu	Ser	Gly	Leu	Thr	Gln	Val	Glu	Phe	Thr	Pro	Gly	
					245					250				255		
caa	aac	ctg	ttt	gcc	ctg	atc	ggc	tcg	gat	acc	gcc	gtg	gcc	ctg		816
Gln	Asn	Leu	Phe	Ala	Leu	Ile	Gly	Ser	Gln	Asp	Thr	Ala	Val	Ala	Leu	
			260					265						270		
tct	ggc	cag	ctc	aag	act	acc	gct	gtg	gca	ctg	atg	aaa	att	gcc	aac	864
Ser	Gly	Gln	Leu	Lys	Thr	Thr	Ala	Val	Ala	Leu	Met	Lys	Ile	Ala	Asn	
			275			280						285				
gac	ctg	cgc	tgg	atg	aac	tcc	ggc	ccg	ctg	gcc	ggc	ctg	ggc	gaa	atc	912
Asp	Leu	Arg	Trp	Met	Asn	Ser	Gly	Pro	Leu	Ala	Gly	Leu	Gly	Glu	Ile	
			290			295					300					
gag	ctg	caa	ggc	ctg	cag	cct	ggc	tct	tcg	atc	atg	ccg	ggc	aag	gtc	960
Glu	Leu	Gln	Gly	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	
305					310					315					320	
aac	ccg	gtg	atc	ccg	gag	gcc	act	gcc	atg	gtc	gcc	gcc	cag	gtg	att	1008
Asn	Pro	Val	Ile	Pro	Glu	Ala	Thr	Ala	Met	Val	Ala	Ala	Gln	Val	Ile	
				325						330				335		
ggc	aac	gac	gcc	acc	atc	gcc	atc	gcg	ggg	cag	tcc	ggc	aac	ttc	gag	1056
Gly	Asn	Asp	Ala	Thr	Ile	Ala	Ile	Ala	Gly	Gln	Ser	Gly	Asn	Phe	Glu	
			340					345						350		
ctg	aac	gtg	atg	ctg	ccg	gtg	atc	gcc	cgc	aac	ctg	ctg	gaa	agc	atc	1104
Leu	Asn	Val	Met	Leu	Pro	Val	Ile	Ala	Arg	Asn	Leu	Leu	Glu	Ser	Ile	
			355			360								365		
gag	ctg	atg	gcc	aac	gtc	agc	cgc	ttg	ctg	gcc	gac	aag	gcc	atc	gcc	1152
Glu	Leu	Met	Ala	Asn	Val	Ser	Arg	Leu	Leu	Ala	Asp	Lys	Ala	Ile	Ala	
			370			375					380					
acc	ttc	aag	gtc	aac	gag	gtc	aag	ctc	aag	gaa	gcc	ctg	gcg	cgc	aac	1200
Thr	Phe	Lys	Val	Asn	Glu	Gly	Lys	Leu	Lys	Glu	Ala	Leu	Ala	Arg	Asn	
385					390					395					400	
ccg	atc	ctg	gtc	act	gcg	ctg	aac	ccg	atc	atc	ggc	tac	ctc	aag	gcc	1248
Pro	Ile	Leu	Val	Thr	Ala	Leu	Asn	Pro	Ile	Ile	Gly	Tyr	Leu	Lys	Ala	
				405						410				415		
gcc	gaa	atc	gcc	aag	acc	gcg	tac	aag	caa	ggc	cgc	ccg	atc	atc	gat	1296
Ala	Glu	Ile	Ala	Lys	Thr	Ala	Tyr	Lys	Gln	Gly	Arg	Pro	Ile	Ile	Asp	
			420					425						430		
gtg	gcg	ctg	gag	cac	acc	gat	ttg	tcg	cgt	gac	cag	ctc	gaa	gca	ctg	1344
Val	Ala	Leu	Glu	His	Thr	Asp	Leu	Ser	Arg	Asp	Gln	Leu	Glu	Ala	Leu	
			435			440								445		
ctg	gac	ccg	gaa	aaa	ctc	acc	gcc	ggc	gga	atc	tga					1380
Leu	Asp	Pro	Glu	Lys	Leu	Thr	Ala	Gly	Gly	Ile						
			450			455										

<210> 9738

<211> 459

<212> PRT

<213> Pseudomonas putida GB-1

PF59083SeqList PF59083.txt

<400> 9738

```

Met Met Ser Asp Thr Arg Ile Glu Arg Asp Ser Met Gly Glu Leu Gln
1      5      10      15
Val Pro Ala Gln Ala Leu Tyr Gly Ala Gln Thr Gln Arg Ala Val Asp
20      25      30
Asn Phe Pro Ile Ser Gly Gln Arg Met Pro Ala Gln Phe Ile Arg Ala
35      40      45
Leu Leu Leu Ala Lys Ala Ala Ala Lys Ala Asn Ile Glu Leu Glu
50      55      60
Gln Leu Ser Ala Ala Gln Gly Gln Ala Ile Val Lys Ala Val Glu Gln
65      70      75      80
Leu Leu Ala Glu Asp Phe Ile Gln His Phe Pro Val Asp Val Phe Gln
85      90      95
Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Ala Asn Glu Val Ile Ala
100      105      110
Thr Leu Ala Ser Arg Val Leu Gly Glu Ala Val Asn Ala Asn Asp His
115      120      125
Val Asn Cys Gly Gln Ser Ser Asn Asp Ile Ile Pro Thr Thr Ile His
130      135      140
Val Ser Ala Ala Leu Ala Leu His Glu Gln Leu Leu Pro Ala Leu Ala
145      150      155      160
His Leu Val Gln Val Ile Glu Ala Lys Ser Ala Gln Val His Gln Tyr
165      170      175
Val Lys Thr Gly Arg Thr His Leu Met Asp Ala Met Pro Val Arg Met
180      185      190
Ser Gln Val Leu Asp Gly Trp Ala Ala Gln Ile Asn Gly Ala Lys Ala
195      200      205
His Leu Glu Ala Thr Leu Leu Ser Leu Gln Ala Leu Ala Gln Gly Gly
210      215      220
Thr Ala Val Gly Thr Gly Ile Asn Ala His Pro Arg Phe Ala Gly Val
225      230      235      240
Phe Ala Arg Gln Leu Ser Gly Leu Thr Gln Val Glu Phe Thr Pro Gly
245      250      255
Gln Asn Leu Phe Ala Leu Ile Gly Ser Gln Asp Thr Ala Val Ala Leu
260      265      270
Ser Gly Gln Leu Lys Thr Thr Ala Val Ala Leu Met Lys Ile Ala Asn
275      280      285
Asp Leu Arg Trp Met Asn Ser Gly Pro Leu Ala Gly Leu Gly Glu Ile
290      295      300
Glu Leu Gln Gly Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys Val
305      310      315      320
Asn Pro Val Ile Pro Glu Ala Thr Ala Met Val Ala Ala Gln Val Ile
325      330      335
Gly Asn Asp Ala Thr Ile Ala Ile Ala Gly Gln Ser Gly Asn Phe Glu
340      345      350
Leu Asn Val Met Leu Pro Val Ile Ala Arg Asn Leu Leu Glu Ser Ile
355      360      365
Glu Leu Met Ala Asn Val Ser Arg Leu Leu Ala Asp Lys Ala Ile Ala
370      375      380
Thr Phe Lys Val Asn Glu Gly Lys Leu Lys Glu Ala Leu Ala Arg Asn
385      390      395      400
Pro Ile Leu Val Thr Ala Leu Asn Pro Ile Ile Gly Tyr Leu Lys Ala
405      410      415
Ala Glu Ile Ala Lys Thr Ala Tyr Lys Gln Gly Arg Pro Ile Ile Asp
420      425      430
Val Ala Leu Glu His Thr Asp Leu Ser Arg Asp Gln Leu Glu Ala Leu
435      440      445
Leu Asp Pro Glu Lys Leu Thr Ala Gly Gly Ile
450      455

```

<210> 9739

<211> 1380

<212> DNA

<213> Marinobacter sp. ELB17

<220>

<221> CDS

<222> (1)..(1380)

<223> transl_table=11

<400> 9739

atg agc aat gaa cgg gta gaa agc gac agc ctt ggc gac gtc agg gtg	48
Met Ser Asn Glu Arg Val Glu Ser Asp Ser Leu Gly Asp Val Arg Val	
1 5 10 15	
ccg gaa aac gca ctt tgg gga gca caa acc caa cgc gcc atc gag aac	96
Pro Glu Asn Ala Leu Trp Gly Ala Gln Thr Gln Arg Ala Ile Glu Asn	
20 25 30	
ttc ccc gtc agc ggg caa ccc atg ccg ccg gcg ttc atc gcc gcc gtg	144
Phe Pro Val Ser Gly Gln Pro Met Pro Pro Ala Phe Ile Ala Ala Val	
35 40 45	
gtg cag ata aaa aaa gcc gcg gcg gaa gct aat gcc agc ctg gcc ttg	192
Val Gln Ile Lys Lys Ala Ala Glu Ala Asn Ala Ser Leu Ala Leu	
50 55 60	
ctc aat ggc ccg gtt cgc gat gct att gtg cta gcc tgt gac cag ttg	240
Leu Asn Gly Pro Val Arg Asp Ala Ile Val Leu Ala Cys Asp Gln Leu	
65 70 75 80	
ctg gcc ggt gat tac tat gat cag ttt ccg gta gac cgc tac cag acc	288
Leu Ala Gly Asp Tyr Tyr Asp Gln Phe Pro Val Asp Arg Tyr Gln Thr	
85 90 95	
ggc tct ggc acc agc acc aac atg aat gtt aac gag gtg atc gcg gca	336
Gly Ser Gly Thr Ser Thr Asn Met Asn Val Asn Glu Val Ile Ala Ala	
100 105 110	
ctg gcc gag ctc agt ggt gtg atg gtt cat ccc aac gac cac gtg aat	384
Leu Ala Glu Leu Ser Gly Val Met Val His Pro Asn Asp His Val Asn	
115 120 125	
atg agc cag agt tct aac gat gtc atc ccg tcg gct atc cat atc agc	432
Met Ser Gln Ser Ser Asn Asp Val Ile Pro Ser Ala Ile His Ile Ser	
130 135 140	
gcg gtg ata gcg att cac cag aat ctg gtg ccg gcg ctg acc cat tta	480
Ala Val Ile Ala Ile His Gln Asn Leu Val Pro Ala Leu Thr His Leu	
145 150 155 160	
caa ggc gtt ctc tac gag cgc gaa gcc atg tat ggc gag cag gta aaa	528
Gln Gly Val Leu Tyr Glu Arg Glu Ala Met Tyr Gly Glu Gln Val Lys	
165 170 175	
acc ggt aga acc cac ctg atg gac gca atg ccg gtg acc ctg ggc caa	576
Thr Gly Arg Thr His Leu Met Asp Ala Met Pro Val Thr Leu Gly Gln	
180 185 190	
gag ctt cgt act tgg cgc gag caa ttg aaa gcg aca cag gcg cgc atc	624
Glu Leu Arg Thr Trp Arg Glu Gln Leu Lys Ala Thr Gln Ala Arg Ile	
195 200 205	
gaa cgt gca gca gat gag ctt ctg gcg ttg ccc cag ggc ggc acg gct	672
Glu Arg Ala Ala Asp Glu Leu Leu Ala Leu Pro Gln Gly Gly Thr Ala	
210 215 220	
gta ggc acc ggg att aat gcc gtt agc gag ttt gcg cct gag ttt acc	720
Val Gly Thr Gly Ile Asn Ala Val Ser Glu Phe Ala Pro Glu Phe Thr	
225 230 235 240	
cgc tgt ctg aaa gcc aat acc ggt ttt ggc ttc aag cca cta gcc cat	768
Arg Cys Leu Lys Ala Asn Thr Gly Phe Gly Phe Lys Pro Leu Ala His	
245 250 255	
aag ttt gtg gca cag agc gca gtg gat gcg ccg gtg gcg ctg tcg gcg	816
Lys Phe Val Ala Gln Ser Ala Val Asp Ala Pro Val Ala Leu Ser Ala	
260 265 270	
cag ctg cgt ggg ctt ggc ata gtg ctg aca aaa atc gcc aac gat ttg	864
Gln Leu Arg Gly Leu Gly Ile Val Leu Thr Lys Ile Ala Asn Asp Leu	
275 280 285	
cgc tgg atg aac agc ggc ccc att cac ggg ctg tca gaa atc agc ctt	912
Arg Trp Met Asn Ser Gly Pro Ile His Gly Leu Ser Glu Ile Ser Leu	
290 295 300	
ccg gta ctt cag cca ggc agc agc att atg cca ggc aaa gtg aac ccg	960
Pro Val Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro	
305 310 315 320	
gtg atc ccc gag tct gtg gct atg gta ggc gcc cag att atg gga ctt	1008
Val Ile Pro Glu Ser Val Ala Met Val Gly Ala Gln Ile Met Gly Leu	
325 330 335	
gat gcc tct atc gct tac gcc ggg cag tct ggt aat ttc cag ctc aac	1056
Asp Ala Ser Ile Ala Tyr Ala Gly Gln Ser Gly Asn Phe Gln Leu Asn	
340 345 350	

PF59083SeqList PF59083.txt

gtg	atg	tta	ccg	ttg	gtc	ggt	gcc	aac	ctg	ctg	gag	atg	att	ggc	ctg	1104
Val	Met	Leu	Pro	Leu	Val	Gly	Ala	Asn	Leu	Leu	Glu	Met	Ile	Gly	Leu	
		355					360					365				
tta	agc	aat	gcc	agc	agt	ctg	ctg	agt	gac	aaa	gca	cta	aaa	ggc	ttt	1152
Leu	Ser	Asn	Ala	Ser	Ser	Leu	Leu	Ser	Asp	Lys	Ala	Leu	Lys	Gly	Phe	
	370					375					380					
acc	gtc	aac	gca	gag	cat	cta	aac	gca	ggt	gtt	ggc	cgt	aat	ccc	gtg	1200
Thr	Val	Asn	Ala	Glu	His	Leu	Asn	Ala	Gly	Val	Gly	Arg	Asn	Pro	Val	
	385				390					395					400	
ctg	gtg	acg	gcg	tta	aac	ccc	gaa	att	ggt	tac	agc	ctg	gcg	tct	gaa	1248
Leu	Val	Thr	Ala	Leu	Asn	Pro	Glu	Ile	Gly	Tyr	Ser	Leu	Ala	Ser	Glu	
				405					410					415		
att	gcc	aaa	gaa	gcc	tac	gcc	agt	ggc	cgc	ccg	gta	att	gat	gtg	gct	1296
Ile	Ala	Lys	Glu	Ala	Tyr	Ala	Ser	Gly	Arg	Pro	Val	Ile	Asp	Val	Ala	
			420					425					430			
gaa	gag	cgc	agt	ggg	ctc	agc	cgc	gag	cgg	ctt	gag	cag	ctt	atg	gac	1344
Glu	Glu	Arg	Ser	Gly	Leu	Ser	Arg	Glu	Arg	Leu	Glu	Gln	Leu	Met	Asp	
		435					440					445				
ccg	tta	aaa	ctg	acc	cgc	ggc	ggg	ttg	gca	ggg	tag					1380
Pro	Leu	Lys	Leu	Thr	Arg	Gly	Gly	Leu	Ala	Gly						
	450					455										

<210> 9740

<211> 459

<212> PRT

<213> Marinobacter sp. ELB17

<400> 9740

Met	Ser	Asn	Glu	Arg	Val	Glu	Ser	Asp	Ser	Leu	Gly	Asp	Val	Arg	Val	
1				5					10					15		
Pro	Glu	Asn	Ala	Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ala	Ile	Glu	Asn	
		20						25					30			
Phe	Pro	Val	Ser	Gly	Gln	Pro	Met	Pro	Pro	Ala	Phe	Ile	Ala	Ala	Val	
		35					40					45				
Val	Gln	Ile	Lys	Lys	Ala	Ala	Glu	Ala	Asn	Ala	Ser	Leu	Ala	Leu		
	50					55				60						
Leu	Asn	Gly	Pro	Val	Arg	Asp	Ala	Ile	Val	Leu	Ala	Cys	Asp	Gln	Leu	
65					70				75					80		
Leu	Ala	Gly	Asp	Tyr	Tyr	Asp	Gln	Phe	Pro	Val	Asp	Arg	Tyr	Gln	Thr	
			85					90					95			
Gly	Ser	Gly	Thr	Ser	Thr	Asn	Met	Asn	Val	Asn	Glu	Val	Ile	Ala	Ala	
			100					105					110			
Leu	Ala	Glu	Leu	Ser	Gly	Val	Met	Val	His	Pro	Asn	Asp	His	Val	Asn	
		115					120					125				
Met	Ser	Gln	Ser	Ser	Asn	Asp	Val	Ile	Pro	Ser	Ala	Ile	His	Ile	Ser	
	130					135					140					
Ala	Val	Ile	Ala	Ile	His	Gln	Asn	Leu	Val	Pro	Ala	Leu	Thr	His	Leu	
145					150					155					160	
Gln	Gly	Val	Leu	Tyr	Glu	Arg	Glu	Ala	Met	Tyr	Gly	Glu	Gln	Val	Lys	
			165					170					175			
Thr	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Met	Pro	Val	Thr	Leu	Gly	Gln	
			180					185					190			
Glu	Leu	Arg	Thr	Trp	Arg	Glu	Gln	Leu	Lys	Ala	Thr	Gln	Ala	Arg	Ile	
		195					200					205				
Glu	Arg	Ala	Ala	Asp	Glu	Leu	Leu	Ala	Leu	Pro	Gln	Gly	Gly	Thr	Ala	
	210					215					220					
Val	Gly	Thr	Gly	Ile	Asn	Ala	Val	Ser	Glu	Phe	Ala	Pro	Glu	Phe	Thr	
225					230					235					240	
Arg	Cys	Leu	Lys	Ala	Asn	Thr	Gly	Phe	Gly	Phe	Lys	Pro	Leu	Ala	His	
			245					250						255		
Lys	Phe	Val	Ala	Gln	Ser	Ala	Val	Asp	Ala	Pro	Val	Ala	Leu	Ser	Ala	
			260					265					270			
Gln	Leu	Arg	Gly	Leu	Gly	Ile	Val	Leu	Thr	Lys	Ile	Ala	Asn	Asp	Leu	
		275					280					285				
Arg	Trp	Met	Asn	Ser	Gly	Pro	Ile	His	Gly	Leu	Ser	Glu	Ile	Ser	Leu	
	290					295					300					
Pro	Val	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	
305					310					315					320	
Val	Ile	Pro	Glu	Ser	Val	Ala	Met	Val	Gly	Ala	Gln	Ile	Met	Gly	Leu	

PF59083SeqList PF59083.txt

```

          325          330          335
Asp Ala Ser Ile Ala Tyr Ala Gly Gln Ser Gly Asn Phe Gln Leu Asn
Val Met Leu Pro Leu Val Gly Ala Asn Leu Leu Glu Met Ile Gly Leu
Leu Ser Asn Ala Ser Ser Leu Ser Asp Lys Ala Leu Lys Gly Phe
Thr Val Asn Ala Glu His Leu Asn Ala Gly Val Gly Arg Asn Pro Val
385 Leu Val Thr Ala Leu Asn Pro Glu Ile Gly Tyr Ser Leu Ala Ser Glu
Ile Ala Lys Glu Ala Tyr Ala Ser Gly Arg Pro Val Ile Asp Val Ala
Glu Glu Arg Ser Gly Leu Ser Arg Glu Arg Leu Glu Gln Leu Met Asp
Pro Leu Lys Leu Thr Arg Gly Gly Leu Ala Gly
450          455

```

<210> 9741
 <211> 1437
 <212> DNA
 <213> Bacillus cereus

<220>
 <221> CDS
 <222> (1)..(1437)
 <223> transl_table=11

```

<400> 9741
atg gca aca tta act gaa gtt aaa aat ggt gtt cga att gaa aaa gat      48
Met Ala Thr Leu Thr Glu Val Lys Asn Gly Val Arg Ile Glu Lys Asp
1          5          10          15
ttt tta ggt gaa aaa gaa gta cca aac tat gca tac tac ggt gta caa      96
Phe Leu Gly Glu Lys Glu Val Pro Asn Tyr Ala Tyr Tyr Gly Val Gln
20          25          30
aca atg cgt gca gtt gaa aac ttc cca att aca gga tac aaa att cat      144
Thr Met Arg Ala Val Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His
35          40          45
gaa ggt tta att aga gcg ttc gca gtt gta aaa aaa gct gca gcg ctt      192
Glu Gly Leu Ile Arg Ala Phe Ala Val Val Lys Lys Ala Ala Ala Leu
50          55          60
gcg aat aca gat gta gga aga ttg gaa ttg aac aag ggc ggc gca atc      240
Ala Asn Thr Asp Val Gly Arg Leu Glu Leu Asn Lys Gly Gly Ala Ile
65          70          75          80
gca gaa gct gct caa gaa att ctt gac ggg aaa tgg cat gat cat ttc      288
Ala Glu Ala Ala Gln Glu Ile Leu Asp Gly Lys Trp His Asp His Phe
85          90          95
atc gta gac cca atc caa ggc gga gca ggt act tca atg aac atg aat      336
Ile Val Asp Pro Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn
100          105          110
gca aat gaa gtc att gcc aat cgt ctc ttg att att agg aat gga aag      384
Ala Asn Glu Val Ile Ala Asn Arg Leu Leu Ile Ile Arg Asn Gly Lys
115          120          125
gga gac tat cat tat att agt cca aat agt cat gta aac atg gcg caa      432
Gly Asp Tyr His Tyr Ile Ser Pro Asn Ser His Val Asn Met Ala Gln
130          135          140
tcc aca aac gat gca ttc cca acg gcg att cat atc gct aca tta aac      480
Ser Thr Asn Asp Ala Phe Pro Thr Ala Ile His Ile Ala Thr Leu Asn
145          150          155          160
gca tta gaa ggt tta tta caa acg atg ggc tat atg cac gat gta ttt      528
Ala Leu Glu Gly Leu Leu Gln Thr Met Gly Tyr Met His Asp Val Phe
165          170          175
gaa tta aaa gca gaa cag ttc gat cat gtg att aaa atg ggt cgt aca      576
Glu Leu Lys Ala Glu Gln Phe Asp His Val Ile Lys Met Gly Arg Thr
180          185          190
cat tta caa gac gct gtt cca att cgt ctt gga caa gaa ttt aaa gca      624
His Leu Gln Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Lys Ala
195          200          205
tac tct cgc gta ctt gaa cgt gat atg aaa cga att cag cag tca cgt      672

```

PF59083SeqList PF59083.txt

Tyr	Ser	Arg	Val	Leu	Glu	Arg	Asp	Met	Lys	Arg	Ile	Gln	Gln	Ser	Arg	
210	210					215				220						
caa	cac	tta	tat	gaa	gtg	aac	atg	gga	gca	act	gca	ggt	ggt	aca	ggc	720
Gln	His	Leu	Tyr	Glu	Val	Asn	Met	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	
225					230					235					240	
tta	aat	gca	gat	cca	gaa	tat	att	caa	gct	ggt	gta	aaa	cat	tta	gct	768
Leu	Asn	Ala	Asp	Pro	Glu	Tyr	Ile	Gln	Ala	Val	Val	Lys	His	Leu	Ala	
				245					250					255		
gca	att	agt	gaa	cta	cca	ctt	ggt	ggt	gca	gac	tta	gta	gat	gca		816
Ala	Ile	Ser		Leu	Pro	Leu	Val	Gly	Ala	Glu	Asp	Leu	Val	Asp	Ala	
			260					265					270			
acg	caa	aat	acg	gat	gca	tat	aca	gaa	gta	tca	gca	gca	ctg	aaa	gta	864
Thr	Gln	Asn	Thr	Asp	Ala	Tyr	Thr	Glu	Val	Ser	Ala	Ala	Leu	Lys	Val	
		275					280					285				
tgt	atg	atg	aat	atg	tct	aaa	att	gcc	aat	gac	ctt	cgc	tta	atg	gca	912
Cys	Met	Met	Asn	Met	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Leu	Met	Ala	
	290					295					300					
tca	ggt	cca	cgt	ggt	ggt	tta	gca	gaa	att	atg	tta	ccg	gct	cgt	caa	960
Ser	Gly	Pro	Arg	Val	Gly	Leu	Ala	Glu	Ile	Met	Leu	Pro	Ala	Arg	Gln	
305					310					315					320	
cca	ggt	tca	tct	att	atg	cca	ggg	aaa	gta	aac	cct	ggt	atg	cca	gag	1008
Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Met	Pro	Glu	
				325					330					335		
gta	att	aat	caa	att	gca	ttc	caa	gta	att	ggt	aat	gac	cat	aca	att	1056
Val	Ile	Asn	Gln	Ile	Ala	Phe	Gln	Val	Ile	Gly	Asn	Asp	His	Thr	Ile	
			340				345						350			
tgt	ctt	gct	tca	gaa	gca	ggt	caa	tta	gaa	ttg	aac	ggt	atg	gaa	cca	1104
Cys	Leu	Ala	Ser	Glu	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	
		355				360						365				
gta	cta	ggt	ttc	aac	tta	ctt	caa	tca	att	agc	att	atg	aat	aac	ggt	1152
Val	Leu	Val	Phe	Asn	Leu	Leu	Gln	Ser	Ile	Ser	Ile	Met	Asn	Asn	Gly	
		370				375					380					
ttc	cgt	gcc	ttt	aca	gat	aat	tgc	tta	aaa	gga	att	gaa	gca	aat	gaa	1200
Phe	Arg	Ala	Phe	Thr	Asp	Asn	Cys	Leu	Lys	Gly	Ile	Glu	Ala	Asn	Glu	
385					390					395					400	
gat	cgc	tta	aaa	gag	tat	ggt	gag	aag	agt	gta	gga	att	att	aca	gcc	1248
Asp	Arg	Leu	Lys	Glu	Tyr	Val	Glu	Lys	Ser	Val	Gly	Ile	Ile	Thr	Ala	
			405						410					415		
gtg	aac	cct	cat	atc	ggt	tat	gaa	gca	gca	gct	cgc	ggt	gca	aaa	gaa	1296
Val	Asn	Pro	His	Ile	Gly	Tyr	Glu	Ala	Ala	Ala	Arg	Val	Ala	Lys	Glu	
			420				425						430			
gca	atc	gca	aca	ggg	caa	tcc	ggt	cga	gaa	ctt	tgt	gtg	aaa	aat	ggt	1344
Ala	Ile	Ala	Thr	Gly	Gln	Ser	Val	Arg	Glu	Leu	Cys	Val	Lys	Asn	Gly	
		435				440						445				
gta	ctg	tca	caa	gaa	gac	tta	gaa	tta	att	cta	gat	cca	ttc	gaa	atg	1392
Val	Leu	Ser	Gln	Glu	Asp	Leu	Glu	Leu	Ile	Leu	Asp	Pro	Phe	Glu	Met	
		450				455					460					
acg	cac	cca	ggg	att	gca	gga	gca	act	ctt	tta	aag	aaa	aat	taa		1437
Thr	His	Pro	Gly	Ile	Ala	Gly	Ala	Thr	Leu	Leu	Lys	Lys	Asn			
465					470					475						

<210> 9742

<211> 478

<212> PRT

<213> Bacillus cereus

<400> 9742

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

PF59083SeqList PF59083.txt

Ile Val Asp Pro Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn
100 105 110
Ala Asn Glu Val Ile Ala Asn Arg Leu Leu Ile Ile Arg Asn Gly Lys
115 120 125
Gly Asp Tyr His Tyr Ile Ser Pro Asn Ser His Val Asn Met Ala Gln
130 135 140
Ser Thr Asn Asp Ala Phe Pro Thr Ala Ile His Ile Ala Thr Leu Asn
145 150 155 160
Ala Leu Glu Gly Leu Leu Gln Thr Met Gly Tyr Met His Asp Val Phe
165 170 175
Glu Leu Lys Ala Glu Gln Phe Asp His Val Ile Lys Met Gly Arg Thr
180 185 190
His Leu Gln Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Lys Ala
195 200 205
Tyr Ser Arg Val Leu Glu Arg Asp Met Lys Arg Ile Gln Gln Ser Arg
210 215 220
Gln His Leu Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly
225 230 235 240
Leu Asn Ala Asp Pro Glu Tyr Ile Gln Ala Val Val Lys His Leu Ala
245 250 255
Ala Ile Ser Glu Leu Pro Leu Val Gly Ala Glu Asp Leu Val Asp Ala
260 265 270
Thr Gln Asn Thr Asp Ala Tyr Thr Glu Val Ser Ala Ala Leu Lys Val
275 280 285
Cys Met Met Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Leu Met Ala
290 295 300
Ser Gly Pro Arg Val Gly Leu Ala Glu Ile Met Leu Pro Ala Arg Gln
305 310 315 320
Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Met Pro Glu
325 330 335
Val Ile Asn Gln Ile Ala Phe Gln Val Ile Gly Asn Asp His Thr Ile
340 345 350
Cys Leu Ala Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro
355 360 365
Val Leu Val Phe Asn Leu Leu Gln Ser Ile Ser Ile Met Asn Asn Gly
370 375 380
Phe Arg Ala Phe Thr Asp Asn Cys Leu Lys Gly Ile Glu Ala Asn Glu
385 390 395 400
Asp Arg Leu Lys Glu Tyr Val Glu Lys Ser Val Gly Ile Ile Thr Ala
405 410 415
Val Asn Pro His Ile Gly Tyr Glu Ala Ala Ala Arg Val Ala Lys Glu
420 425 430
Ala Ile Ala Thr Gly Gln Ser Val Arg Glu Leu Cys Val Lys Asn Gly
435 440 445
Val Leu Ser Gln Glu Asp Leu Glu Leu Ile Leu Asp Pro Phe Glu Met
450 455 460
Thr His Pro Gly Ile Ala Gly Ala Thr Leu Leu Lys Lys Asn
465 470 475

<210> 9743

<211> 1416

<212> DNA

<213> Wolinella succinogenes

<220>

<221> CDS

<222> (1)..(1416)

<223> transl_table=11

<400> 9743

atg gca tct aca cga ata gaa cac gat ctt att ggg gac tta gag gta	48
Met Ala Ser Thr Arg Ile Glu His Asp Leu Ile Gly Asp Leu Glu Val	
1 5 10 15	
agt aac gac tgc tat tat gga gtt caa act gct aga gcg aaa gag aac	96
Ser Asn Asp Cys Tyr Tyr Gly Val Thr Ala Arg Ala Lys Glu Asn	
20 25 30	
ttc cac atc tca ggc gtc cta ctc tca agc atg ccc act ttc att gct	144
Phe His Ile Ser Gly Val Leu Leu Ser Ser Met Pro Thr Phe Ile Ala	
35 40 45	

PF59083SeqList PF59083.txt																
tca	ctc	gct	aaa	gtc	aaa	aaa	gcc	gct	gca	ctc	gcc	aac	ttt	gag	ctt	192
Ser	Leu	Ala	Lys	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Phe	Glu	Leu	
	50					55					60					
ggg	ctc	ttg	gat	gag	aag	atc	aaa	aac	gcc	atc	tgc	gaa	gcg	tgc	gat	240
Gly	Leu	Leu	Asp	Glu	Lys	Ile	Lys	Asn	Ala	Ile	Cys	Glu	Ala	Cys	Asp	
	65				70					75					80	
ctc	atc	atc	gct	gga	aaa	tat	cac	gac	caa	ttc	gtc	gtg	gat	gcc	atc	288
Leu	Ile	Ile	Ala	Gly	Lys	Tyr	His	Asp	Gln	Phe	Val	Val	Asp	Ala	Ile	
			85						90					95		
caa	gga	ggc	gct	gga	act	tcc	acc	aac	atg	aac	gcc	aat	gaa	gtg	atc	336
Gln	Gly	Gly	Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	
			100					105					110			
gcc	aac	gtc	gca	ctt	gag	ctc	atg	gga	cat	aaa	aag	ggg	gaa	tat	aaa	384
Ala	Asn	Val	Ala	Leu	Glu	Leu	Met	Gly	His	Lys	Lys	Gly	Glu	Tyr	Lys	
		115				120						125				
cat	tgc	cac	ccc	aac	aac	cac	gtc	aac	ctc	tca	caa	tct	act	aat	gat	432
His	Cys	His	Pro	Asn	Asn	His	Val	Asn	Leu	Ser	Gln	Ser	Thr	Asn	Asp	
	130				135						140					
gcc	tat	cct	acg	gca	ttc	cgc	gtt	gcc	ctg	tat	gaa	aaa	ctc	atc	gag	480
Ala	Tyr	Pro	Thr	Ala	Phe	Arg	Val	Ala	Leu	Tyr	Glu	Lys	Leu	Ile	Glu	
	145				150					155					160	
ctc	acc	gtc	tcc	atg	gga	atc	cta	aga	gac	tct	ttt	gcc	aaa	aag	gcc	528
Leu	Thr	Val	Ser	Met	Gly	Ile	Leu	Arg	Asp	Ser	Phe	Ala	Lys	Lys	Ala	
			165						170					175		
gag	gaa	ttc	aaa	gat	atc	atc	aag	atg	ggg	cga	acc	cag	ctc	caa	gac	576
Glu	Glu	Phe	Lys	Asp	Ile	Ile	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	Asp	
			180					185					190			
gct	gtg	ccc	atg	acc	cta	ggg	caa	gag	ttt	aaa	acc	tac	gcc	gtc	atg	624
Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Lys	Thr	Tyr	Ala	Val	Met	
		195				200						205				
atg	acc	gaa	gat	atc	gat	cgc	gtg	cta	gag	gct	aga	aac	ctt	gtt	cga	672
Met	Thr	Glu	Asp	Ile	Asp	Arg	Val	Leu	Glu	Ala	Arg	Asn	Leu	Val	Arg	
	210					215					220					
gag	atg	aac	ctt	ggg	gca	acc	gcg	att	gga	aca	gga	atc	aac	tct	cac	720
Glu	Met	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Ser	His	
	225				230				235						240	
cct	gac	tac	gct	acg	ctt	gta	gag	aaa	aaa	ctt	caa	gag	gtc	aca	ggc	768
Pro	Asp	Tyr	Ala	Thr	Leu	Val	Glu	Lys	Lys	Leu	Gln	Glu	Val	Thr	Gly	
			245						250					255		
cga	ccc	ttt	atc	acc	gcc	agc	gat	ctt	gtt	gag	gcg	act	caa	gac	aca	816
Arg	Pro	Phe	Ile	Thr	Ala	Ser	Asp	Leu	Val	Glu	Ala	Thr	Gln	Asp	Thr	
			260				265						270			
ggg	gct	tat	gtc	caa	atc	tct	ggg	gtt	ctt	aag	cgt	gtc	tcc	acc	aaa	864
Gly	Ala	Tyr	Val	Gln	Ile	Ser	Gly	Val	Leu	Lys	Arg	Val	Ser	Thr	Lys	
		275					280					285				
gtc	tcc	aaa	atc	tgc	aac	gat	cta	aga	ctc	ctt	agc	tca	ggc	cca	aga	912
Val	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	
	290					295					300					
gcg	gga	ctt	agc	gag	atc	aat	ctt	ccc	cct	atg	cag	cct	ggg	agc	tcc	960
Ala	Gly	Leu	Ser	Glu	Ile	Asn	Leu	Pro	Pro	Met	Gln	Pro	Gly	Ser	Ser	
	305				310					315					320	
att	atg	cct	gga	aag	gtt	aat	cct	gtg	att	ccc	gaa	gtg	gtc	aat	cag	1008
Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln	
			325						330					335		
gtc	tgc	tac	cac	gtt	att	ggc	gcc	gac	atg	act	gta	act	att	gcc	tct	1056
Val	Cys	Tyr	His	Val	Ile	Gly	Ala	Asp	Met	Thr	Val	Thr	Ile	Ala	Ser	
			340					345					350			
gaa	ggg	ggg	cag	ctt	cag	ctc	aac	gtt	ttt	gag	ccc	gtc	atc	gcc	ttt	1104
Glu	Gly	Gly	Gln	Leu	Gln	Leu	Asn	Val	Phe	Glu	Pro	Val	Ile	Ala	Phe	
		355					360					365				
agc	ctc	ttt	agc	tct	atc	aac	atg	atg	aga	aga	gct	ttt	gaa	act	ttg	1152
Ser	Leu	Phe	Ser	Ser	Ile	Asn	Met	Met	Arg	Arg	Ala	Phe	Glu	Thr	Leu	
	370					375					380					
gct	gaa	aaa	tgc	gtg	aat	gga	atc	acc	gcc	aac	gct	gac	aac	tgc	cgc	1200
Ala	Glu	Lys	Cys	Val	Asn	Gly	Ile	Thr	Ala	Asn	Ala	Asp	Asn	Cys	Arg	
	385				390					395					400	
gac	tat	gtc	ctt	aag	agc	atc	gga	ctc	gtc	aca	gcg	ctc	aac	ccc	tac	1248
Asp	Tyr	Val	Leu	Lys	Ser	Ile	Gly	Leu	Val	Thr	Ala	Leu	Asn	Pro	Tyr	
			405						410					415		

PF59083SeqList PF59083.txt

atc	gga	tat	gag	aac	tcc	act	tca	gtg	gcc	aaa	gag	gcg	cta	gag	tca	1296
Ile	Gly	Tyr	Glu	Asn	Ser	Thr	Ser	Val	Ala	Lys	Glu	Ala	Leu	Glu	Ser	
			420					425					430			
ggc	aag	tcc	gtc	cac	gat	atc	gtc	cta	gag	cgc	aaa	ctt	ctt	agc	aaa	1344
Gly	Lys	Ser	Val	His	Asp	Ile	Val	Leu	Glu	Arg	Lys	Leu	Leu	Ser	Lys	
			435				440					445				
gaa	gag	cta	gaa	gag	att	att	cga	ccc	gaa	aac	atg	atc	aag	ccc	aaa	1392
Glu	Glu	Leu	Glu	Glu	Ile	Ile	Arg	Pro	Glu	Asn	Met	Ile	Lys	Pro	Lys	
			450			455					460					
gtc	gtc	act	cta	aca	aaa	aaa	taa									1416
Val	Val	Thr	Leu	Thr	Lys	Lys										
465					470											

<210> 9744

<211> 471

<212> PRT

<213> Wolinella succinogenes

<400> 9744

Met	Ala	Ser	Thr	Arg	Ile	Glu	His	Asp	Leu	Ile	Gly	Asp	Leu	Glu	Val
1				5					10					15	
Ser	Asn	Asp	Cys	Tyr	Tyr	Gly	Val	Gln	Thr	Ala	Arg	Ala	Lys	Glu	Asn
			20					25					30		
Phe	His	Ile	Ser	Gly	Val	Leu	Leu	Ser	Ser	Met	Pro	Thr	Phe	Ile	Ala
		35				40						45			
Ser	Leu	Ala	Lys	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Phe	Glu	Leu
	50				55					60					
Gly	Leu	Leu	Asp	Glu	Lys	Ile	Lys	Asn	Ala	Ile	Cys	Glu	Ala	Cys	Asp
65					70				75					80	
Leu	Ile	Ile	Ala	Gly	Lys	Tyr	His	Asp	Gln	Phe	Val	Val	Asp	Ala	Ile
				85					90					95	
Gln	Gly	Gly	Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile
			100					105					110		
Ala	Asn	Val	Ala	Leu	Glu	Leu	Met	Gly	His	Lys	Lys	Gly	Glu	Tyr	Lys
		115				120						125			
His	Cys	His	Pro	Asn	Asn	His	Val	Asn	Leu	Ser	Gln	Ser	Thr	Asn	Asp
	130					135					140				
Ala	Tyr	Pro	Thr	Ala	Phe	Arg	Val	Ala	Leu	Tyr	Glu	Lys	Leu	Ile	Glu
145					150					155				160	
Leu	Thr	Val	Ser	Met	Gly	Ile	Leu	Arg	Asp	Ser	Phe	Ala	Lys	Lys	Ala
				165					170					175	
Glu	Glu	Phe	Lys	Asp	Ile	Ile	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	Asp
			180					185					190		
Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Lys	Thr	Tyr	Ala	Val	Met
		195				200						205			
Met	Thr	Glu	Asp	Ile	Asp	Arg	Val	Leu	Glu	Ala	Arg	Asn	Leu	Val	Arg
	210					215					220				
Glu	Met	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Ser	His
225					230					235				240	
Pro	Asp	Tyr	Ala	Thr	Leu	Val	Glu	Lys	Lys	Leu	Gln	Glu	Val	Thr	Gly
				245					250					255	
Arg	Pro	Phe	Ile	Thr	Ala	Ser	Asp	Leu	Val	Glu	Ala	Thr	Gln	Asp	Thr
			260					265					270		
Gly	Ala	Tyr	Val	Gln	Ile	Ser	Gly	Val	Leu	Lys	Arg	Val	Ser	Thr	Lys
		275					280					285			
Val	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg
	290					295					300				
Ala	Gly	Leu	Ser	Glu	Ile	Asn	Leu	Pro	Pro	Met	Gln	Pro	Gly	Ser	Ser
305					310					315				320	
Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln
				325					330					335	
Val	Cys	Tyr	His	Val	Ile	Gly	Ala	Asp	Met	Thr	Val	Thr	Ile	Ala	Ser
			340					345					350		
Glu	Gly	Gly	Gln	Leu	Gln	Leu	Asn	Val	Phe	Glu	Pro	Val	Ile	Ala	Phe
		355					360					365			
Ser	Leu	Phe	Ser	Ser	Ile	Asn	Met	Met	Arg	Arg	Ala	Phe	Glu	Thr	Leu
	370					375					380				
Ala	Glu	Lys	Cys	Val	Asn	Gly	Ile	Thr	Ala	Asn	Ala	Asp	Asn	Cys	Arg
385					390					395					400

PF59083SeqList PF59083.txt

Asp Tyr Val Leu Lys Ser Ile Gly Leu Val Thr Ala Leu Asn Pro Tyr
 405 410 415
 Ile Gly Tyr Glu Asn Ser Thr Ser Val Ala Lys Glu Ala Leu Glu Ser
 420 425 430
 Gly Lys Ser Val His Asp Ile Val Leu Glu Arg Lys Leu Leu Ser Lys
 435 440 445
 Glu Glu Leu Glu Glu Ile Ile Arg Pro Glu Asn Met Ile Lys Pro Lys
 450 455 460
 Val Val Thr Leu Thr Lys Lys
 465 470

<210> 9745

<211> 1650

<212> DNA

<213> *Aspergillus oryzae*

<220>

<221> CDS

<222> (1)..(1650)

<400> 9745

atg ttg gca ccc tcg aac tcc cga gcc gcg gtg cgg tcg atg gct tct	48
Met Leu Ala Pro Ser Asn Ser Arg Ala Ala Val Arg Ser Met Ala Ser	
1 5 10 15	
ttg gcg cat gca gca tcg aga gcg tct gcc agt tcc ccc gca gtc gca	96
Leu Ala His Ala Ala Ser Arg Ala Ser Ala Ser Pro Ala Val Ala	
20 25 30	
cgc tct gct tta gct tgt gct gcc cgg tcc ccc gct tct ctc ggt tgc	144
Arg Ser Ala Leu Ala Cys Ala Ala Arg Ser Pro Ala Ser Leu Gly Cys	
35 40 45	
cgt cgc gct ctg agc acc aat agc cga caa ctc cag ttc ccc cgc ctt	192
Arg Arg Ala Leu Ser Thr Asn Ser Arg Gln Leu Gln Phe Pro Arg Leu	
50 55 60	
cag tcc ttg aac acc atc tcc agc aag aga act ttt ggt aca acc gca	240
Gln Ser Leu Asn Thr Ile Ser Ser Lys Arg Thr Phe Gly Thr Thr Ala	
65 70 75 80	
aga atg gct tcg gaa act cgc gtt gaa act gac gcc ttt ggc gag att	288
Arg Met Ala Ser Glu Thr Arg Val Glu Thr Asp Ala Phe Gly Glu Ile	
85 90 95	
gag gtc cct gcc gac aag tac tgg ggt gcc cag acc cag cgt tcc ctg	336
Glu Val Pro Ala Asp Lys Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu	
100 105 110	
ggt aac ttt gac atc aac cag cct cag gac cgt atg cct gag ggt gtt	384
Gly Asn Phe Asp Ile Asn Gln Pro Gln Asp Arg Met Pro Glu Gly Val	
115 120 125	
gtc aag gct ttc ggt atc ctg aag ggt gct gct gct acc gtg aac atg	432
Val Lys Ala Phe Gly Ile Leu Lys Gly Ala Ala Ala Thr Val Asn Met	
130 135 140	
aag ttt ggc ctt gac ccc aag att ggt gag gct att cag aag gct gcc	480
Lys Phe Gly Leu Asp Pro Lys Ile Gly Glu Ala Ile Gln Lys Ala Ala	
145 150 155 160	
gcc gag gtt gcc gag ggc aag ctc atg gac cac ttc cct ctt gtc gtt	528
Ala Glu Val Ala Glu Gly Lys Leu Met Asp His Phe Pro Leu Val Val	
165 170 175	
tgg cag act ggt tcc ggc acc cag tcc aac tcc aac gag gtc	576
Trp Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ser Asn Glu Val	
180 185 190	
atc tcg aac cgt gcc atc gag atc ttg ggt ggc aag atg gga tct aag	624
Ile Ser Asn Arg Ala Ile Glu Ile Leu Gly Gly Lys Met Gly Ser Lys	
195 200 205	
aag cct gtg cac ccc aac gac cac gtc aac atg tct gct tcc tcc aac	672
Lys Pro Val His Pro Asn Asp His Val Asn Met Ser Ala Ser Ser Asn	
210 215 220	
gac tct ttc cct act gct atg cac atc gct gct ttg gag ctc gag	720
Asp Ser Phe Pro Thr Ala Met His Ile Ala Ala Val Leu Glu Leu Glu	
225 230 235 240	
gga act ttg ctg cct tcc ctc aag agc ctt cgc gat gct ctc cag gtg	768
Gly Thr Leu Leu Pro Ser Leu Lys Ser Leu Arg Asp Ala Leu Gln Val	
245 250 255	

PF59083SeqList PF59083.txt

aag	gtg	gag	aac	ttt	gag	aag	atc	atc	aag	atc	ggt	cgt	acc	cat	ctg	816
Lys	Val	Glu	Asn	Phe	Glu	Lys	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	
			260					265					270			
cag	gat	gct	act	cct	ctt	act	ctt	ggt	cag	gag	ttc	tcc	ggc	tac	gtt	864
Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val	
			275					280					285			
gcc	cag	ctt	gat	cgc	aac	att	gag	cgc	gtt	cag	aac	tct	ctt	ccc	cac	912
Ala	Gln	Leu	Asp	Arg	Asn	Ile	Glu	Arg	Val	Gln	Asn	Ser	Leu	Pro	His	
			290			295					300					
ctc	cgc	tat	ctt	gct	cag	ggt	gga	act	gct	gtc	ggt	act	ggt	ctg	aac	960
Leu	Arg	Tyr	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	
					310					315					320	
acc	ttc	aag	ggc	ttt	gat	gag	gcc	att	gcc	gcc	gag	gtc	acc	aag	atg	1008
Thr	Phe	Lys	Gly	Phe	Asp	Glu	Ala	Ile	Ala	Ala	Glu	Val	Thr	Lys	Met	
				325				330						335		
act	ggc	acc	gaa	ttc	aag	acc	gcc	ccc	aac	aag	ttc	gag	gtt	ctc	gct	1056
Thr	Gly	Thr	Glu	Phe	Lys	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Val	Leu	Ala	
			340					345					350			
gct	cac	gat	gcg	atc	gtc	gag	gcc	tct	ggt	tcc	ctt	aac	acc	ctt	gct	1104
Ala	His	Asp	Ala	Ile	Val	Glu	Ala	Ser	Gly	Ser	Leu	Asn	Thr	Leu	Ala	
			355				360						365			
tgc	tct	ctc	ttc	aag	atc	gcc	cag	gat	atc	cgt	tac	ctc	ggt	tct	gga	1152
Cys	Ser	Leu	Phe	Lys	Ile	Ala	Gln	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	
			370			375					380					
cct	cgt	tgc	ggt	ctg	ggc	gag	ctg	atc	ctc	ccc	gag	aac	gag	ccc	ggc	1200
Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn	Glu	Pro	Gly	
					390					395					400	
tcc	tct	atc	atg	cct	gga	aag	gtc	aac	ccc	act	cag	tgc	gag	tcc	ctt	1248
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ser	Leu	
				405					410					415		
acc	atg	atc	tgc	tcc	cag	gtt	atg	ggt	aac	cac	gtc	gct	gct	acc	gtt	1296
Thr	Met	Ile	Cys	Ser	Gln	Val	Met	Gly	Asn	His	Val	Ala	Ala	Thr	Val	
			420					425					430			
ggt	ggt	atg	aac	ggt	cag	ttc	gag	ctt	aac	gtg	ttc	aag	ccc	gtc	atg	1344
Gly	Gly	Met	Asn	Gly	Gln	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Met	
			435				440						445			
atc	cgc	aac	ctt	ctg	cac	agc	tcg	cgc	att	ctt	tcg	gat	ggc	atg	aag	1392
Ile	Arg	Asn	Leu	Leu	His	Ser	Ser	Arg	Ile	Leu	Ser	Asp	Gly	Met	Lys	
			450			455					460					
agc	ttc	gag	aag	aac	ctg	gtg	cac	ggt	ctc	gag	gcc	aac	gag	ccc	aga	1440
Ser	Phe	Glu	Lys	Asn	Leu	Val	His	Gly	Leu	Glu	Ala	Asn	Glu	Pro	Arg	
					470					475					480	
atc	aac	tcc	ctg	ctc	cac	gag	agt	ctg	atg	ctc	gtc	acc	tgc	ttg	aac	1488
Ile	Asn	Ser	Leu	Leu	His	Glu	Ser	Leu	Met	Leu	Val	Thr	Cys	Leu	Asn	
					485				490					495		
ccc	gtt	atc	ggt	tac	gac	atg	gcg	tcc	aag	gtc	gct	aag	aac	gcc	cac	1536
Pro	Val	Ile	Gly	Tyr	Asp	Met	Ala	Ser	Lys	Val	Ala	Lys	Asn	Ala	His	
			500				505						510			
aag	aag	ggt	ctc	act	ctg	aag	cag	agt	gct	atg	gag	ctg	cag	gcc	ctt	1584
Lys	Lys	Gly	Leu	Thr	Leu	Lys	Gln	Ser	Ala	Met	Glu	Leu	Gln	Ala	Leu	
			515				520					525				
agc	gag	gag	gac	ttc	gac	acc	cat	gtc	cgc	cct	gag	ctg	atg	ctt	gct	1632
Ser	Glu	Glu	Asp	Phe	Asp	Thr	His	Val	Arg	Pro	Glu	Leu	Met	Leu	Ala	
			530			535					540					
cct	aag	gag	aag	aaa	tag											1650
Pro	Lys	Glu	Lys	Lys												

<210> 9746

<211> 549

<212> PRT

<213> Aspergillus oryzae

<400> 9746

Met	Leu	Ala	Pro	Ser	Asn	Ser	Arg	Ala	Ala	Val	Arg	Ser	Met	Ala	Ser
1				5				10						15	
Leu	Ala	His	Ala	Ala	Ser	Arg	Ala	Ser	Ala	Ser	Ser	Pro	Ala	Val	Ala
			20					25					30		
Arg	Ser	Ala	Leu	Ala	Cys	Ala	Ala	Arg	Ser	Pro	Ala	Ser	Leu	Gly	Cys

PF59083SeqList PF59083.txt

			35				40					45			
Arg	Arg	Ala	Leu	Ser	Thr	Asn	Ser	Arg	Gln	Leu	Gln	Phe	Pro	Arg	Leu
	50					55					60				
Gln	Ser	Leu	Asn	Thr	Ile	Ser	Ser	Lys	Arg	Thr	Phe	Gly	Thr	Thr	Ala
65				85	70					75					80
Arg	Met	Ala	Ser	Glu	Thr	Arg	Val	Glu	Thr	Asp	Ala	Phe	Gly	Glu	Ile
								90						95	
Glu	Val	Pro	Ala	Asp	Lys	Tyr	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu
			100					105					110		
Gly	Asn	Phe	Asp	Ile	Asn	Gln	Pro	Gln	Asp	Arg	Met	Pro	Glu	Gly	Val
			115				120					125			
Val	Lys	Ala	Phe	Gly	Ile	Leu	Lys	Gly	Ala	Ala	Ala	Thr	Val	Asn	Met
	130					135					140				
Lys	Phe	Gly	Leu	Asp	Pro	Lys	Ile	Gly	Glu	Ala	Ile	Gln	Lys	Ala	Ala
145					150					155					160
Ala	Glu	Val	Ala	Glu	Gly	Lys	Leu	Met	Asp	His	Phe	Pro	Leu	Val	Val
			165						170					175	
Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ser	Asn	Glu	Val
			180					185					190		
Ile	Ser	Asn	Arg	Ala	Ile	Glu	Ile	Leu	Gly	Gly	Lys	Met	Gly	Ser	Lys
		195				200						205			
Lys	Pro	Val	His	Pro	Asn	Asp	His	Val	Asn	Met	Ser	Ala	Ser	Ser	Asn
	210					215					220				
Asp	Ser	Phe	Pro	Thr	Ala	Met	His	Ile	Ala	Ala	Val	Leu	Glu	Leu	Glu
225					230				235						240
Gly	Thr	Leu	Leu	Pro	Ser	Leu	Lys	Ser	Leu	Arg	Asp	Ala	Leu	Gln	Val
			245						250					255	
Lys	Val	Glu	Asn	Phe	Glu	Lys	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu
			260					265					270		
Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Val
		275					280					285			
Ala	Gln	Leu	Asp	Arg	Asn	Ile	Glu	Arg	Val	Gln	Asn	Ser	Leu	Pro	His
	290					295					300				
Leu	Arg	Tyr	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn
305					310				315						320
Thr	Phe	Lys	Gly	Phe	Asp	Glu	Ala	Ile	Ala	Ala	Glu	Val	Thr	Lys	Met
			325						330				335		
Thr	Gly	Thr	Glu	Phe	Lys	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Val	Leu	Ala
			340					345					350		
Ala	His	Asp	Ala	Ile	Val	Glu	Ala	Ser	Gly	Ser	Leu	Asn	Thr	Leu	Ala
		355					360					365			
Cys	Ser	Leu	Phe	Lys	Ile	Ala	Gln	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly
	370					375					380				
Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn	Glu	Pro	Gly
385															

<210>	9747
<211>	1865
<212>	DNA

PF59083SeqList PF59083.txt

<213> Solanum tuberosum

<220>

<221> CDS

<222> (66)..(1547)

<400> 9747

```
ctcagactca gcatcaacat tcccaccaac tcgcatacag gcggcggcgc attgactgct      60

gagat atg gcg atg tta aat gcg gct cgt cga tta tca gct gga tca gct      110
      Met Ala Met Leu Asn Ala Ala Arg Arg Leu Ser Ala Gly Ser Ala
      1      5      10      15
tta tca gat tca ctg cgt tat act tct tcc tgg agg ttt ttc tct acg      158
Leu Ser Asp Ser Leu Arg Tyr Thr Ser Ser Trp Arg Phe Phe Thr
      20      25      30
tct ttc agg gag gaa aga gat acg ttt ggt cct att ctc gtt cca tcg      206
Ser Phe Arg Glu Glu Arg Asp Thr Phe Gly Pro Ile Leu Val Pro Ser
      35      40      45
gac aag tta tgg ggg gct caa act caa aga tca ttg cag aat ttt gaa      254
Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn Phe Glu
      50      55      60
att ggg ggt gat cgt gaa aga atg cct gag cca atc ata cgt gca ttc      302
Ile Gly Gly Asp Arg Glu Arg Met Pro Glu Pro Ile Ile Arg Ala Phe
      65      70      75
ggt att att aaa aag tgt gca gcc aag gtg aac atg gac tat ggc ctt      350
Gly Ile Ile Lys Lys Cys Ala Ala Lys Val Asn Met Asp Tyr Gly Leu
      80      85      90
gac caa tct att gga aaa gca ata atg caa gca gct gaa gag gtt gca      398
Asp Gln Ser Ile Gly Lys Ala Ile Met Gln Ala Ala Glu Glu Val Ala
      100      105      110
gaa gga aaa tta aat gac cat ttt cct ttg gtg gtt tgg cag act ggc      446
Glu Gly Lys Leu Asn Asp His Phe Pro Leu Val Val Trp Gln Thr Gly
      115      120      125
agt ggc act caa agt aac atg aat gct aac gag gtt att gca aat cga      494
Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ala Asn Arg
      130      135      140
gca gct gaa ata ctt ggc cat aac cgc gga gac aaa cat gtg cat cca      542
Ala Ala Glu Ile Leu Gly His Asn Arg Gly Asp Lys His Val His Pro
      145      150      155
aat gac cat gta aat aaa tcg caa tct tca aat gat act ttc tct acg      590
Asn Asp His Val Asn Lys Ser Gln Ser Ser Asn Asp Thr Phe Ser Thr
      160      165      170
gtg atg cac att gct gca gca atg gag cta aat aaa aga tta gta cca      638
Val Met His Ile Ala Ala Met Glu Leu Asn Lys Arg Leu Val Pro
      180      185      190
aac ctt gaa aca gtt gca tac tca cta aat tca aag tca gtc gaa ttc      686
Asn Leu Glu Thr Val Ala Tyr Ser Leu Asn Ser Lys Ser Val Glu Phe
      195      200      205
aag gac att atc aag att ggg cga acc cac aca caa gat gca aca cct      734
Lys Asp Ile Ile Lys Ile Gly Arg Thr His Thr Gln Asp Ala Thr Pro
      210      215      220
ttg act ctt gga caa gag ttt agt ggc tat gca act caa gtg aaa tat      782
Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Ala Thr Gln Val Lys Tyr
      225      230      235
gga atc gat aga gtc tta tgc acg ctt cag cgc atg tat cag ctc gca      830
Gly Ile Asp Arg Val Leu Cys Thr Leu Gln Arg Met Tyr Gln Leu Ala
      240      245      250
caa ggg ggc aca gca gta ggg aca gga ttg aat aca aag aaa ggg ttt      878
Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Lys Lys Gly Phe
      260      265      270
gac ata aaa att gct gca gca gtt gca gag gaa aca aat ttc cca ttt      926
Asp Ile Lys Ile Ala Ala Val Ala Glu Glu Thr Asn Phe Pro Phe
      275      280      285
gtt aca gct gaa aac aag ttt gaa gca ttg gct gct cat gat gca ttt      974
Val Thr Ala Glu Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Phe
      290      295      300
gct gaa act agt gga gcc tta aat acc ctg gct gct tcc ctt atg aag      1022
Ala Glu Thr Ser Gly Ala Leu Asn Thr Leu Ala Ala Ser Leu Met Lys
```

PF59083SeqList PF59083.txt

```

305          310          315
att ggg aat gat ata cgc ttc ttg gga agt ggt ccc cgc tgt ggt ctt      1070
Ile Gly Asn Asp Ile Arg Phe Leu Gly Ser Gly Pro Arg Cys Gly Leu
320          325          330          335
ggc gag ctc agt ctt cct gaa aat gaa ccc gga agc agt ata atg cct      1118
Gly Glu Leu Ser Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro
          340          345          350
ggc aag gta aat cct act cag tgt gag gct ctc acc atg gtc tgt gct      1166
Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys Ala
          355          360          365
cag gtt atg ggg aat cat gtg gct gtt act gtt ggt gca tca aat ggc      1214
Gln Val Met Gly Asn His Val Ala Val Thr Val Gly Ala Ser Asn Gly
          370          375          380
cat ttt gag ctg aat gtc ttc aag ccg atg att gct aat gct ctc cta      1262
His Phe Glu Leu Asn Val Phe Lys Pro Met Ile Ala Asn Ala Leu Leu
          385          390          395
cat tca gta aga ttg cta ggc gat gca tct gct tcc ttt gaa aag aat      1310
His Ser Val Arg Leu Leu Gly Asp Ala Ser Ala Ser Phe Glu Lys Asn
400          405          410          415
tgt gtg agg gat atc caa gct aac aga gac aga att gct aaa ttg ttg      1358
Cys Val Arg Asp Ile Gln Ala Asn Arg Asp Arg Ile Ala Lys Leu Leu
          420          425          430
cac gag tca ctc atg ctc gtt aca tgt ttg aac cca aaa att ggt tat      1406
His Glu Ser Leu Met Leu Val Thr Cys Leu Asn Pro Lys Ile Gly Tyr
          435          440          445
gat aat gct gct gca gtt gcc aag aaa gcc cac aag gag gga acc agt      1454
Asp Asn Ala Ala Ala Val Ala Lys Lys Ala His Lys Glu Gly Thr Ser
          450          455          460
ttg aag gaa gct gct ctc aat cta gga gtc ctc acc agt gaa gag ttt      1502
Leu Lys Glu Ala Ala Leu Asn Leu Gly Val Leu Thr Ser Glu Glu Phe
          465          470          475
gat caa ctt gta gtc cct gag aaa atg att ggt cca act gac tgatctgatt      1554
Asp Gln Leu Val Val Pro Glu Lys Met Ile Gly Pro Thr Asp
480          485          490
cattagctct tcgaaatgag aaagaggacc atggctagct tcttctgtcc atcagattcg      1614

aacgaggggaa ataaacattt gacacaattc ttgaggtttt cttattcctg gtaatttatc      1674

agtgttttttt actgtgagaa tgcctccatt tttttttttg taatgagtcg ctggagcgat      1734

agccaagtaa ataatgaact gaattagtat tttttatgag gttgggccat gaataatgag      1794

ggagaaaatc atctttttatg aaatggagac ggggaaatga tcaaaatggt cttatgtatg      1854

ggttttgatt c      1865

```

<210> 9748

<211> 493

<212> PRT

<213> Solanum tuberosum

<400> 9748

```

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

```

PF59083SeqList PF59083.txt

Ile Ile Lys Lys Cys 85 Ala Ala Lys Val Asn 90 Met Asp Tyr Gly Leu 95 Asp
Gln Ser Ile Gly Lys 100 Ala Ile Met Gln Ala 105 Ala Glu Glu Val 110 Ala Glu
Gly Lys 115 Asn Asp His Phe 120 Leu Val Val Trp 125 Gln Thr Gly Ser
Gly Thr Gln Ser Asn Met 135 Asn Ala Asn Glu Val 140 Ile Ala Asn Arg Ala
Ala Glu Ile Leu Gly His 150 Asn Arg Gly Asp Lys 155 His Val His Pro Asn
145 Asp His Val Asn Lys 165 Ser Gln Ser Ser Asn 170 Asp Thr Phe Ser Thr Val
Met His Ile Ala Ala 180 Ala Met Glu Leu Asn Lys Arg Leu Val 190 Pro Asn
Leu Glu Thr Val Ala Tyr Ser 200 Asn Ser Lys Ser Val 205 Glu Phe Lys
Asp Ile Ile Lys Ile Gly Arg 215 Thr His Thr Gln Asp Ala Thr Pro Leu
210 Thr Leu Gly Gln Glu Phe 230 Ser Gly Tyr Ala Thr Gln Val Lys Tyr Gly
225 Ile Asp Arg Val Leu 245 Cys Thr Leu Gln Arg 250 Met Tyr Gln Leu Ala Gln
Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Lys Lys Gly Phe Asp
260 Ile Lys Ile Ala Ala Ala Val 280 Glu Glu Thr Asn Phe Pro Phe Val
275 Thr Ala Glu Asn Lys Phe 295 Glu Ala Leu Ala Ala His Asp Ala Phe Ala
290 Glu Thr Ser Gly Ala Leu 310 Asn Thr Leu Ala Ala Ser Leu Met Lys Ile
305 Gly Asn Asp Ile Arg 325 Phe Leu Gly Ser Gly 330 Pro Arg Cys Gly Leu Gly
Glu Leu Ser Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly
340 Lys Val Asn Pro Thr Gln Cys Glu 360 Ala Leu Thr Met Val Cys Ala Gln
355 Val Met Gly Asn His Val 375 Ala Val Thr Val Gly Ala Ser Asn Gly His
370 Phe Glu Leu Asn Val Phe 390 Lys Pro Met Ile Ala Asn Ala Leu Leu His
385 Ser Val Arg Leu Leu Gly Asp Ala Ser Ala Ser Phe Glu Lys Asn Cys
405 Val Arg Asp Ile Gln Ala Asn Arg Asp Arg Ile Ala Lys Leu Leu His
420 Glu Ser Leu Met Leu Val Thr Cys 440 Leu Asn Pro Lys Ile Gly Tyr Asp
435 Asn Ala Ala Ala Val Ala Lys 455 Lys Ala His Lys Glu Gly Thr Ser Leu
450 Lys Glu Ala Ala Leu Asn 470 Leu Gly Val Leu Thr Ser Glu Glu Phe Asp
465 Gln Leu Val Val Pro Glu Lys Met Ile Gly 490 Pro Thr Asp
485

<210> 9749

<211> 1434

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1434)

<223> transl_table=11

<400> 9749

atg tca aac aac att cgt atc gaa gaa gat cgg ttg ggt acc agg gaa 48
Met Ser Asn Asn Ile Arg Ile Glu Glu Asp Arg Leu Gly Thr Arg Glu
1 5 10 15
gtt gga gct gat gcc tac tat ggt gtt cac act ctg aga gcg att gaa 96
Val Gly Ala Asp Ala Tyr Tyr Gly Val His Thr Arg Ala Ile Glu

PF59083SeqList PF59083.txt

	20	25	30	
aac ttc tat atc agc aac aac aaa atc agt gat att cct gaa ttt gtt	144			
Asn Phe Tyr Ile Ser Asn Asn Lys Ile Ser Asp Ile Pro Glu Phe Val				
cgc ggt atg gta atg gtt aaa aaa gcc gca gct atg gca aac aaa gag	192			
Arg Gly Met Val Met Val Lys Lys Ala Ala Ala Met Ala Asn Lys Glu				
ctg caa acc aat cct aaa agt gta gcg aat gcc atc att ccc gca tgt	240			
Leu Gln Thr Asn Pro Lys Ser Val Ala Asn Ala Ile Ile Pro Ala Cys				
gat gaa gac ctg aac aac gga aaa tgc atg gat cag ttc ccg gta gac	288			
Asp Glu Asp Leu Asn Asn Gly Lys Cys Met Asp Gln Phe Pro Val Asp				
gtc tac cag ggc ggc gca cgt act tcc gta aac atg aac acc aac gaa	336			
Val Tyr Gln Gly Gly Ala Arg Thr Val Asn Met Asn Thr Asn Glu				
gtg ctg gcc aat atc ggt ctg gaa ctg atg gga cac cag aaa gct gaa	384			
Val Leu Ala Asn Ile Gly Leu Glu Leu Met Gly His Gln Lys Ala Glu				
tat cag tac ctg aac ccg aac gac cat gtt aac aaa tgt cag tcc act	432			
Tyr Gln Tyr Leu Asn Pro Asn Asp His Val Asn Lys Cys Gln Ser Thr				
aac gac gcc cac ccg acc ggt ttc cgt atc gca gtt tac tct tct atg	480			
Asn Asp Ala His Pro Thr Gly Phe Arg Ile Ala Val Tyr Ser Ser Met				
att aag ctg gta gat gcg att aac caa ctg cgt gaa ggc ttt gaa cgt	528			
Ile Lys Leu Val Asp Ala Ile Asn Gln Leu Arg Glu Gly Phe Glu Arg				
aaa gct gtc gaa ttg cag gac atc ctg aaa atg ggt cgt acc cag ccg	576			
Lys Ala Val Glu Leu Gln Asp Ile Leu Lys Met Gly Arg Thr Gln Pro				
cag gac gca gta ccg atg acc ctg ggt cag gaa ttc cgc act ttc agc	624			
Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Arg Thr Phe Ser				
atc ctg ctg aaa gaa gaa gtg aaa aac atc caa cgt acc gct gaa ctg	672			
Ile Leu Leu Lys Glu Glu Val Lys Asn Ile Gln Arg Thr Ala Glu Leu				
ctg ctg gaa gtt aac ctt ggc gca aca gca atc ggt act ggt ccc aac	720			
Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Pro Asn				
acg ccg aaa gag tac cgt ccg ctg gca gtg aaa aaa ctg gct gaa gtc	768			
Thr Pro Lys Glu Tyr Arg Pro Leu Ala Val Lys Lys Leu Ala Glu Val				
act ggc ttc cca tgc gta ccg gct gaa cac ctg atc gaa gcg acc tct	816			
Thr Gly Phe Pro Cys Val Pro Ala Glu His Leu Ile Glu Ala Thr Ser				
gac tgc ggc gct tat gtt atg gtt cac ggc gcg ctg aaa cgc ctg gct	864			
Asp Cys Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Leu Ala				
gtg aag atg tcc aaa atc tgt aac gac ctg cgc ttg ctc tct tct ggc	912			
Val Lys Met Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly				
cca cgt gcc ggc ctg aac gag atc aac ctg ccg gaa ctg cag gcg ggc	960			
Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly				
tct tcc atc atg cca gct aaa gta aac ccg gtt gtt ccg gaa gtg gtt	1008			
Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val				
aac cag gta tgc aac aaa gtc atc ggt aac gac acc act gtt acc atg	1056			
Asn Gln Val Cys Asn Lys Val Ile Gly Asn Asp Thr Thr Val Thr Met				
gca gca gaa gca ggt cag ctg cag ttg aac gtt atg gag ccg gtc act	1104			
Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Thr				
ggc cag gct atg ttc gaa tcc gtt cac att ctg acc gct tgc tac	1152			
Gly Gln Ala Met Phe Glu Ser Val His Ile Leu Thr Asn Ala Cys Tyr				
aac ctg ctg gta aaa tgc att aac ggc atc act gct aac aaa gaa gtg	1200			
Asn Leu Leu Val Lys Cys Ile Asn Gly Ile Thr Ala Asn Lys Glu Val				

PF59083SeqList PF59083.txt

385	390	395	400	
tgc gaa ggt tac gtt tac aac act atc ggt atc gtt act tac ctg aac				1248
Cys Glu Gly Tyr Val Tyr Asn Thr Ile Gly Ile Val Thr Tyr Leu Asn				
	405	410	415	
ccg ttc atc ggt cac cac aac ggt gac atc gcg ggt aaa atc tgt gcc				1296
Pro Phe Ile Gly His His Asn Gly Asp Ile Ala Gly Lys Ile Cys Ala				
	420	425	430	
gaa acc ggt aag agt gta cgt gaa gtc ctg gaa cgc ggt ctg ttg tat				1344
Glu Thr Gly Lys Ser Val Arg Glu Val Leu Glu Arg Gly Leu Leu Tyr				
	435	440	445	
gaa gcg gaa ctt gac gat att ttc gta cag aat ctg atg cac ccg				1392
Glu Ala Glu Leu Asp Asp Ile Phe Ser Val Gln Asn Leu Met His Pro				
	450	455	460	
gct tac aaa gct aaa cgc tat act gat gaa agc gaa cag taa				1434
Ala Tyr Lys Ala Lys Arg Tyr Thr Asp Glu Ser Glu Gln				
465	470	475		

<210> 9750

<211> 477

<212> PRT

<213> Escherichia coli

<400> 9750

Met Ser Asn Asn Ile Arg Ile Glu Glu Asp Arg Leu Gly Thr Arg Glu	
1 Val Gly Ala Asp Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Ile Glu	
	5 20 25 30
Asn Phe Tyr Ile Ser Asn Asn Lys Ile Ser Asp Ile Pro Glu Phe Val	
	35 40 45
Arg Gly Met Val Met Val Lys Lys Ala Ala Ala Met Ala Asn Lys Glu	
	50 55 60
Leu Gln Thr Asn Pro Lys Ser Val Ala Asn Ala Ile Ile Pro Ala Cys	
65 Asp Glu Asp Leu Asn Asn Gly Lys Cys Met Asp Gln Phe Pro Val Asp	
	70 75 80 85 90 95
Val Tyr Gln Gly Gly Ala Arg Thr Ser Val Asn Met Asn Thr Asn Glu	
	100 105 110
Val Leu Ala Asn Ile Gly Leu Glu Leu Met Gly His Gln Lys Ala Glu	
	115 120 125
Tyr Gln Tyr Leu Asn Pro Asn Asp His Val Asn Lys Cys Gln Ser Thr	
	130 135 140
Asn Asp Ala His Pro Thr Gly Phe Arg Ile Ala Val Tyr Ser Ser Met	
145 Ile Lys Leu Val Asp Ala Ile Asn Gln Leu Arg Glu Gly Phe Glu Arg	
	150 155 160 165 170 175
Lys Ala Val Glu Leu Gln Asp Ile Leu Lys Met Gly Arg Thr Gln Pro	
	180 185 190
Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Arg Thr Phe Ser	
	195 200 205
Ile Leu Leu Lys Glu Glu Val Lys Asn Ile Gln Arg Thr Ala Glu Leu	
	210 215 220
Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Pro Asn	
225 Thr Pro Lys Glu Tyr Arg Pro Leu Ala Val Lys Lys Leu Ala Glu Val	
	230 235 240 245 250 255
Thr Gly Phe Pro Cys Val Pro Ala Glu His Leu Ile Glu Ala Thr Ser	
	260 265 270
Asp Cys Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Leu Ala	
	275 280 285
Val Lys Met Ser Lys Ile Cys Asn Asp Leu Arg Leu Ser Ser Gly	
	290 295 300
Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly	
305 Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val	
	310 315 320 325 330 335
Asn Gln Val Cys Asn Lys Val Ile Gly Asn Asp Thr Thr Val Thr Met	
	340 345 350
Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Thr	
	355 360 365

PF59083SeqList PF59083.txt

Gly Gln Ala Met Phe Glu Ser Val His Ile Leu Thr Asn Ala Cys Tyr
 370 375 380
 Asn Leu Leu Val Lys Cys Ile Asn Gly Ile Thr Ala Asn Lys Glu Val
 385 390 395 400
 Cys Glu Gly Tyr Val Tyr Asn Thr Ile Gly Ile Val Thr Tyr Leu Asn
 405 410 415
 Pro Phe Ile Gly His His Asn Gly Asp Ile Ala Gly Lys Ile Cys Ala
 420 425 430
 Glu Thr Gly Lys Ser Val Arg Glu Val Leu Glu Arg Gly Leu Leu Tyr
 435 440 445
 Glu Ala Glu Leu Asp Asp Ile Phe Ser Val Gln Asn Leu Met His Pro
 450 455 460
 Ala Tyr Lys Ala Lys Arg Tyr Thr Asp Glu Ser Glu Gln
 465 470 475

<210> 9751
 <211> 1389
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1)..(1389)
 <223> transl_table=11

<400> 9751
 atg agc acc cgc acc gaa cac gac acc atg ggc aat gtc gaa gtc ccg 48
 Met Ser Thr Arg Thr Glu His Asp Thr Met Gly Asn Val Glu Val Pro
 1 5 10 15
 tcc gaa gcc tat tgg ggc gcg cag acc cag cgc agc cgc aac aat ttc 96
 Ser Glu Ala Tyr Trp Gly Ala Gln Thr Arg Ser Arg Asn Asn Phe
 20 25 30
 aaa atc ggc ggc gaa acc ctg ccg cag ccg ctg att tat gct ttg gcg 144
 Lys Ile Gly Gly Glu Thr Leu Pro Gln Pro Leu Ile Tyr Ala Leu Ala
 35 40 45
 ctg gtg aaa aaa gcc gct gcc gcg acc aat gtt tcc ctc ggc agg att 192
 Leu Val Lys Lys Ala Ala Ala Thr Asn Val Ser Leu Gly Arg Ile
 50 55 60
 aag ccg gaa cag gcg gat ttg att acg cag gcg gcg gat gat gtg ttg 240
 Lys Pro Glu Gln Ala Asp Leu Ile Thr Gln Ala Asp Asp Val Leu
 65 70 75 80
 aac ggc agg ctt gac gga cag ttt cct tta gtg gtt tgg cag acc ggc 288
 Asn Gly Arg Leu Asp Gly Gln Phe Pro Leu Val Val Trp Gln Thr Gly
 85 90 95
 tcc ggc acg cag tcc aat atg aac atg aac gaa gtg ctg gcg aac cgc 336
 Ser Gly Thr Gln Ser Asn Met Asn Met Asn Glu Val Leu Ala Asn Arg
 100 105 110
 gcc aac gaa atc gcc ggt acg ggt ttg gcg gcg tat cag ccc gtc cat 384
 Ala Asn Glu Ile Ala Gly Thr Gly Leu Ala Ala Tyr Gln Pro Val His
 115 120 125
 ccc aac gac cat gtg aac cac gcg caa tcg acc aac gac gca ttc ccg 432
 Pro Asn Asp His Val Asn His Ala Gln Ser Thr Asn Asp Ala Phe Pro
 130 135 140
 acc gcc atc cac gtt gcc gcc gcg att gaa atc aac cgc cac ctc atc 480
 Thr Ala Ile His Val Ala Ala Ala Ile Glu Ile Asn Arg His Leu Ile
 145 150 155 160
 ccc gcc gta aaa gcc ctg cgc gac acc ttg gac aaa aaa gcc caa gcc 528
 Pro Ala Val Lys Ala Leu Arg Asp Thr Leu Asp Lys Lys Ala Gln Ala
 165 170 175
 ttc gcc ccc atc gtc aaa atc ggc cgc acc cac ttg cag gac gcg acg 576
 Phe Ala Pro Ile Val Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr
 180 185 190
 ccg ctg act tta ggc caa gaa ttt tcc ggc tac gtt tcc cag ctc gac 624
 Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Val Ser Gln Leu Asp
 195 200 205
 cac ggc tta ggc cgt ctg aat gac gcg ctt aaa gac ttg tat gaa ctt 672
 His Gly Leu Gly Arg Leu Asn Asp Ala Leu Lys Asp Leu Tyr Glu Leu
 210 215 220
 gct ttg ggc ggt acg gcg gtc ggc acg ggt ttg aac agc cat ccc gaa 720

PF59083SeqList PF59083.txt

Ala 225	Leu	Gly	Gly	Thr	Ala 230	Val	Gly	Thr	Gly	Leu 235	Asn	Ser	His	Pro	Glu 240	
tac	gcc	gaa	aaa	gcc	gcc	gcc	aaa	ctc	gcc	gaa	ttg	tcc	ggc	ttg	ccg	768
Tyr	Ala	Glu	Lys	Ala 245	Ala	Ala	Lys	Leu	Ala 250	Glu	Leu	Ser	Gly	Leu 255	Pro	
ttt	gtc	agc	gcg	ccg	aac	aaa	ttt	gaa	gcc	ttg	ggc	gga	cgc	gat	gcc	816
Phe	Val	Ser	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Gly	Gly	Arg	Asp	Ala	
gcc	gtt	gcc	gct	tcg	ggc	gca	ttg	aaa	acg	ctg	gcg	gca	agc	ctg	aat	864
Ala	Val	Ala	Ala	Ser	Gly	Ala	Leu	Lys	Thr	Leu	Ala	Ala	Ser	Leu	Asn	
aaa	atc	gcc	aac	gac	atc	cgc	tggt	ctg	gca	agc	ggc	ccg	cgc	tgc	ggt	912
Lys	Ile	Ala	Asn	Asp	Ile	Arg	Trp	Leu	Ala	Ser	Gly	Pro	Arg	Cys	Gly	
ttt	ggc	gaa	atc	aaa	atc	ccc	gaa	aac	gag	ccg	ggt	tcg	tcc	atc	atg	960
Leu	Gly	Glu	Ile	Lys	Ile	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	
ccg	ggc	aaa	gtc	aac	ccg	acc	caa	tgc	gaa	gcg	atg	acc	atg	gtg	tgc	1008
Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Met	Thr	Met	Val	Cys	
tgc	caa	gtg	ttc	ggc	aac	gac	gtt	acc	atc	ggc	atg	gcg	ggc	gcg	tcg	1056
Cys	Gln	Val	Phe	Gly	Asn	Asp	Val	Thr	Ile	Gly	Met	Ala	Gly	Ala	Ser	
ggc	aat	ttc	gag	ctg	aac	gtc	tat	atg	ccc	gtt	atc	gcc	tac	aac	ctc	1104
Gly	Asn	Phe	Glu	Leu	Asn	Val	Tyr	Met	Pro	Val	Ile	Ala	Tyr	Asn	Leu	
ttt	caa	tcc	atc	cgc	ctg	ttg	ggc	gac	gcg	tgc	aac	agc	ttc	aac	gaa	1152
Leu	Gln	Ser	Ile	Arg	Leu	Leu	Gly	Asp	Ala	Cys	Asn	Ser	Phe	Asn	Glu	
cac	tgc	gcc	gtc	ggc	atc	gaa	ccc	gta	ccg	gaa	aaa	atc	gac	tat	ttc	1200
His	Cys	Ala	Val	Gly	Ile	Glu	Pro	Val	Pro	Glu	Lys	Ile	Asp	Tyr	Phe	
ctg	cac	cat	tcc	ctg	atg	ctg	gtt	act	gcg	tta	aac	cgt	aaa	atc	ggc	1248
Leu	His	His	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Arg	Lys	Ile	Gly	
tac	gaa	aac	gcc	gcc	aaa	gtc	gcc	aaa	acc	gcc	tac	aaa	aac	aac	aaa	1296
Tyr	Glu	Asn	Ala	Ala	Lys	Val	Ala	Lys	Thr	Ala	Tyr	Lys	Asn	Asn	Lys	
tcg	ttg	cgc	gaa	acc	gcc	gtt	gag	ttg	ggc	ttg	ctg	acg	ggc	gaa	gaa	1344
Ser	Leu	Arg	Glu	Thr	Ala	Val	Glu	Leu	Gly	Leu	Leu	Thr	Gly	Glu	Glu	
ttt	gac	gaa	ctg	gtc	gtt	cct	gcc	gat	atg	gtt	cat	ccg	cgc	taa		1389
Phe	Asp	Glu	Leu	Val	Val	Pro	Ala	Asp	Met	Val	His	Pro	Arg			

<210> 9752

<211> 462

<212> PRT

<213> Neisseria meningitidis

<400> 9752

Met 1	Ser	Thr	Arg	Thr 5	Glu	His	Asp	Thr	Met 10	Gly	Asn	Val	Glu	Val 15	Pro
Ser	Glu	Ala	Tyr 20	Trp	Gly	Ala	Gln	Thr 25	Gln	Arg	Ser	Arg	Asn 30	Asn	Phe
Lys	Ile	Gly	Gly 35	Glu	Thr	Leu	Pro 40	Gln	Pro	Leu	Ile	Tyr 45	Ala	Leu	Ala
Leu	Val 50	Lys	Lys	Ala	Ala	Ala 55	Ala	Thr	Asn	Val	Ser 60	Leu	Gly	Arg	Ile
Lys 65	Pro	Glu	Gln	Ala	Asp 70	Leu	Ile	Thr	Gln	Ala 75	Ala	Asp	Asp	Val	Leu
Asn	Gly	Arg	Leu	Asp 85	Gly	Gln	Phe	Pro	Leu 90	Val	Val	Trp	Gln	Thr 95	Gly
Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Met 105	Asn	Glu	Val	Leu	Ala	Asn	Arg
Ala	Asn	Glu	Ile	Ala	Gly	Thr	Gly	Leu	Ala	Ala	Tyr	Gln	Pro	Val	His
Pro	Asn 130	Asp	His	Val	Asn	His 135	Ala	Gln	Ser	Thr	Asn	Asp	Ala	Phe	Pro

PF59083SeqList PF59083.txt

Thr Ala Ile His Val Ala Ala Ala Ile Glu Ile Asn Arg His Leu Ile
145 150 155 160
Pro Ala Val Lys Ala Leu Arg Asp Thr Leu Asp Lys Lys Ala Gln Ala
165 170 175
Phe Ala Pro Ile Val Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr
180 185 190
Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Val Ser Gln Leu Asp
195 200 205
His Gly Leu Gly Arg Leu Asn Asp Ala Leu Lys Asp Leu Tyr Glu Leu
210 215 220
Ala Leu Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Ser His Pro Glu
225 230 235 240
Tyr Ala Glu Lys Ala Ala Ala Lys Leu Ala Glu Leu Ser Gly Leu Pro
245 250 255
Phe Val Ser Ala Pro Asn Lys Phe Glu Ala Leu Gly Gly Arg Asp Ala
260 265 270
Ala Val Ala Ala Ser Gly Ala Leu Lys Thr Leu Ala Ala Ser Leu Asn
275 280 285
Lys Ile Ala Asn Asp Ile Arg Trp Leu Ala Ser Gly Pro Arg Cys Gly
290 295 300
Leu Gly Glu Ile Lys Ile Pro Glu Asn Glu Pro Gly Ser Ser Ile Met
305 310 315 320
Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Met Thr Met Val Cys
325 330 335
Cys Gln Val Phe Gly Asn Asp Val Thr Ile Gly Met Ala Gly Ala Ser
340 345 350
Gly Asn Phe Glu Leu Asn Val Tyr Met Pro Val Ile Ala Tyr Asn Leu
355 360 365
Leu Gln Ser Ile Arg Leu Leu Gly Asp Ala Cys Asn Ser Phe Asn Glu
370 375 380
His Cys Ala Val Gly Ile Glu Pro Val Pro Glu Lys Ile Asp Tyr Phe
385 390 395 400
Leu His His Ser Leu Met Leu Val Thr Ala Leu Asn Arg Lys Ile Gly
405 410 415
Tyr Glu Asn Ala Ala Lys Val Ala Lys Thr Ala Tyr Lys Asn Asn Lys
420 425 430
Ser Leu Arg Glu Thr Ala Val Glu Leu Gly Leu Leu Thr Gly Glu Glu
435 440 445
Phe Asp Glu Leu Val Val Pro Ala Asp Met Val His Pro Arg
450 455 460

<210> 9753
<211> 1395
<212> DNA
<213> Eikenella corrodens

<220>
<221> CDS
<222> (1)..(1395)
<223> transl_table=11

<400> 9753
atg aca acc cga acc gaa cac gac ttc ttc ggc gaa cgc gaa atc ccc 48
Met Thr Thr Arg Thr Glu His Asp Phe Phe Gly Glu Arg Glu Ile Pro 15
1 5 10
gca acc gct tat tgg ggt atc cac acc ctg cgc gca gtg gaa aac ttc 96
Ala Thr Ala Tyr Trp Gly Ile His Thr Leu Arg Ala Val Glu Asn Phe 20 25 30
caa atc tcc ggg cag aag att tcc gac gta ccc cag ttt gtg cgc agc 144
Gln Ile Ser Gly Gln Lys Ile Ser Asp Val Pro Gln Phe Val Arg Ser 35 40 45
atg gtg atg gtg aaa aaa gcc gct gcc cag gcc aac ggc gag ctg ggc 192
Met Val Met Val Lys Lys Ala Ala Ala Gln Ala Asn Gly Glu Leu Gly 50 55 60
gca ctc aag ccc gaa atc gcc gcc att gcc caa gct tgc gac gag 240
Ala Leu Lys Pro Glu Ile Ala Ala Ala Ile Ala Gln Ala Cys Asp Glu 65 70 75 80
gtg ctg ctc aaa ggc cgt tgc ctc gac cag ttc cca tcc gac gta ttc 288
Val Leu Leu Lys Gly Arg Cys Leu Asp Gln Phe Pro Ser Asp Val Phe
Seite 10243

PF59083SeqList PF59083.txt

														85															90															95							
caa	ggc	ggc	ggc	ggc	act	tcg	gtg	aac	atg	aac	acc	aac	gaa	gtg	atc	336																																			
Gln	Gly	Gly	Ala	Gly	Thr	Ser	Val	Asn	Met	Asn	Thr	Asn	Glu	Val	Ile																																				
																100																	105																	110	
gcc	aac	ctc	ggc	ttg	gaa	gcc	tta	ggc	caa	gcc	aaa	ggc	cgc	tac	gac	384																																			
Ala	Asn	Leu	Ala	Leu	Glu	Ala	Leu	Gly	Gln	Ala	Lys	Gly	Arg	Tyr	Asp																																				
																115																	120																	125	
atc	gtc	aat	ccc	atg	gat	cat	gtg	aac	gcc	agc	caa	ttt	acc	aac	gac	432																																			
Ile	Val	Asn	Pro	Met	Asp	His	Val	Asn	Ala	Ser	Gln	Phe	Thr	Asn	Asp																																				
																130																	135																	140	
gct	tac	cct	acc	ggc	ttc	cgg	ctg	gct	gta	tac	acc	agc	atc	ggc	gaa	480																																			
Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Leu	Ala	Val	Tyr	Thr	Ser	Ile	Gly	Glu																																				
																145																	150																	155	
ctg	cta	gac	aaa	ctg	gca	tac	ctg	aaa	aac	acc	ttt	gct	gcc	aaa	gct	528																																			
Leu	Leu	Asp	Lys	Leu	Ala	Tyr	Leu	Lys	Asn	Thr	Phe	Ala	Ala	Lys	Ala																																				
																165																	170																	175	
gat	gaa	ttc	aaa	gac	ata	tta	aaa	atg	ggc	cgc	acc	cag	ctg	caa	gat	576																																			
Asp	Glu	Phe	Lys	Asp	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	Asp																																				
																180																	185																	190	
gcc	gtg	ccc	atg	act	gcc	ggc	caa	gaa	ttc	caa	tcc	ttc	caa	gtg	ctg	624																																			
Ala	Val	Pro	Met	Thr	Ala	Gly	Gln	Glu	Phe	Gln	Ser	Phe	Gln	Val	Leu																																				
																195																	200																	205	
ctg	gca	gaa	gag	gaa	acc	aac	ctc	gaa	cgc	acc	cgc	caa	ctg	ctg	ctg	672																																			
Leu	Ala	Glu	Glu	Glu	Thr	Asn	Leu	Glu	Arg	Thr	Arg	Gln	Leu	Leu	Leu																																				
																210																	215																	220	
gaa	gtg	aac	ctc	ggc	gcc	aca	gcc	atc	ggc	aca	ggc	atc	aat	acg	ccg	720																																			
Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Thr	Pro																																				
																225																	230																	235	
caa	ggc	tac	gcg	ccg	ctg	gcc	gta	caa	aaa	ctc	tcc	gaa	atc	agc	ggc	768																																			
Gln	Gly	Tyr	Ala	Pro	Leu	Ala	Val	Gln	Lys	Leu	Ser	Glu	Ile	Ser	Gly																																				
																245																	250																	255	
ctg	ccc	tgc	aag	ctc	acc	gaa	aac	ctg	att	gaa	gcc	act	tcc	gac	tgc	816																																			
Leu	Pro	Cys	Lys	Leu	Thr	Glu	Asn	Leu	Ile	Glu	Ala	Thr	Ser	Asp	Cys																																				
																260																	265																	270	
ggg	gcc	tat	gtg	atg	gtg	cac	ggc	ctc	aag	cgc	acc	gcc	gtg	aag		864																																			
Gly	Ala	Tyr	Val	Met	Val	His	Gly	Ala	Leu	Lys	Arg	Thr	Ala	Val	Lys																																				
																275																	280																	285	
ctc	tcc	aaa	atc	tgc	aac	gac	ctg	cgc	cta	ctc	tcc	tcc	ggc	ccg	cgt	912																																			
Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg																																				
																290																	295																	300	
gcc	ggc	ctg	aaa	gaa	atc	aac	ctg	ccg	gaa	atg	cag	gcc	ggc	tca	tcg	960																																			
Ala	Gly	Leu	Lys	Glu	Ile	Asn	Leu	Pro	Glu	Met	Gln	Ala	Gly	Ser	Ser																																				
																305																	310																	315	
att	atg	ccc	ggc	aag	gtg	aat	ccc	gtg	att	ccc	gaa	gtg	gtg	aac	caa	1008																																			
Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln																																				
																325																	330																	335	
gtt	tgt	ttc	aaa	gta	atc	ggc	aac	gac	acc	acc	atc	acc	ttc	gcc	gcc	1056																																			
Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Thr	Ile	Thr	Phe	Ala	Ala																																				
																340																	345																	350	
gaa	gcc	ggc	cag	ctc	cat	caa	cgt	gat	gga	gcc	ggt	tat	ccg	caa	tcc	1104																																			
Glu	Ala	Gly	Gln	Leu	His	Gln	Arg	Asp	Gly	Ala	Gly	Tyr	Pro	Gln	Ser																																				
																355																	360																	365	
atg	ttt	gaa	agc	atc	tcg	ctt	tta	ggc	aac	gcc	gcc	att	acg	ttg	gcc	1152																																			
Met	Phe	Glu	Ser	Ile	Ser	Leu	Leu	Gly	Asn	Ala	Ala	Ile	Thr	Leu	Ala																																				
																370																	375																	380	
gac	aaa	tgc	gtg	cgc	ggc	atc	acg	gta	aac	cgc	gaa	atc	tgc	gaa	cgc	1200																																			
Asp	Lys	Cys	Val	Arg	Gly	Ile	Thr	Val	Asn	Arg	Glu	Ile	Cys	Glu	Arg																																				
																385																	390																	395	
tac	gtc	ttc	aac	tcc	atc	ggc	ctg	gta	acc	tat	ctc	aac	ccc	tat	atc	1248																																			
Tyr	Val	Phe	Asn	Ser	Ile	Gly	Leu	Val	Thr	Tyr	Leu	Asn	Pro	Tyr	Ile																																				
																405																	410																	415	
ggc	cac	gaa	aac	ggc	gac	ctg	gtg	ggc	aaa	atc	tgc	gct	caa	acc	ggc	1296																																			
Gly	His	Glu	Asn	Gly	Asp	Leu	Val	Gly	Lys	Ile	Cys	Ala	Gln	Thr	Gly																																				
																420																	425																	430	
aaa	acc	gtg	cgc	gaa	gtg	gta	ctg	gag	cgc	cag	ctc	ttg	agc	gaa	gcg	1344																																			
Lys	Thr	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gln	Leu	Leu	Ser	Glu	Ala																																				
																435																	440																	445	
gag	ctc	gac	cgt	atc	ctg	tcg	cca	caa	aac	ttg	gcc	aat	ccg	cat	ttg	1392																																			
Glu	Leu	Asp	Arg	Ile	Leu	Ser	Pro	Gln	Asn	Leu	Ala	Asn	Pro	His	Leu																																				

450
taa

455 460

1395

<210> 9754
<211> 464
<212> PRT
<213> Eikenella corrodens

<400> 9754
Met Thr Thr Arg Thr Glu His Asp Phe Phe Gly Glu Arg Glu Ile Pro
1 5 10 15
Ala Thr Ala Tyr Trp Gly Ile His Thr Leu Arg Ala Val Glu Asn Phe
20 25 30
Gln Ile Ser Gly Gln Lys Ile Ser Asp Val Pro Gln Phe Val Arg Ser
35 40 45
Met Val Met Val Lys Lys Ala Ala Ala Gln Ala Asn Gly Glu Leu Gly
50 55 60
Ala Leu Lys Pro Glu Ile Ala Ala Ala Ile Ala Gln Ala Cys Asp Glu
65 70 75 80
Val Leu Leu Lys Gly Arg Cys Leu Asp Gln Phe Pro Ser Asp Val Phe
85 90 95
Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val Ile
100 105 110
Ala Asn Leu Ala Leu Glu Ala Leu Gly Gln Ala Lys Gly Arg Tyr Asp
115 120 125
Ile Val Asn Pro Met Asp His Val Asn Ala Ser Gln Phe Thr Asn Asp
130 135 140
Ala Tyr Pro Thr Gly Phe Arg Leu Ala Val Tyr Thr Ser Ile Gly Glu
145 150 155 160
Leu Leu Asp Lys Leu Ala Tyr Leu Lys Asn Thr Phe Ala Ala Lys Ala
165 170 175
Asp Glu Phe Lys Asp Ile Leu Lys Met Gly Arg Thr Gln Leu Gln Asp
180 185 190
Ala Val Pro Met Thr Ala Gly Gln Glu Phe Gln Ser Phe Gln Val Leu
195 200 205
Leu Ala Glu Glu Glu Thr Asn Leu Glu Arg Thr Arg Gln Leu Leu Leu
210 215 220
Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Ile Asn Thr Pro
225 230 235 240
Gln Gly Tyr Ala Pro Leu Ala Val Gln Lys Leu Ser Glu Ile Ser Gly
245 250 255
Leu Pro Cys Lys Leu Thr Glu Asn Leu Ile Glu Ala Thr Ser Asp Cys
260 265 270
Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Thr Ala Val Lys
275 280 285
Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg
290 295 300
Ala Gly Leu Lys Glu Ile Asn Leu Pro Glu Met Gln Ala Gly Ser Ser
305 310 315 320
Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln
325 330 335
Val Cys Phe Lys Val Ile Gly Asn Asp Thr Thr Ile Thr Phe Ala Ala
340 345 350
Glu Ala Gly Gln Leu His Gln Arg Asp Gly Ala Gly Tyr Pro Gln Ser
355 360 365
Met Phe Glu Ser Ile Ser Leu Leu Gly Asn Ala Ala Ile Thr Leu Ala
370 375 380
Asp Lys Cys Val Arg Gly Ile Thr Val Asn Arg Glu Ile Cys Glu Arg
385 390 395 400
Tyr Val Phe Asn Ser Ile Gly Leu Val Thr Tyr Leu Asn Pro Tyr Ile
405 410 415
Gly His Glu Asn Gly Asp Leu Val Gly Lys Ile Cys Ala Gln Thr Gly
420 425 430
Lys Thr Val Arg Glu Val Val Leu Glu Arg Gln Leu Leu Ser Glu Ala
435 440 445
Glu Leu Asp Arg Ile Leu Ser Pro Gln Asn Leu Ala Asn Pro His Leu
450 455 460

PF59083SeqList PF59083.txt

<210> 9755
 <211> 1380
 <212> DNA
 <213> Pseudomonas putida

<220>
 <221> CDS
 <222> (1)..(1380)
 <223> transl_table=11

```

<400> 9755
atg atg agt gat acc cgt atc gag cgt gac agc atg ggc gaa ctg cag      48
Met Met Ser Asp Thr Arg Ile Glu Arg Asp Ser Met Gly Glu Leu Gln
 1      5      10      15
gtg ccg gcc cag gcc ctg tac ggt gcc cag act cag cgc gcg gtc gac      96
Val Pro Ala Gln Ala Leu Tyr Gly Ala Gln Thr Gln Arg Ala Val Asp
 20      25      30
aac ttc ccg gtc agc ggc cag cgc atg ccg gcc cag ttc att cgc gcg      144
Asn Phe Pro Val Ser Gly Gln Arg Met Pro Ala Gln Phe Ile Arg Ala
 35      40      45
ctg ttg ctg gcc aag gcg gct gcc gcc aag gcc aac gtc gag ctg gag      192
Leu Leu Leu Ala Lys Ala Ala Ala Lys Ala Asn Val Glu Leu Glu
 50      55      60
caa ttg tct gcc gcg cag ggc aat gcc atc gtc aag gcg gtc gag caa      240
Gln Leu Ser Ala Ala Gln Gly Asn Ala Ile Val Lys Ala Val Glu Gln
 65      70      75      80
ctg ctg gcc gag gac ttc atc cag cac ttc ccg gtg gat gtg ttc cag      288
Leu Leu Ala Glu Asp Phe Ile Gln His Phe Pro Val Asp Val Phe Gln
 85      90      95
acc ggc tcc ggc acc agc tcg aac atg aac gcc aac gag gtg atc gcc      336
Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Ala Asn Glu Val Ile Ala
100      105      110
acc ctg gcc agc cgt gta ctg ggt gat gcg gtc aac gcc aac gac cac      384
Thr Leu Ala Ser Arg Val Leu Gly Asp Ala Val Asn Ala Asn Asp His
115      120      125
gtc aac tgt ggc cag agc agc aac gac atc atc ccg acc acc att cac      432
Val Asn Cys Gly Gln Ser Ser Asn Asp Ile Ile Pro Thr Thr Ile His
130      135      140
gtc agt gct gca ctg gcc ctg cac gaa caa ctg ctt ccg gcc ctg agc      480
Val Ser Ala Ala Leu Ala Leu His Glu Gln Leu Leu Pro Ala Leu Ser
145      150      155      160
cac ctg gtg cag gtg atc gag acc aag tcg gtg cag gtg cat cag tac      528
His Leu Val Gln Val Ile Glu Thr Lys Ser Val Gln Val His Gln Tyr
165      170      175
gtg aaa acc ggc cgt acc cac ttg atg gac gcc atg ccg gtg cgc atg      576
Val Lys Thr Gly Arg Thr His Leu Met Asp Ala Met Pro Val Arg Met
180      185      190
agc cag gtg ctg gat ggc tgg gcc gcg cag atc aac gct gcc aag gcg      624
Ser Gln Val Leu Asp Gly Trp Ala Ala Gln Ile Asn Ala Ala Lys Ala
195      200      205
cac atc gag gcg acc ctg ccg agc ttg cag gcg ctg gcc cag ggt ggc      672
His Ile Glu Ala Thr Leu Pro Ser Leu Gln Ala Leu Ala Gln Gly Gly
210      215      220
acg gcc gtg ggt acc ggc atc aac gcc cac cca cag ttc gcg gcc ggt      720
Thr Ala Val Gly Thr Gly Ile Asn Ala His Pro Gln Phe Ala Ala Gly
225      230      235      240
ttc gcc cgc cag ctc agc ggc ctg acc cag gtc gag ttc acc ccg ggc      768
Phe Ala Arg Gln Leu Ser Gly Leu Thr Gln Val Glu Phe Thr Pro Gly
245      250      255
cag aac ctg ttt gcc ctg atc ggc tcg caa gac act gcc gtg gcg ctg      816
Gln Asn Leu Phe Ala Leu Ile Gly Ser Gln Asp Thr Ala Val Ala Leu
260      265      270
tct ggc cag ctc aag acc act gct gtg gcg ctg atg aag atc gcc aac      864
Ser Gly Gln Leu Lys Thr Thr Ala Val Ala Leu Met Lys Ile Ala Asn
275      280      285      290
gac ctg cgc tgg atg aac tcc ggc ccg ctc gcc ggc ctg ggc gaa att      912
Asp Leu Arg Trp Met Asn Ser Gly Pro Leu Ala Gly Leu Gly Glu Ile
290      295      300
    
```

PF59083SeqList PF59083.txt

gag	ctg	caa	ggc	ctg	caa	ccg	ggc	tct	tcg	atc	atg	cct	ggc	aag	gtc	960
Glu	Leu	Gln	Gly	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	
305				310				315							320	
aac	ccg	gtg	att	cct	gag	gcc	acc	gcc	atg	gtt	gct	gcc	cag	gtg	atc	1008
Asn	Pro	Val	Ile	Pro	Glu	Ala	Thr	Ala	Met	Val	Ala	Ala	Gln	Val	Ile	
				325				330						335		
ggc	aac	gac	gcc	acc	atc	gct	gtc	gct	ggc	cag	tcc	ggc	aac	ttc	gag	1056
Gly	Asn	Asp	Ala	Thr	Ile	Ala	Val	Ala	Gly	Gln	Ser	Gly	Asn	Phe	Glu	
			340					345					350			
ctg	aac	gtg	atg	ctg	ccg	gtg	atc	gcc	cgc	aac	ctg	ctg	gaa	agc	atc	1104
Leu	Asn	Val	Met	Leu	Pro	Val	Ile	Ala	Arg	Asn	Leu	Leu	Glu	Ser	Ile	
			355				360						365			
gag	ctg	atg	gcc	aac	gtc	agc	cgt	ctg	ctg	gcc	gac	aag	gcc	atc	gcc	1152
Glu	Leu	Met	Ala	Asn	Val	Ser	Arg	Leu	Leu	Ala	Asp	Lys	Ala	Ile	Ala	
			370			375					380					
acg	ttc	agg	gtc	aac	gag	ggc	aag	ctc	aag	gaa	gcc	ctg	gcg	cgc	aac	1200
Thr	Phe	Arg	Val	Asn	Glu	Gly	Lys	Leu	Lys	Glu	Ala	Leu	Ala	Arg	Asn	
385				390				395							400	
ccg	att	ctg	gtc	act	gcg	ctg	aac	ccg	atc	atc	ggc	tac	ctc	aag	gcc	1248
Pro	Ile	Leu	Val	Thr	Ala	Leu	Asn	Pro	Ile	Ile	Gly	Tyr	Leu	Lys	Ala	
				405				410						415		
gcc	gaa	atc	gcc	aag	acc	gcc	tac	aag	cag	ggc	cgc	ccg	atc	atc	gac	1296
Ala	Glu	Ile	Ala	Lys	Thr	Ala	Tyr	Lys	Gln	Gly	Arg	Pro	Ile	Ile	Asp	
			420				425						430			
gtg	gcg	ctg	gag	cac	acc	gac	ctg	tcg	cgg	gac	cag	ctg	gaa	gca	ctg	1344
Val	Ala	Leu	Glu	His	Thr	Asp	Leu	Ser	Arg	Asp	Gln	Leu	Glu	Ala	Leu	
			435				440					445				
ctg	gac	ccg	gaa	aaa	ctc	acc	gct	ggc	ggg	atc	tga					1380
Leu	Asp	Pro	Glu	Lys	Leu	Thr	Ala	Gly	Gly	Ile						
	450					455										

<210> 9756

<211> 459

<212> PRT

<213> Pseudomonas putida

<400> 9756

Met	Met	Ser	Asp	Thr	Arg	Ile	Glu	Arg	Asp	Ser	Met	Gly	Glu	Leu	Gln	
1				5					10					15		
Val	Pro	Ala	Gln	Ala	Leu	Tyr	Gly	Ala	Gln	Thr	Gln	Arg	Ala	Val	Asp	
			20					25					30			
Asn	Phe	Pro	Val	Ser	Gly	Gln	Arg	Met	Pro	Ala	Gln	Phe	Ile	Arg	Ala	
		35				40						45				
Leu	Leu	Leu	Ala	Lys	Ala	Ala	Ala	Lys	Ala	Asn	Val	Glu	Leu	Glu		
		50				55					60					
Gln	Leu	Ser	Ala	Ala	Gln	Gly	Asn	Ala	Ile	Val	Lys	Ala	Val	Glu	Gln	
65				70					75					80		
Leu	Leu	Ala	Glu	Asp	Phe	Ile	Gln	His	Phe	Pro	Val	Asp	Val	Phe	Gln	
				85					90					95		
Thr	Gly	Ser	Gly	Thr	Ser	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	
			100					105					110			
Thr	Leu	Ala	Ser	Arg	Val	Leu	Gly	Asp	Ala	Val	Asn	Ala	Asn	Asp	His	
		115					120					125				
Val	Asn	Cys	Gly	Gln	Ser	Ser	Asn	Asp	Ile	Ile	Pro	Thr	Thr	Ile	His	
		130				135					140					
Val	Ser	Ala	Ala	Leu	Ala	Leu	His	Glu	Gln	Leu	Leu	Pro	Ala	Leu	Ser	
145				150					155					160		
His	Leu	Val	Gln	Val	Ile	Glu	Thr	Lys	Ser	Val	Gln	Val	His	Gln	Tyr	
			165					170					175			
Val	Lys	Thr	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Met	Pro	Val	Arg	Met	
			180					185					190			
Ser	Gln	Val	Leu	Asp	Gly	Trp	Ala	Ala	Gln	Ile	Asn	Ala	Ala	Lys	Ala	
		195					200					205				
His	Ile	Glu	Ala	Thr	Leu	Pro	Ser	Leu	Gln	Ala	Leu	Ala	Gln	Gly	Gly	
		210				215					220					
Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Ala	His	Pro	Gln	Phe	Ala	Ala	Gly	
225				230					235					240		
Phe	Ala	Arg	Gln	Leu	Ser	Gly	Leu	Thr	Gln	Val	Glu	Phe	Thr	Pro	Gly	
				245					250					255		

PF59083SeqList PF59083.txt

Gln Asn Leu Phe Ala Leu Ile Gly Ser Gln Asp Thr Ala Val Ala Leu
 260 265 270
 Ser Gly Gln Leu Lys Thr Thr Ala Val Ala Leu Met Lys Ile Ala Asn
 275 280 285
 Asp Leu Arg Trp Met Asn Ser Gly Pro Leu Ala Gly Leu Gly Glu Ile
 290 295 300
 Glu Leu Gln Gly Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys Val
 305 310 315 320
 Asn Pro Val Ile Pro Glu Ala Thr Ala Met Val Ala Ala Gln Val Ile
 325 330 335
 Gly Asn Asp Ala Thr Ile Ala Val Ala Gly Gln Ser Gly Asn Phe Glu
 340 345 350
 Leu Asn Val Met Leu Pro Val Ile Ala Arg Asn Leu Leu Glu Ser Ile
 355 360 365
 Glu Leu Met Ala Asn Val Ser Arg Leu Leu Ala Asp Lys Ala Ile Ala
 370 375 380
 Thr Phe Arg Val Asn Glu Gly Lys Leu Lys Glu Ala Leu Ala Arg Asn
 385 390 395 400
 Pro Ile Leu Val Thr Ala Leu Asn Pro Ile Ile Gly Tyr Leu Lys Ala
 405 410 415
 Ala Glu Ile Ala Lys Thr Ala Tyr Lys Gln Gly Arg Pro Ile Ile Asp
 420 425 430
 Val Ala Leu Glu His Thr Asp Leu Ser Arg Asp Gln Leu Glu Ala Leu
 435 440 445
 Leu Asp Pro Glu Lys Leu Thr Ala Gly Gly Ile
 450 455

<210> 9757

<211> 1428

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1428)

<223> transl_table=11

<400> 9757

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

PF59083SeqList PF59083.txt

Glu	Lys	Leu	Leu	Lys	Thr	Met	Glu	Asp	Met	His	Ser	Val	Phe	Lys	Gln	
aaa	gca	cag	gag	ttt	cac	tct	ggt	att	aaa	atg	ggc	cgg	aca	cac	ctt	576
Lys	Ala	Gln	Glu	Phe	His	Ser	Val	Ile	Lys	Met	Gly	Arg	Thr	His	Leu	
caa	gat	gcg	ggt	ccg	atc	cgt	ctt	ggc	cag	gaa	ttc	gaa	gct	tac	agc	624
Gln	Asp	Ala	Val	Pro	Ile	Arg	Leu	Gly	Gln	Glu	Phe	Glu	Ala	Tyr	Ser	
cgt	gtt	ctc	gag	cgt	gat	atc	aaa	cga	atc	aag	caa	tcg	cgc	cag	cac	672
Arg	Val	Leu	Glu	Arg	Asp	Ile	Lys	Arg	Ile	Lys	Gln	Ser	Arg	Gln	His	
ctg	tat	gaa	gtc	aac	atg	ggc	gca	act	gct	gtt	ggg	aca	ggg	ctg	aac	720
Leu	Tyr	Glu	Val	Asn	Met	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	
225					230					235					240	
gct	gat	cct	gaa	tat	atc	aaa	cag	gta	gta	aag	cac	ctt	gct	gat	att	768
Ala	Asp	Pro	Glu	Tyr	Ile	Lys	Gln	Val	Val	Lys	His	Leu	Ala	Asp	Ile	
245									250					255		
agc	ggg	ctt	cct	ctt	gtc	ggc	gct	gat	cat	ctt	gtt	gat	gcg	aca	caa	816
Ser	Gly	Leu	Pro	Leu	Val	Gly	Ala	Asp	His	Leu	Val	Asp	Ala	Thr	Gln	
260								265					270			
aat	aca	gat	gcc	tat	aca	gag	gta	gct	tca	tta	aaa	gtc	tgc	atg		864
Asn	Thr	Asp	Ala	Tyr	Thr	Glu	Val	Ser	Ala	Ser	Leu	Lys	Val	Cys	Met	
275							280					285				
atg	aac	atg	tcg	aag	atc	gca	aac	gac	ctg	cgc	tta	atg	gcg	tcg	gga	912
Met	Asn	Met	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Leu	Met	Ala	Ser	Gly	
290						295					300					
ccg	cgc	gcc	gga	ctt	gcg	gaa	att	tct	ctg	cct	gca	cgt	cag	ccg	ggt	960
Pro	Arg	Ala	Gly	Leu	Ala	Glu	Ile	Ser	Leu	Pro	Ala	Arg	Gln	Pro	Gly	
305					310					315					320	
tca	tct	att	atg	ccg	ggg	aaa	gtc	aat	ccg	gtt	atg	gcg	gag	ctg	atc	1008
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Leu	Ile	
325									330					335		
aac	caa	att	gcg	ttc	cag	gtt	atc	gga	aat	gac	aat	aca	atc	tgc	ctt	1056
Asn	Gln	Ile	Ala	Phe	Gln	Val	Ile	Gly	Asn	Asp	Asn	Thr	Ile	Cys	Leu	
340								345					350			
gct	tca	gaa	gcc	ggc	cag	ctt	gag	ttg	aac	gtc	atg	gag	ccc	gtg	ctt	1104
Ala	Ser	Glu	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Leu	
355							360					365				
gtc	ttt	aat	ttg	ctt	caa	tcc	atc	agc	atc	atg	aac	aac	ggc	ttc	cgt	1152
Val	Phe	Asn	Leu	Leu	Gln	Ser	Ile	Ser	Ile	Met	Asn	Asn	Gly	Phe	Arg	
370						375					380					
tcg	ttc	act	gac	aac	tgc	tta	aaa	ggc	att	gaa	gcc	aac	gaa	aag	cgt	1200
Ser	Phe	Thr	Asp	Asn	Cys	Leu	Lys	Gly	Ile	Glu	Ala	Asn	Glu	Lys	Arg	
385					390					395					400	
atg	aag	caa	tac	gta	gaa	aaa	agc	gca	ggc	gtg	atc	aca	gct	gtc	aat	1248
Met	Lys	Gln	Tyr	Val	Glu	Lys	Ser	Ala	Gly	Val	Ile	Thr	Ala	Val	Asn	
405									410					415		
ccg	cat	ctt	ggg	tat	gaa	gcg	gca	gct	aga	att	gcc	agg	gaa	gca	att	1296
Pro	His	Leu	Gly	Tyr	Glu	Ala	Ala	Ala	Arg	Ile	Ala	Arg	Glu	Ala	Ile	
420								425					430			
atg	aca	ggg	caa	tct	gtc	cgg	gat	ctt	tgt	ctg	cag	cat	gat	gtg	ctg	1344
Met	Thr	Gly	Gln	Ser	Val	Arg	Asp	Leu	Cys	Leu	Gln	His	Asp	Val	Leu	
435							440					445				
act	gaa	gaa	gaa	ttg	gat	att	att	tta	aac	cca	tat	gag	atg	acc	aaa	1392
Thr	Glu	Glu	Glu	Leu	Asp	Ile	Ile	Leu	Asn	Pro	Tyr	Glu	Met	Thr	Lys	
450						455					460					
cca	ggt	atc	gca	ggg	aaa	gaa	cta	tta	gaa	aaa	taa					1428
Pro	Gly	Ile	Ala	Gly	Lys	Glu	Leu	Leu	Glu	Lys						
465					470					475						

<210> 9758

<211> 475

<212> PRT

<213> Bacillus subtilis

<400> 9758

Met	Leu	Asn	Gly	Gln	Lys	Glu	Tyr	Arg	Val	Glu	Lys	Asp	Phe	Leu	Gly
1				5					10					15	
Glu	Lys	Gln	Ile	Glu	Ala	Asp	Val	Tyr	Tyr	Gly	Ile	Gln	Thr	Leu	Arg

PF59083SeqList PF59083.txt

			20					25					30		
Ala	Ser	Glu	Asn	Phe	Pro	Ile	Thr	Gly	Tyr	Lys	Ile	His	Glu	Glu	Met
		35					40					45			
Ile	Asn	Ala	Leu	Ala	Ile	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Met
	50					55					60				
Asp	Val	Lys	Arg	Leu	Tyr	Glu	Gly	Ile	Gly	Gln	Ala	Ile	Val	Gln	Ala
65					70					75					80
Ala	Asp	Glu	Ile	Leu	Glu	Gly	Lys	Trp	His	Asp	Gln	Phe	Ile	Val	Asp
				85					90					95	
Pro	Ile	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Met	Asn	Met	Asn	Ala	Asn	Gln
			100					105					110		
Val	Ile	Gly	Asn	Arg	Ala	Leu	Glu	Ile	Met	Gly	His	Lys	Lys	Gly	Asp
		115					120					125			
Tyr	Ile	His	Leu	Ser	Pro	Asn	Thr	His	Val	Asn	Met	Ser	Gln	Ser	Gln
	130					135					140				
Asn	Asp	Val	Phe	Pro	Thr	Ala	Ile	His	Ile	Ser	Thr	Leu	Lys	Leu	Leu
145					150					155					160
Glu	Lys	Leu	Leu	Lys	Thr	Met	Glu	Asp	Met	His	Ser	Val	Phe	Lys	Gln
				165					170					175	
Lys	Ala	Gln	Glu	Phe	His	Ser	Val	Ile	Lys	Met	Gly	Arg	Thr	His	Leu
			180					185					190		
Gln	Asp	Ala	Val	Pro	Ile	Arg	Leu	Gly	Gln	Glu	Phe	Glu	Ala	Tyr	Ser
		195					200					205			
Arg	Val	Leu	Glu	Arg	Asp	Ile	Lys	Arg	Ile	Lys	Gln	Ser	Arg	Gln	His
	210					215					220				
Leu	Tyr	Glu	Val	Asn	Met	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn
225				230						235					240
Ala	Asp	Pro	Glu	Tyr	Ile	Lys	Gln	Val	Val	Lys	His	Leu	Ala	Asp	Ile
				245					250					255	
Ser	Gly	Leu	Pro	Leu	Val	Gly	Ala	Asp	His	Leu	Val	Asp	Ala	Thr	Gln
			260					265					270		
Asn	Thr	Asp	Ala	Tyr	Thr	Glu	Val	Ser	Ala	Ser	Leu	Lys	Val	Cys	Met
		275				280						285			
Met	Asn	Met	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Leu	Met	Ala	Ser	Gly
	290					295					300				
Pro	Arg	Ala	Gly	Leu	Ala	Glu	Ile	Ser	Leu	Pro	Ala	Arg	Gln	Pro	Gly
					310					315					320
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Leu	Ile
				325					330					335	
Asn	Gln	Ile	Ala	Phe	Gln	Val	Ile	Gly	Asn	Asp	Asn	Thr	Ile	Cys	Leu
			340					345					350		
Ala	Ser	Glu	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Leu
		355					360					365			
Val	Phe	Asn	Leu	Leu	Gln	Ser	Ile	Ser	Ile	Met	Asn	Asn	Gly	Phe	Arg
	370														

<210> 9759

<211> 1407

<212> DNA

<213> Helicobacter pylori

$\langle 220 \rangle$

<221> CDS

<222> (1) . . (1407)

```
<223> trans1_table=11
```

<400> 9759

PF59083SeqList PF59083.txt																
atg	cgt	att	gag	cat	gat	ttc	att	ggg	caa	atg	gaa	att	agc	gac	gag	48
Met	Arg	Ile	Glu	His	Asp	Phe	Ile	Gly	Gln	Met	Glu	Ile	Ser	Asp	Glu	
1				5				10						15		
ggt	tat	tac	ggg	att	caa	act	tta	aga	gcg	agt	gaa	aat	ttt	ttc	atc	96
Val	Tyr	Tyr	Gly	Ile	Gln	Thr	Leu	Arg	Ala	Ser	Glu	Asn	Phe	Phe	Ile	
			20					25					30			
acc	aac	gac	aag	ctt	tgc	agt	tat	cct	gtt	ttt	atc	aaa	tct	ttc	gct	144
Thr	Asn	Asp	Lys	Leu	Cys	Ser	Tyr	Pro	Val	Phe	Ile	Lys	Ser	Phe	Ala	
			35				40					45				
caa	gtc	aaa	aaa	gcg	gct	act	tta	gcg	aac	gtg	caa	tta	ggc	ttg	att	192
Gln	Val	Lys	Lys	Ala	Ala	Thr	Leu	Ala	Asn	Val	Gln	Leu	Gly	Leu	Ile	
	50					55					60					
gat	gaa	aag	ctt	aaa	att	gcg	att	tgc	cat	gcg	tgc	gat	ttg	ctc	att	240
Asp	Glu	Lys	Leu	Lys	Ile	Ala	Ile	Cys	His	Ala	Cys	Asp	Leu	Leu	Ile	
65					70					75					80	
gat	ggc	aaa	tac	cat	gat	caa	ttc	att	gtg	gat	atg	att	caa	ggg	ggg	288
Asp	Gly	Lys	Tyr	His	Asp	Gln	Phe	Ile	Val	Asp	Met	Ile	Gln	Gly	Gly	
				85				90						95		
gct	ggc	aca	agc	acg	aac	atg	aac	atg	aac	gaa	gtg	att	gct	aat	ttg	336
Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Met	Asn	Glu	Val	Ile	Ala	Asn	Leu	
			100				105						110			
gct	tta	gaa	tac	atg	ggg	cat	caa	aag	ggc	gag	tat	caa	ttt	tgc	cac	384
Ala	Leu	Glu	Tyr	Met	Gly	His	Gln	Lys	Gly	Glu	Tyr	Gln	Phe	Cys	His	
			115				120					125				
cca	aac	gac	cat	gtc	aac	cgc	tct	caa	tcc	act	aat	gac	gcc	tat	cct	432
Pro	Asn	Asp	His	Val	Asn	Arg	Ser	Gln	Ser	Thr	Asn	Asp	Ala	Tyr	Pro	
	130					135					140					
agt	gcg	tta	aaa	atc	gct	att	tat	gag	cgc	ttg	agc	aat	cta	gtc	gcc	480
Ser	Ala	Leu	Lys	Ile	Ala	Ile	Tyr	Glu	Arg	Leu	Ser	Asn	Leu	Val	Ala	
145					150					155					160	
ccc	atg	aaa	gcc	tta	agg	gat	gct	ttc	gct	caa	aag	gct	aag	gaa	ttc	528
Pro	Met	Lys	Ala	Leu	Arg	Asp	Ala	Phe	Ala	Gln	Lys	Ala	Lys	Glu	Phe	
			165				170							175		
gct	cat	gtg	att	aaa	atg	ggg	cgc	acc	cag	ctt	caa	gac	gct	gtg	cct	576
Ala	His	Val	Ile	Lys	Met	Gly	Arg	Gln	Thr	Leu	Gln	Asp	Ala	Val	Pro	
			180				185						190			
atg	act	tta	ggc	caa	gag	ttt	gaa	act	tat	gcc	ttg	atg	ggt	gat	agg	624
Met	Thr	Leu	Gly	Gln	Glu	Phe	Glu	Thr	Tyr	Ala	Leu	Met	Val	Asp	Arg	
			195				200					205				
gat	att	gag	cag	ggt	tta	gac	agg	aat	tgg	gta	aga	gag	ctt	aat		672
Asp	Ile	Glu	Gln	Val	Leu	Asp	Ala	Arg	Asn	Trp	Val	Arg	Glu	Leu	Asn	
	210					215				220						
tta	ggc	ggc	acg	gct	att	ggc	aca	ggg	atc	aat	tcg	cac	ccg	gat	tat	720
Leu	Gly	Gly	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Ser	His	Pro	Asp	Tyr	
					230					235				240		
cgc	agt	ttg	att	gaa	aag	aaa	atc	caa	gaa	gta	acg	ggc	cgc	ccc	ttt	768
Arg	Ser	Leu	Ile	Glu	Lys	Lys	Ile	Gln	Glu	Val	Thr	Gly	Arg	Pro	Phe	
			245						250					255		
gtc	atg	gct	aat	aac	ttg	att	gaa	gcc	act	caa	agc	acg	ggg	gcg	tat	816
Val	Met	Ala	Asn	Asn	Leu	Ile	Glu	Ala	Thr	Gln	Ser	Thr	Gly	Ala	Tyr	
			260				265						270			
gtg	caa	gtg	agc	ggg	gtg	tta	aag	cgt	att	gcg	gtg	aaa	ctt	tct	aag	864
Val	Gln	Val	Ser	Gly	Val	Leu	Lys	Arg	Ile	Ala	Val	Lys	Leu	Ser	Lys	
			275				280					285				
gtt	tgt	aac	gat	ctc	agg	cta	ctc	agt	tca	ggc	cct	aga	gcc	ggg	ttg	912
Val	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Ala	Gly	Leu	
	290					295					300					
aat	gaa	atc	aat	ttg	cct	aaa	atg	cag	ccg	ggt	agt	tct	atc	atg	ccc	960
Asn	Glu	Ile	Asn	Leu	Pro	Lys	Met	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	
					310					315				320		
ggt	aaa	gtc	aat	ccg	gtg	atc	cct	gaa	gtg	gtc	aat	cag	gtg	tgc	ttt	1008
Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln	Val	Cys	Phe	
				325					330					335		
gcg	gtg	att	ggg	aat	gat	ttg	agc	gtg	gcg	tta	gcc	gca	gaa	ggc	ggg	1056
Ala	Val	Ile	Gly	Asn	Asp	Leu	Ser	Val	Ala	Leu	Ala	Ala	Glu	Gly	Gly	
			340				345						350			
cag	ttg	caa	ctc	aat	gtg	ttt	gag	ccg	gtg	atc	gct	tac	aag	cta	ttc	1104
Gln	Leu	Gln	Leu	Asn	Val	Phe	Glu	Pro	Val	Ile	Ala	Tyr	Lys	Leu	Phe	
			355				360					365				

PF59083SeqList PF59083.txt

cat	tcc	ttt	gtg	att	tta	ggg	cgt	gcg	att	gaa	act	tta	acg	act	aaa	1152
His	Ser	Phe	Val	Ile	Leu	Gly	Arg	Ala	Ile	Glu	Thr	Leu	Thr	Thr	Lys	
	370					375					380					
tgt	gtg	gaa	ggc	atc	acg	gct	aat	gaa	aag	att	tgc	cac	gat	tat	gtc	1200
Cys	Val	Glu	Gly	Ile	Thr	Ala	Asn	Glu	Lys	Ile	Cys	His	Asp	Tyr	Val	
385					390					395					400	
ttt	aac	agc	att	ggc	att	gtt	acc	gcg	cta	aac	cct	cat	atc	ggc	tat	1248
Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	
			405					410						415		
gaa	aaa	tcc	gct	atg	atc	gct	aaa	gaa	gcc	tta	aaa	agc	gat	cgc	tct	1296
Glu	Lys	Ser	Ala	Met	Ile	Ala	Lys	Glu	Ala	Leu	Lys	Ser	Asp	Arg	Ser	
			420					425					430			
att	tat	gac	atc	gct	tta	gaa	aag	aaa	atc	tta	act	aaa	gag	caa	ctg	1344
Ile	Tyr	Asp	Ile	Ala	Leu	Glu	Lys	Lys	Ile	Leu	Thr	Lys	Glu	Gln	Leu	
		435					440					445				
gac	gat	att	ttc	aag	cca	gaa	aac	atg	cta	agc	cct	cac	gct	ttc	aaa	1392
Asp	Asp	Ile	Phe	Lys	Pro	Glu	Asn	Met	Leu	Ser	Pro	His	Ala	Phe	Lys	
	450					455					460					
aag	cat	aaa	gac	tga												1407
Lys	His	Lys	Asp													
465																

<210> 9760

<211> 468

<212> PRT

<213> Helicobacter pylori

<400> 9760

Met	Arg	Ile	Glu	His	Asp	Phe	Ile	Gly	Gln	Met	Glu	Ile	Ser	Asp	Glu	
1				5					10					15		
Val	Tyr	Tyr	Gly	Ile	Gln	Thr	Leu	Arg	Ala	Ser	Glu	Asn	Phe	Phe	Ile	
			20					25					30			
Thr	Asn	Asp	Lys	Leu	Cys	Ser	Tyr	Pro	Val	Phe	Ile	Lys	Ser	Phe	Ala	
		35				40						45				
Gln	Val	Lys	Lys	Ala	Ala	Thr	Leu	Ala	Asn	Val	Gln	Leu	Gly	Leu	Ile	
	50					55					60					
Asp	Glu	Lys	Leu	Lys	Ile	Ala	Ile	Cys	His	Ala	Cys	Asp	Leu	Leu	Ile	
65					70				75						80	
Asp	Gly	Lys	Tyr	His	Asp	Gln	Phe	Ile	Val	Asp	Met	Ile	Gln	Gly	Gly	
				85				90					95			
Ala	Gly	Thr	Ser	Thr	Asn	Met	Asn	Met	Asn	Glu	Val	Ile	Ala	Asn	Leu	
			100				105						110			
Ala	Leu	Glu	Tyr	Met	Gly	His	Gln	Lys	Gly	Glu	Tyr	Gln	Phe	Cys	His	
	115						120					125				
Pro	Asn	Asp	His	Val	Asn	Arg	Ser	Gln	Ser	Thr	Asn	Asp	Ala	Tyr	Pro	
	130					135					140					
Ser	Ala	Leu	Lys	Ile	Ala	Ile	Tyr	Glu	Arg	Leu	Ser	Asn	Leu	Val	Ala	
145					150				155						160	
Pro	Met	Lys	Ala	Leu	Arg	Asp	Ala	Phe	Ala	Gln	Lys	Ala	Lys	Glu	Phe	
			165					170					175			
Ala	His	Val	Ile	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	
			180				185						190			
Met	Thr	Leu	Gly	Gln	Glu	Phe	Glu	Thr	Tyr	Ala	Leu	Met	Val	Asp	Arg	
	195					200						205				
Asp	Ile	Glu	Gln	Val	Leu	Asp	Ala	Arg	Asn	Trp	Val	Arg	Glu	Leu	Asn	
	210					215					220					
Leu	Gly	Gly	Thr	Ala	Ile	Gly	Thr	Gly	Ile	Asn	Ser	His	Pro	Asp	Tyr	
225					230				235					240		
Arg	Ser	Leu	Ile	Glu	Lys	Lys	Ile	Gln	Glu	Val	Thr	Gly	Arg	Pro	Phe	
			245					250						255		
Val	Met	Ala	Asn	Asn	Leu	Ile	Glu	Ala	Thr	Gln	Ser	Thr	Gly	Ala	Tyr	
			260					265					270			
Val	Gln	Val	Ser	Gly	Val	Leu	Lys	Arg	Ile	Ala	Val	Lys	Leu	Ser	Lys	
	275						280					285				
Val	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Ala	Gly	Leu	
	290					295					300					
Asn	Glu	Ile	Asn	Leu	Pro	Lys	Met	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	
305					310					315					320	
Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Val	Val	Asn	Gln	Val	Cys	Phe	

PF59083SeqList PF59083.txt

325 330 335
 Ala Val Ile Gly Asn Asp Leu Ser Val Ala Leu Ala Ala Glu Gly Gly
 340 345 350
 Gln Leu Gln Leu Asn Val Phe Glu Pro Val Ile Ala Tyr Lys Leu Phe
 355 360 365
 His Ser Phe Val Ile Leu Gly Arg Ala Ile Glu Thr Leu Thr Thr Lys
 370 375 380
 Cys Val Glu Gly Ile Thr Ala Asn Glu Lys Ile Cys His Asp Tyr Val
 385 390 400
 Phe Asn Ser Ile Gly Ile Val Thr Ala Leu Asn Pro His Ile Gly Tyr
 405 410 415
 Glu Lys Ser Ala Met Ile Ala Lys Glu Ala Leu Lys Ser Asp Arg Ser
 420 425 430
 Ile Tyr Asp Ile Ala Leu Glu Lys Lys Ile Leu Thr Lys Glu Gln Leu
 435 440 445
 Asp Asp Ile Phe Lys Pro Glu Asn Met Leu Ser Pro His Ala Phe Lys
 450 455 460
 Lys His Lys Asp
 465

<210> 9761
 <211> 1425
 <212> DNA
 <213> Pseudomonas aeruginosa

<220>
 <221> CDS
 <222> (1)..(1425)
 <223> transl_table=11

<400> 9761
 atg tcc ccc gtt gca tct tcc cgt atc gag aaa gac ctg ctc ggc acc 48
 Met Ser Pro Val Ala Ser Ser Arg Ile Glu Lys Asp Leu Leu Gly Thr
 1 5 10 15
 ctc gaa gtg ccc gct gac gcc tac tac ggc atc cag acc ctg cgc gcc 96
 Leu Glu Val Pro Ala Asp Ala Tyr Tyr Gly Ile Gln Thr Leu Arg Ala
 20 25 30
 gtg aac aac ttc cgc ctc tcc ggg gtg ccg ctg tcg cac tac ccg aag 144
 Val Asn Asn Phe Arg Leu Ser Gly Val Pro Leu Ser His Tyr Pro Lys
 35 40 45
 ctg gtc gtt gcc ctg gcc atg gtc aag cag gcc gcc gcc gac gcc aac 192
 Leu Val Val Ala Leu Ala Met Val Lys Gln Ala Ala Ala Asp Ala Asn
 50 55 60
 cgt cag ctc ggc cat ctc ccg gaa gac aag cac gcc gcc atc agc gag 240
 Arg Gln Leu Gly His Leu Pro Glu Asp Lys His Ala Ala Ile Ser Glu
 65 70 75 80
 gcc tgc gcc cgc ctg atc cgc ggc gat ttc cac gag cag ttc gtg gtg 288
 Ala Cys Ala Arg Leu Ile Arg Gly Asp Phe His Glu Gln Phe Val Val
 85 90 95
 gac atg atc cag ggc ggc gcc ggc acc tcc acc aac atg aac gcg aac 336
 Asp Met Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn
 100 105 110
 gaa gtg atc gcg aac atc gcg ctg gaa gcc atg ggc cac acc aag ggt 384
 Glu Val Ile Ala Asn Ile Ala Leu Glu Ala Met Gly His Thr Lys Gly
 115 120 125
 gag tac aag tac ctg cac ccg aac aac gat gtg aac atg gcg cag tcg 432
 Glu Tyr Lys Tyr Leu His Pro Asn Asn Asp Val Asn Met Ala Gln Ser
 130 135 140
 acc aac gac gcc tac cca acc gcc atc cgc ctg ggc ctg ctg ctc ggc 480
 Thr Asn Asp Ala Tyr Pro Thr Ala Ile Arg Leu Gly Leu Leu Leu Gly
 145 150 155 160
 cac gac acc ctg ctg gcc agc ctc gac agc ctg atc cag gcc ttc gcc 528
 His Asp Thr Leu Leu Ala Ser Leu Asp Ser Leu Ile Gln Ala Phe Ala
 165 170 175
 gcc aag ggc gtc gaa ttc gcc ggc gta ctg aag atg ggc cgc acc cag 576
 Ala Lys Gly Val Glu Phe Ala Gly Val Leu Lys Met Gly Arg Thr Gln
 180 185 190
 ttg cag gac gcc gtg ccg atg acc ctc ggc cag gaa ttc cac gct ttc 624
 Leu Gln Asp Ala Val Pro Met Thr Leu Gly Gln Phe His Ala Phe

PF59083SeqList PF59083.txt

195	200	205	
gcc acc acc ctc ggc gaa gac ctc gac cgc ctg cgt cgc ctg gcg ccg	210	215	220
Ala Thr Thr Leu Gly Glu Asp Leu Asp Arg Leu Arg Arg Leu Ala Pro	225	230	235
gag ctg ctc acc gaa gtg aac ctc ggt ggc acc gcc atc ggc acc ggc	240	245	250
Glu Leu Leu Thr Glu Val Asn Leu Gly Gly Thr Ala Ile Gly Thr Gly	255	260	265
atc aac gcc gac ccc ggc tac cag aag ctc gcc gtc gag cgc ctg gcc	270	275	280
Ile Asn Ala Asp Pro Gly Tyr Gln Lys Leu Ala Val Glu Arg Leu Ala	285	290	295
gcc atc agc ggg cag ccg ctg aag ccg gcc gac ctg atc gaa gcc	300	305	310
Ala Ile Ser Gly Gln Pro Leu Lys Pro Ala Ala Asp Leu Ile Glu Ala	315	320	325
acc tcc gac atg ggc gcc ttc gtg ctg ttc tcc ggc atg ctc aag cgc	330	335	340
Thr Ser Asp Met Gly Ala Phe Val Leu Phe Ser Gly Met Leu Lys Arg	345	350	355
acc gcg gtc aag ctg tgc aag atc tgc aac gac ctg cgc ctg ctc tcc	360	365	370
Thr Ala Val Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser	375	380	385
agc ggc ccg cgc acc ggc atc aac gag atc aac ctg ccg ccg cgc cag	390	395	400
Ser Gly Pro Arg Thr Gly Ile Asn Glu Ile Asn Leu Pro Pro Arg Gln	405	410	415
ccg ggc agt tgc atc atg ccg ggc aag gtc aac ccg gtg atc ccg gaa	420	425	430
Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu	435	440	445
gcg gtc aac cag gtc gcc ttc gaa gtg atc ggc aac gac ctc gcc ctg	450	455	460
Ala Val Asn Gln Val Ala Phe Glu Val Ile Gly Asn Asp Leu Ala Leu	465	470	
acc ctg gcg gcc gaa ggc ggc cag ttg caa ctg aac gtg atg gag ccg			
Thr Leu Ala Glu Gly Gly Gln Leu Gln Leu Asn Val Met Glu Pro			
ctg atc gcc tac aag atc ttc gac tgc atc cgc ctg ctg caa cgc gcc			
Leu Ile Ala Tyr Lys Ile Phe Asp Ser Ile Arg Leu Leu Gln Arg Ala			
atg gac atg ctc cgc gag cac tgc atc acc ggc atc acc gcc aac gtc			
Met Asp Met Leu Arg Glu His Cys Ile Thr Gly Ile Thr Ala Asn Val			
gag cgc tgc cac gaa ctg gtc gag cac agc atc ggt ctg gtc acc gcg			
Glu Arg Cys His Glu Leu Val Glu His Ser Ile Gly Leu Val Thr Ala			
ctg aac ccg tac atc ggc tac gag aac tcc acg cgg atc gcc aag acc			
Leu Asn Pro Tyr Ile Gly Tyr Glu Asn Ser Thr Arg Ile Ala Lys Thr			
gcc ctg gag agc ggc cgc ggc gtc ctg gaa ctg gta cgc gag gaa aag			
Ala Leu Glu Ser Gly Arg Gly Val Leu Glu Leu Val Arg Glu Glu Lys			
ctg ctg gac gaa gcc acc ctg gcc gac atc ctg ctg ccg gaa aac atg			
Leu Leu Asp Glu Ala Thr Leu Ala Asp Ile Leu Leu Pro Glu Asn Met			
atc gcg ccg cgc ctg att ccg ctg cgc gcc tga			
Ile Ala Pro Arg Leu Ile Pro Leu Arg Ala			

<210> 9762
 <211> 474
 <212> PRT
 <213> Pseudomonas aeruginosa

<400> 9762
 Met Ser Pro Val Ala Ser Ser Arg Ile Glu Lys Asp Leu Leu Gly Thr
 1 5 10 15
 Leu Glu Val Pro Ala Asp Ala Tyr Tyr Gly Ile Gln Thr Leu Arg Ala
 20 25 30
 Val Asn Asn Phe Arg Leu Ser Gly Val Pro Leu Ser His Tyr Pro Lys
 35 40 45
 Leu Val Val Ala Leu Ala Met Val Lys Gln Ala Ala Ala Asp Ala Asn
 50 55 60
 Arg Gln Leu Gly His Leu Pro Glu Asp Lys His Ala Ala Ile Ser Glu
 65 70 75 80

PF59083SeqList PF59083.txt

Ala Cys Ala Arg Leu Ile Arg Gly Asp Phe His Glu Gln Phe Val Val
 85 90 95
 Asp Met Ile Gln Gly Gly Ala Gly Thr Ser Thr Asn Met Asn Ala Asn
 100 105 110
 Glu Val Ile Ala Asn Ile Ala Leu Glu Ala Met Gly His Thr Lys Gly
 115 120 125
 Glu Tyr Lys Tyr Leu His Pro Asn Asn Asp Val Asn Met Ala Gln Ser
 130 135 140
 Thr Asn Asp Ala Tyr Pro Thr Ala Ile Arg Leu Gly Leu Leu Leu Gly
 145 150 155 160
 His Asp Thr Leu Leu Ala Ser Leu Asp Ser Leu Ile Gln Ala Phe Ala
 165 170 175
 Ala Lys Gly Val Glu Phe Ala Gly Val Leu Lys Met Gly Arg Thr Gln
 180 185 190
 Leu Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe His Ala Phe
 195 200 205
 Ala Thr Thr Leu Gly Glu Asp Leu Asp Arg Leu Arg Arg Leu Ala Pro
 210 215 220
 Glu Leu Leu Thr Glu Val Asn Leu Gly Gly Thr Ala Ile Gly Thr Gly
 225 230 235 240
 Ile Asn Ala Asp Pro Gly Tyr Gln Lys Leu Ala Val Glu Arg Leu Ala
 245 250 255
 Ala Ile Ser Gly Gln Pro Leu Lys Pro Ala Ala Asp Leu Ile Glu Ala
 260 265 270
 Thr Ser Asp Met Gly Ala Phe Val Leu Phe Ser Gly Met Leu Lys Arg
 275 280 285
 Thr Ala Val Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser
 290 295 300
 Ser Gly Pro Arg Thr Gly Ile Asn Glu Ile Asn Leu Pro Pro Arg Gln
 305 310 315 320
 Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Ile Pro Glu
 325 330 335
 Ala Val Asn Gln Val Ala Phe Glu Val Ile Gly Asn Asp Leu Ala Leu
 340 345 350
 Thr Leu Ala Glu Gly Gly Gln Leu Gln Leu Asn Val Met Glu Pro
 355 360 365
 Leu Ile Ala Tyr Lys Ile Phe Asp Ser Ile Arg Leu Leu Gln Arg Ala
 370 375 380
 Met Asp Met Leu Arg Glu His Cys Ile Thr Gly Ile Thr Ala Asn Val
 385 390 395 400
 Glu Arg Cys His Glu Leu Val Glu His Ser Ile Gly Leu Val Thr Ala
 405 410 415
 Leu Asn Pro Tyr Ile Gly Tyr Glu Asn Ser Thr Arg Ile Ala Lys Thr
 420 425 430
 Ala Leu Glu Ser Gly Arg Gly Val Leu Glu Leu Val Arg Glu Glu Lys
 435 440 445
 Leu Leu Asp Glu Ala Thr Leu Ala Asp Ile Leu Leu Pro Glu Asn Met
 450 455 460
 Ile Ala Pro Arg Leu Ile Pro Leu Arg Ala
 465 470

<210> 9763

<211> 2066

<212> DNA

<213> Pseudomonas fluorescens

<220>

<221> CDS

<222> (323)..(1759)

<223> transl_table=11

<400> 9763

gttgaccagc gtcagcccca acgcggcttc caggctgcgg atacgccgac tgaacgccgg

60

ctgggtgaca aagcgccgct cagccgcctg ggaaaaacta cgcgtcgccg ccagggcgct

120

gaagtcttcc aaccacttgc tctcaagggt catcactgcc tcccacggaa tgcaccattt

180

PF59083SeqList PF59083.txt

tggcacacac gcccgccaag ataaccgggt cacatccaca ttatgccgtt tgtgcatagg	240
ccagtgttta acagcattgg cccaaaaagt cctacaagcc tagcattcgc agcgttccgg	300
ccagtcccgg gtccatattg ag atg atc tcc gtc atg tcc tct gct gca tct	352
Met Ile Ser Val Met Ser Ser Ala Ala Ser	
1 5 10	
ttc cgt acc gaa aaa gac ctg ctt ggc gta ctc gaa gta ccg gct caa	400
Phe Arg Thr Glu Lys Asp Leu Leu Gly Val Leu Glu Val Pro Ala Gln	
15 20 25	
gcg tat tac ggc atc cag acc ctg cga gcg gtg aat aac ttc cgc ctc	448
Ala Tyr Tyr Gly Ile Gln Thr Leu Arg Ala Val Asn Asn Phe Arg Leu	
30 35 40	
tcg ggc gtt ccg att tcg cat tac ccg aaa ttg gtg gtc ggt ctg gca	496
Ser Gly Val Pro Ile Ser His Tyr Pro Lys Leu Val Val Gly Leu Ala	
45 50 55	
atg gtc aag caa gca gcg gct gac gcc aac cgc gag ttg ggc cag ctc	544
Met Val Lys Gln Ala Ala Ala Asp Ala Asn Arg Glu Leu Gly Gln Leu	
60 65 70	
agc gaa cgc aag cac gct gcc atc agc gaa gcc tgc gct cgt ctg atc	592
Ser Glu Arg Lys His Ala Ala Ile Ser Glu Ala Cys Ala Arg Leu Ile	
75 80 85 90	
cgc ggc gat ttc cac gaa gag ttc gtg gtg gac atg att caa ggc ggc	640
Arg Gly Asp Phe His Glu Glu Phe Val Val Asp Met Ile Gln Gly Gly	
95 100 105	
gct ggc act tca aac aat atg aat gcc aac gaa gtc atc gcc aac atc	688
Ala Gly Thr Ser Thr Asn Met Asn Ala Asn Glu Val Ile Ala Asn Ile	
110 115 120	
gcg ctg gag gcc atg ggt cac cag aag ggc gaa tac cag tac ctg cac	736
Ala Leu Glu Ala Met Gly His Gln Lys Gly Glu Tyr Gln Tyr Leu His	
125 130 135	
ccc aac aac gac gtg aac atg gcg cag tcg acc aac gac gcc tac ccg	784
Pro Asn Asn Asp Val Asn Met Ala Gln Ser Thr Asn Asp Ala Tyr Pro	
140 145 150	
acc gcg atc cgc ctg ggt ctg ctg ctg ggc cat gac gcg ctg ctg gcc	832
Thr Ala Ile Arg Leu Gly Leu Leu Leu Gly His Asp Ala Leu Leu Ala	
155 160 165 170	
agc ctc gac agc ctg atc cag gcg ttc gcc gcc aaa ggc gcc gag ttc	880
Ser Leu Asp Ser Leu Ile Gln Ala Phe Ala Ala Lys Gly Ala Glu Phe	
175 180 185	
agc cat gtg ctg gaa atg ggc cgc aca caa ttg caa gac gcc gtg ccg	928
Ser His Val Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro	
190 195 200	
atg acc ctc ggc cag gaa ttc cgc gcg ttc gcc acc acc ctg ggt gaa	976
Met Thr Leu Gly Gln Glu Phe Arg Ala Phe Ala Thr Thr Leu Gly Glu	
205 210 215	
gac ctg gcc cgc ctg aaa acc ctg gcg cca gag ctg ctg acc gaa gtg	1024
Asp Leu Ala Arg Leu Lys Thr Leu Ala Pro Glu Leu Leu Thr Glu Val	
220 225 230	
aac ctg ggc gga acc gcg atc ggt acc ggc atc aac gcc gac ccg cgc	1072
Asn Leu Gly Gly Thr Ala Ile Gly Thr Gly Ile Asn Ala Asp Pro Arg	
235 240 245 250	
tac cag gcc ctc gcc gta caa cgc ctg gcc acc atc agc ggt cag ccg	1120
Tyr Gln Ala Leu Ala Val Gln Arg Leu Ala Thr Ile Ser Gly Gln Pro	
255 260 265	
ctg gta ccg gcg gcc gac ctg atc gaa gcc acc tcc gac atg ggc gct	1168
Leu Val Pro Ala Ala Asp Leu Ile Glu Ala Thr Ser Asp Met Gly Ala	
270 275 280	
ttc gta ctg ttc tcc ggc atg ctc aag cgt act gcc gtg aag ctg tcc	1216
Phe Val Leu Phe Ser Gly Met Leu Lys Arg Thr Ala Val Lys Leu Ser	
285 290 295	
aag atc tgc aac gac ctg cgc ctg ctg tcc agc ggc cca cgc acc ggc	1264
Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Thr Gly	
300 305 310	
atc aac gag atc aac ctg ccg gct cgc cag cca ggc agc tcg atc atg	1312

PF59083SeqList PF59083.txt

Ile	Asn	Glu	Ile	Asn	Leu	Pro	Ala	Arg	Gln	Pro	Gly	Ser	Ser	Ile	Met	
315					320					325					330	
ccc	ggc	aag	gtc	aac	ccg	gtc	atc	ccg	gaa	gcg	gtc	aac	cag	gta	gcg	1360
Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Ala	Val	Asn	Gln	Val	Ala	
				335					340					345		
ttc	caa	gtc	atc	ggg	aac	gac	ctg	gcc	ctg	acc	atg	gca	gcc	gaa	ggc	1408
Phe	Gln	Val	Ile	Gly	Asn	Asp	Leu	Ala	Leu	Thr	Met	Ala	Ala	Glu	Gly	
			350					355					360			
ggc	caa	ctg	cag	ttg	aac	gtg	atg	gag	ccg	ctg	atc	gcc	ttc	aag	atc	1456
Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Leu	Ile	Ala	Phe	Lys	Ile	
			365				370						375			
ttc	gac	tcg	atc	cgc	ctg	ctg	caa	cgc	gcc	atg	gac	atg	ctg	cgc	gag	1504
Phe	Asp	Ser	Ile	Arg	Leu	Leu	Gln	Arg	Ala	Met	Asp	Met	Leu	Arg	Glu	
			380			385					390					
cac	tgc	atc	gtc	ggc	atc	acc	gcc	aac	gaa	gcc	cgc	tgc	cgc	gaa	ctg	1552
His	Cys	Ile	Val	Gly	Ile	Thr	Ala	Asn	Glu	Ala	Arg	Cys	Arg	Glu	Leu	
395					400				405						410	
gtg	gaa	cat	tcc	atc	ggc	ctg	gtc	acc	gcg	ctg	aac	cca	tac	atc	ggc	1600
Val	Glu	His	Ser	Ile	Gly	Leu	Val	Thr	Ala	Leu	Asn	Pro	Tyr	Ile	Gly	
				415					420					425		
tat	gaa	aac	gcc	acc	cgc	att	gcg	cgt	atc	gcg	ctt	gaa	agc	ggg	cgc	1648
Tyr	Glu	Asn	Ala	Thr	Arg	Ile	Ala	Arg	Ile	Ala	Leu	Glu	Ser	Gly	Arg	
			430					435					440			
ggc	gtg	ctg	gaa	ctg	gtg	cgt	gaa	gaa	ggc	ttg	ctc	gac	gac	gcc	atg	1696
Gly	Val	Leu	Glu	Leu	Val	Arg	Glu	Glu	Gly	Leu	Leu	Asp	Asp	Ala	Met	
			445				450					455				
ctc	gac	gac	atc	ctg	cgc	ccc	gaa	aac	atg	att	gcc	cca	cgc	ttg	gtc	1744
Leu	Asp	Asp	Ile	Leu	Arg	Pro	Glu	Asn	Met	Ile	Ala	Pro	Arg	Leu	Val	
			460			465					470					
ccg	ctg	aag	gcc	taagcgtttg	ttgcaccgct	caccaggctg	agggactaga									1796
Pro	Leu	Lys	Ala													
475																
cacctctcac	cttttgaggg	cttgaagact	cgttcttcag	gccctttttt	ttgctcgtaa											1856
ttcctctcct	tatataaagc	gctgttagtg	cgtttcacct	ataaaacatc	acgcctgcgg											1916
cgttacttga	aaaagcattc	attcattgca	aattcccatt	gcgtgcacaa	acggtgtgca											1976
gtttcgtgcc	atataaaaac	aatggtttca	tatatgaaac	gctcaataag	taaccttaat											2036
ctcgcaacta	attaatttaa	aagggaattc														2066

<210> 9764

<211> 478

<212> PRT

<213> Pseudomonas fluorescens

<400> 9764

Met	Ile	Ser	Val	Met	Ser	Ser	Ala	Ala	Ser	Phe	Arg	Thr	Glu	Lys	Asp	
1				5					10					15		
Leu	Leu	Gly	Val	Leu	Glu	Val	Pro	Ala	Gln	Ala	Tyr	Tyr	Gly	Ile	Gln	
			20					25					30			
Thr	Leu	Arg	Ala	Val	Asn	Asn	Phe	Arg	Leu	Ser	Gly	Val	Pro	Ile	Ser	
			35				40					45				
His	Tyr	Pro	Lys	Leu	Val	Val	Gly	Leu	Ala	Met	Val	Lys	Gln	Ala	Ala	
			50			55				60						
Ala	Asp	Ala	Asn	Arg	Glu	Leu	Gly	Gln	Leu	Ser	Glu	Arg	Lys	His	Ala	
65				70					75					80		
Ala	Ile	Ser	Glu	Ala	Cys	Ala	Arg	Leu	Ile	Arg	Gly	Asp	Phe	His	Glu	
			85					90						95		
Glu	Phe	Val	Val	Asp	Met	Ile	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Thr	Asn	
			100				105					110				
Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Ile	Ala	Leu	Glu	Ala	Met	Gly	

PF59083SeqList PF59083.txt

ctgcatctgc acgaaggttt tcatgccctg attgcgacc agcgaaatgc cgacgcagga	300
gctgaacacc accagcagca gggtagacagc cacgccgagc acggcggcga ctttgataaa	360
gatggatatt tctatgtaag ccagcagaaa tatcagcagt agcggtaacc agcgcacctg	420
gttctcctat cggtaggtaa ggcacggccg ccacggggcg acggcgcgaa aaaagaggcc	480
gtaaacggcc gacactatta caatgagggc atccccccac catttcaacc gagagccggt	540
ttttattgct aaagttcaca aacgtgaaag aagtcacaga accgaaaaag ggcatatcct	600
taaacacccat aaggtgatct ggattcagtc atttcttacc aaccagcata tgatctgggc	660
agctacgggc gatttgggta atcgtttcac gccccaagcc ttcggcaata ttaatttagg	720
ctgtgccctt actagccttg acctgacaaa ttattaattc ggcagcaaca catagagaag	780
gttctc atg tca aac aac att cgt atc gaa gaa gac ctg tta gga aca	828
Met Ser Asn Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Thr	
1 5 10	
cgt gaa gtc ccc gca gac gct tac tac gga gtt cac act ctg cgt gcg	876
Arg Glu Val Pro Ala Asp Ala Tyr Tyr Gly Val His Thr Leu Arg Ala	
15 20 25 30	
att gaa aac ttc tac atc agc aac agc aaa atc agc gat gtc ccc gag	924
Ile Glu Asn Phe Tyr Ile Ser Asn Ser Lys Ile Ser Asp Val Pro Glu	
35 40 45	
ttc gtt cgc ggc atg gtg atg gtg aaa aag gcc gcg gcg atg gcc aac	972
Phe Val Arg Gly Met Val Met Val Lys Lys Ala Ala Ala Met Ala Asn	
50 55 60	
aaa gaa ctc aaa acc atc ccg cgc aaa atc gcc gac gtg atc atc cag	1020
Lys Glu Leu Lys Thr Ile Pro Arg Lys Ile Ala Asp Val Ile Ile Gln	
65 70 75	
gcc tgc gac gag gtg ctg gat aaa ggc aag tgc atg gat cag ttc ccg	1068
Ala Cys Asp Glu Val Leu Asp Lys Gly Lys Cys Met Asp Gln Phe Pro	
80 85 90	
gtg gac gta ttc cag ggc ggc gcg ggc acc tcg ctg aac atg aac acc	1116
Val Asp Val Phe Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr	
95 100 105 110	
aac gaa gtg ctg gcg aac atc ggc ctg gag ctg atg ggc cat caa aaa	1164
Asn Glu Val Leu Ala Asn Ile Gly Leu Leu Met Gly His Gln Lys	
115 120 125	
ggc gaa tac cag tac ctg aac ccg aac gat cac ctc aat aag tgt cag	1212
Gly Glu Tyr Gln Tyr Leu Asn Pro Asn Asp His Leu Asn Lys Cys Gln	
130 135 140	
tcc acc aac gac gcc tac ccg acc ggg ttc cgc atc gcg gtg tac gcc	1260
Ser Thr Asn Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Ala	
145 150 155	
tcc aac cag aaa ctg atc gac gcc atc aac cag ctg cgc gaa ggc ttc	1308
Ser Asn Gln Lys Leu Ile Asp Ala Ile Asn Gln Leu Arg Glu Gly Phe	
160 165 170	
gat cgc aag gcg aaa gag ttc gaa acc atc ctg aaa atg ggc gcg acc	1356
Asp Arg Lys Ala Lys Glu Phe Glu Thr Ile Leu Lys Met Gly Arg Thr	
175 180 185 190	
cag ctg cag gac gcg ctg ccg atg acc cta ggc cag gaa ttc cac gcc	1404
Gln Leu Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe His Ala	
195 200 205	
ttc agc gtg ctg ctg aac gaa gag acc cgc aat ctg cac cgc acc gcg	1452
Phe Ser Val Leu Leu Asn Glu Glu Thr Arg Asn Leu His Arg Thr Ala	
210 215 220	

PF59083SeqList PF59083.txt

acg	ctg	ctg	ctg	gaa	gtg	aac	ctc	ggc	gcc	acc	gcc	atc	ggc	acc	gcg	1500
Thr	Leu	Leu	Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Ala	
		225					230					235				
ctc	aac	acc	ccg	gaa	ggc	tac	cag	ccg	ctg	gcg	gtg	caa	aaa	ctg	gcg	1548
Leu	Asn	Thr	Pro	Glu	Gly	Tyr	Gln	Pro	Leu	Ala	Val	Gln	Lys	Leu	Ala	
	240					245					250					
gaa	gtc	agc	ggc	ctg	ccg	gtg	gtg	ccg	gca	gaa	gac	ctg	atc	gaa	gcc	1596
Glu	Val	Ser	Gly	Leu	Pro	Val	Val	Pro	Ala	Glu	Asp	Leu	Ile	Glu	Ala	
255				260				265							270	
acc	tcc	gac	tgc	ggc	gcc	tac	gtg	atg	gtg	cac	agc	gcg	ctc	aaa	cgc	1644
Thr	Ser	Asp	Cys	Gly	Ala	Tyr	Val	Met	Val	His	Ser	Ala	Leu	Lys	Arg	
			275					280						285		
ctg	gcg	gtg	aaa	ctg	tcc	aaa	atc	tgt	aac	gac	ctg	cgc	ctg	ctc	tcc	1692
Leu	Ala	Val	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	
		290						295					300			
tcc	ggc	ccg	cgc	ggc	ggc	ctg	aac	gaa	atc	aac	ttg	ccg	gag	ctg	cag	1740
Ser	Gly	Pro	Arg	Ala	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Glu	Leu	Gln	
		305				310						315				
gcg	gga	tgc	tcc	atc	atg	ccg	gcc	aaa	gtg	aat	ccg	gtg	gtg	ccg	gaa	1788
Ala	Gly	Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Val	Pro	Glu	
	320					325					330					
gtg	gtc	aat	cag	gtg	tgt	ttc	aag	gtg	att	ggc	aac	gac	act	tgc	gtt	1836
Val	Val	Asn	Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Cys	Val	
335				340				345							350	
acc	atg	gcg	gcc	gaa	ggc	ggc	cag	ctg	cag	ctg	aac	gtg	atg	gag	ccg	1884
Thr	Met	Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	
			355					360						365		
gtg	atc	ggc	cag	gcg	atg	ttc	gag	tcg	atc	cac	atc	ctg	acc	aac	gcc	1932
Val	Ile	Gly	Gln	Ala	Met	Phe	Glu	Ser	Ile	His	Ile	Leu	Thr	Asn	Ala	
		370					375						380			
tgc	tac	aac	ctg	ctg	gaa	aaa	tgc	att	aac	ggc	atc	acc	gcg	aat	aaa	1980
Cys	Tyr	Asn	Leu	Leu	Glu	Lys	Cys	Ile	Asn	Gly	Ile	Thr	Ala	Asn	Lys	
		385					390					395				
gaa	gtc	tgc	gaa	cac	tac	gtc	ttc	aac	tcg	atc	ggt	atc	gtc	acc	tat	2028
Glu	Val	Cys	Glu	His	Tyr	Phe	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr		
	400					405					410					
ctg	aac	ccg	ttc	atc	ggc	cac	cat	aac	ggt	gac	atc	gtc	ggg	aag	atc	2076
Leu	Asn	Pro	Phe	Ile	Gly	His	His	Asn	Gly	Asp	Ile	Val	Gly	Lys	Ile	
415				420				425							430	
tgc	gcc	gaa	acc	ggc	aag	agc	gtg	cgc	gaa	gtg	gtg	ctg	gaa	cgc	ggc	2124
Cys	Ala	Glu	Thr	Gly	Lys	Ser	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gly	
			435					440						445		
ctg	ctg	acc	gaa	gcc	gag	ctg	gat	gac	atc	ttc	tcc	gtg	gag	aac	ctg	2172
Leu	Leu	Thr	Glu	Ala	Glu	Leu	Asp	Asp	Ile	Phe	Ser	Val	Glu	Asn	Leu	
		450					455						460			
atg	cac	ccg	gcc	tat	aaa	gcc	aaa	cgc	tat	acg	gat	gaa	aat	gaa	caa	2220
Met	His	Pro	Ala	Tyr	Lys	Ala	Lys	Arg	Tyr	Thr	Asp	Glu	Asn	Glu	Gln	
		465				470					475					
taacagac	ctt	acccgg	tagc	cctgaa	aggc	acgcta	aatc	ctctgg	atag	cgtgc	ctttt					2280
tacttttagg	tgcccc	acaaa	atttta	acgt	tttatt	tttca	atttac	accc	taaat	cattg						2340
ggactg	catc	aaggcg	gcaa	gagcg	caagt	ccccag	gagc	ttactc	aagt	aagt	gact	gg				2400
ggtgag	cgct	cgagcc	aac	accgat	gcag	tttca	aggat	gacggg	aaat	ctcatt	tttaa					2460
ggagtaa	aca	ctatg	ctagc	cgtaga	attg	gttat	cggtc	tgctgg	ccat	cttttt	taggg					2520
gccaggt	tgg	gcggt	atcgg	tatcgg	gttc	gcgggg	gggac	tgggcg	tatt	ggcgct	ggcg					2580
ctgatc	ggcg	tcaaacc	ggg	caacatt	ccc	ttcgac	gtca	tctccat	cat	catggc	ggtg					2640

PF59083SeqList PF59083.txt

attgcggcga tctccgcat gcaggatgcc ggggggatgg actacctggt gcaacagacc 2700

gaaaaactgc tgcgcaagaa cccaagcac atcaccattc tcgcccctat cgtcacctac 2760

ttcctgacca tcttcgccgg caccggcaac atctcgctct cggcgctgcc ggtgatcgcc 2820

gaggtggcga aagaacaggg catcaagcct tgccgccgcg tgtcgac 2867

<210> 9766
 <211> 478
 <212> PRT
 <213> *Serratia marcescens*

<400> 9766
 Met Ser Asn Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Thr Arg Glu
 1 5 10 15
 Val Pro Ala Asp Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Ile Glu
 20 25 30
 Asn Phe Tyr Ile Ser Asn Ser Lys Ile Ser Asp Val Pro Glu Phe Val
 35 40 45
 Arg Gly Met Val Met Val Lys Lys Ala Ala Ala Met Ala Asn Lys Glu
 50 55 60
 Leu Lys Thr Ile Pro Arg Lys Ile Ala Asp Val Ile Ile Gln Ala Cys
 65 70 75 80
 Asp Glu Val Leu Asp Lys Gly Lys Cys Met Asp Gln Phe Pro Val Asp
 85 90 95
 Val Phe Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr Asn Glu
 100 105 110
 Val Leu Ala Asn Ile Gly Leu Glu Leu Met Gly His Gln Lys Gly Glu
 115 120 125
 Tyr Gln Tyr Leu Asn Pro Asn Asp His Leu Asn Lys Cys Gln Ser Thr
 130 135 140
 Asn Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Ala Ser Asn
 145 150 155 160
 Gln Lys Leu Ile Asp Ala Ile Asn Gln Leu Arg Glu Gly Phe Asp Arg
 165 170 175
 Lys Ala Lys Glu Phe Glu Thr Ile Leu Lys Met Gly Arg Thr Gln Leu
 180 185 190
 Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe His Ala Phe Ser
 195 200 205
 Val Leu Leu Asn Glu Glu Thr Arg Asn Leu His Arg Thr Ala Thr Leu
 210 215 220
 Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Ala Leu Asn
 225 230 235 240
 Thr Pro Glu Gly Tyr Gln Pro Leu Ala Val Gln Lys Leu Ala Glu Val
 245 250 255
 Ser Gly Leu Pro Val Val Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser
 260 265 270
 Asp Cys Gly Ala Tyr Val Met Val His Ser Ala Leu Lys Arg Leu Ala
 275 280 285
 Val Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly
 290 295 300
 Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly
 305 310 315 320
 Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val
 325 330 335
 Asn Gln Val Cys Phe Lys Val Ile Gly Asn Asp Thr Cys Val Thr Met
 340 345 350
 Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile
 355 360 365
 Gly Gln Ala Met Phe Glu Ser Ile His Ile Leu Thr Asn Ala Cys Tyr
 370 375 380
 Asn Leu Leu Glu Lys Cys Ile Asn Gly Ile Thr Ala Asn Lys Glu Val
 385 390 395 400

PF59083SeqList PF59083.txt

Cys Glu His Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn
 405 410 415
 Pro Phe Ile Gly His His Asn Gly Asp Ile Val Gly Lys Ile Cys Ala
 420 425 430
 Glu Thr Gly Lys Ser Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu
 435 440 445
 Thr Glu Ala Glu Leu Asp Asp Ile Phe Ser Val Glu Asn Leu Met His
 450 455 460
 Pro Ala Tyr Lys Ala Lys Arg Tyr Thr Asp Glu Asn Glu Gln
 465 470 475

<210> 9767

<211> 1479

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1479)

<400> 9767

atg	tcg	att	tac	gtc	gcg	tcg	cga	cgg	ctc	tcc	ggc	gga	aca	act	gtg	48
Met	Ser	Ile	Tyr	Val	Ala	Ser	Arg	Arg	Leu	Ser	Gly	Gly	Thr	Thr	Val	
1				5					10					15		
acg	gcg	ctg	cgt	tat	gcc	acc	tct	ctg	aga	tct	tat	tcg	acc	tcg	ttt	96
Thr	Ala	Leu	Arg	Tyr	Ala	Thr	Ser	Leu	Arg	Ser	Tyr	Ser	Thr	Ser	Phe	
			20					25					30			
agg	gag	gag	agg	gac	acc	ttc	ggg	ccg	att	caa	ggt	cct	tcc	gat	aaa	144
Arg	Glu	Glu	Arg	Asp	Thr	Phe	Gly	Pro	Ile	Gln	Val	Pro	Ser	Asp	Lys	
		35					40					45				
ttg	tgg	gga	gcc	cag	acg	cag	aga	tcg	ctg	cag	aac	ttc	gaa	atc	ggt	192
Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	Glu	Ile	Gly	
	50					55				60						
ggt	gag	cgc	gag	cga	atg	cct	gaa	cca	att	gtc	cgc	gct	ttt	ggc	gtc	240
Gly	Glu	Arg	Glu	Arg	Met	Pro	Glu	Pro	Ile	Val	Arg	Ala	Phe	Gly	Val	
65					70				75					80		
ttg	aag	aaa	tgc	gct	gcc	aag	gtt	aac	atg	gaa	tac	ggc	ctt	gat	ccg	288
Leu	Lys	Lys	Cys	Ala	Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	Leu	Asp	Pro	
			85					90					95			
acg	att	ggg	aaa	gca	att	atg	caa	gct	gct	cag	gaa	gta	gct	gag	gga	336
Thr	Ile	Gly	Lys	Ala	Ile	Met	Gln	Ala	Ala	Gln	Glu	Val	Ala	Glu	Gly	
			100					105					110			
aag	ctc	aat	gat	cat	ttc	ccc	ctt	gtt	gtc	tgg	caa	act	ggt	agt	ggg	384
Lys	Leu	Asn	Asp	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser	Gly	
			115				120					125				
act	cag	agt	aat	atg	aat	gct	aat	gag	gtc	att	gct	aat	aga	gca	gct	432
Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	Ala	Ala	
			130			135					140					
gag	att	ctt	ggt	cgc	aaa	cgt	ggt	gag	aaa	tgt	gtg	cac	cca	aat	gac	480
Glu	Ile	Leu	Gly	Arg	Lys	Arg	Gly	Glu	Lys	Cys	Val	His	Pro	Asn	Asp	
145					150				155					160		
cat	gtg	aac	aga	tca	caa	tct	tct	aac	gac	act	ttt	cct	acc	gtc	atg	528
His	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val	Met	
			165					170						175		
cac	att	gca	gct	gca	acc	gag	att	aat	tcg	agg	ctc	atc	cct	agt	tta	576
His	Ile	Ala	Ala	Ala	Thr	Glu	Ile	Asn	Ser	Arg	Leu	Ile	Pro	Ser	Leu	
			180					185					190			
aaa	act	ttg	cat	agc	act	ttg	gaa	tct	aag	tcc	ttc	gag	ttc	aaa	gat	624
Lys	Thr	Leu	His	Ser	Thr	Leu	Glu	Ser	Lys	Ser	Phe	Glu	Phe	Lys	Asp	
		195					200					205				
att	gtg	aaa	att	gga	aga	act	cac	act	caa	gat	gct	aca	cct	ttg	aca	672
Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	Leu	Thr	
		210				215					220					
cta	gga	caa	gaa	ttt	ggt	ggc	tat	gct	act	caa	ggt	aag	tat	gga	cta	720
Leu	Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Thr	Gln	Val	Lys	Tyr	Gly	Leu	
225					230				235					240		
aat	aga	gtc	acc	tgc	act	ctt	cct	cgc	ctc	tat	cag	ctt	gca	caa	ggt	768
Asn	Arg	Val	Thr	Cys	Thr	Leu	Pro	Arg	Leu	Tyr	Gln	Leu	Ala	Gln	Gly	
				245					250					255		

PF59083SeqList PF59083.txt

gga	act	gcg	gtt	ggg	aca	gga	tta	aac	act	aag	aaa	ggg	ttt	gat	gta	816
Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	Asp	Val	
			260				265						270			
aag	ata	gct	gct	gca	gta	gct	gaa	gaa	aca	aac	ttg	cca	ttt	gtc	act	864
Lys	Ile	Ala	Ala	Ala	Val	Ala	Glu	Glu	Thr	Asn	Leu	Pro	Phe	Val	Thr	
			275				280						285			
gca	gaa	aac	aag	ttt	gaa	gct	ctg	gct	gca	cac	gat	gct	tgt	gtt	gaa	912
Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Cys	Val	Glu	
			290			295					300					
acc	agt	ggg	tca	ctt	aac	aca	atc	gcc	aca	tcg	ctg	atg	aag	atc	gcc	960
Thr	Ser	Gly	Ser	Leu	Asn	Thr	Ile	Ala	Thr	Ser	Leu	Met	Lys	Ile	Ala	
305					310					315					320	
aat	gat	ata	cgt	ttt	ctt	gga	agt	ggc	cca	aga	tgt	ggg	ctt	ggg	gaa	1008
Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	Glu	
				325					330					335		
ctt	gta	cta	cct	gaa	aat	gag	cca	gga	agc	agt	atc	atg	cct	ggg	aag	1056
Leu	Val	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	
			340					345					350			
gta	aat	cct	aca	cag	tgt	gag	gcc	ttg	act	atg	gtt	tgt	gca	cag	gtt	1104
Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	Gln	Val	
			355				360					365				
atg	gga	aac	cat	gta	gct	gtg	aca	gtt	ggg	ggg	tca	aat	ggg	cat	ttc	1152
Met	Gly	Asn	His	Val	Ala	Val	Thr	Val	Gly	Gly	Ser	Asn	Gly	His	Phe	
			370			375					380					
gaa	ttg	aat	gta	ttc	aag	ccg	gtg	atc	gcg	agt	gct	ctt	tta	cat	tcc	1200
Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Ile	Ala	Ser	Ala	Leu	Leu	His	Ser	
385					390					395					400	
gtc	aga	tta	ata	gca	gat	gct	tca	gct	tcg	ttc	gag	aaa	aac	tgt	gtg	1248
Val	Arg	Leu	Ile	Ala	Asp	Ala	Ser	Ala	Ser	Phe	Glu	Lys	Asn	Cys	Val	
				405					410					415		
agg	ggc	att	gag	gcc	aac	aga	gaa	aga	atc	tca	aag	cta	ttg	cac	gag	1296
Arg	Gly	Ile	Glu	Ala	Asn	Arg	Glu	Arg	Ile	Ser	Lys	Leu	Leu	His	Glu	
			420				425						430			
tct	ctt	atg	ctt	gtg	aca	tca	ttg	aat	ccg	aaa	atc	ggg	tat	gac	aat	1344
Ser	Leu	Met	Leu	Val	Thr	Ser	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	Asp	Asn	
			435				440					445				
gct	gca	gca	gtt	gcc	aag	aaa	gct	cac	aaa	gaa	gga	tgt	aca	ttg	aag	1392
Ala	Ala	Ala	Val	Ala	Lys	Lys	Ala	His	Lys	Glu	Gly	Cys	Thr	Leu	Lys	
			450			455					460					
gaa	gcg	gct	ctg	aat	tta	ggc	gtg	ctt	act	gcg	gaa	gag	ttt	gat	aca	1440
Glu	Ala	Ala	Leu	Asn	Leu	Gly	Val	Leu	Thr	Ala	Glu	Glu	Phe	Asp	Thr	
465					470					475					480	
ctt	gtt	gtt	cct	gag	aag	atg	att	ggg	ccc	tcc	gat	tga				1479
Leu	Val	Val	Pro	Glu	Lys	Met	Ile	Gly	Pro	Ser	Asp					
				485					490							

<210> 9768
 <211> 492
 <212> PRT
 <213> Arabidopsis thaliana

<400> 9768
 Met Ser Ile Tyr Val Ala Ser Arg Arg Leu Ser Gly Gly Thr Thr Val
 1 5 10 15
 Thr Ala Leu Arg Tyr Ala Thr Ser Leu Arg Ser Tyr Ser Thr Ser Phe
 20 25 30
 Arg Glu Glu Arg Asp Thr Phe Gly Pro Ile Gln Val Pro Ser Asp Lys
 35 40 45
 Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn Phe Glu Ile Gly
 50 55 60
 Gly Glu Arg Glu Arg Met Pro Glu Pro Ile Val Arg Ala Phe Gly Val
 65 70 75 80
 Leu Lys Lys Cys Ala Lys Val Asn Met Glu Tyr Gly Leu Asp Pro
 85 90 95
 Thr Ile Gly Lys Ala Ile Met Gln Ala Ala Gln Glu Val Ala Glu Gly
 100 105 110
 Lys Leu Asn Asp His Phe Pro Leu Val Val Trp Gln Thr Gly Ser Gly
 115 120 125
 Thr Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ala Asn Arg Ala Ala
 Seite 10263

PF59083SeqList PF59083.txt

130 135 140
 Glu Ile Leu Gly Arg Lys Arg Gly Glu Lys Cys Val His Pro Asn Asp
 145 150 155 160
 His Val Asn Arg Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr Val Met
 165 170 175
 His Ile Ala Ala Thr Glu Ile Asn Ser Arg Leu Ile Pro Ser Leu
 180 185 190
 Lys Thr Leu His Ser Thr Leu Glu Ser Lys Ser Phe Glu Phe Lys Asp
 195 200 205
 Ile Val Lys Ile Gly Arg Thr His Thr Gln Asp Ala Thr Pro Leu Thr
 210 215 220
 Leu Gly Gln Glu Phe Gly Gly Tyr Ala Thr Gln Val Lys Tyr Gly Leu
 225 230 235 240
 Asn Arg Val Thr Cys Thr Leu Pro Arg Leu Tyr Gln Leu Ala Gln Gly
 245 250 255
 Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Lys Lys Gly Phe Asp Val
 260 265 270
 Lys Ile Ala Ala Ala Val Ala Glu Glu Thr Asn Leu Pro Phe Val Thr
 275 280 285
 Ala Glu Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Cys Val Glu
 290 295 300
 Thr Ser Gly Ser Leu Asn Thr Ile Ala Thr Ser Leu Met Lys Ile Ala
 305 310 315 320
 Asn Asp Ile Arg Phe Leu Gly Ser Gly Pro Arg Cys Gly Leu Gly Glu
 325 330 335
 Leu Val Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys
 340 345 350
 Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys Ala Gln Val
 355 360 365
 Met Gly Asn His Val Ala Val Thr Val Gly Gly Ser Asn Gly His Phe
 370 375 380
 Glu Leu Asn Val Phe Lys Pro Val Ile Ala Ser Ala Leu Leu His Ser
 385 390 395 400
 Val Arg Leu Ile Ala Asp Ala Ser Ala Ser Phe Glu Lys Asn Cys Val
 405 410 415
 Arg Gly Ile Glu Ala Asn Arg Glu Arg Ile Ser Lys Leu Leu His Glu
 420 425 430
 Ser Leu Met Leu Val Thr Ser Leu Asn Pro Lys Ile Gly Tyr Asp Asn
 435 440 445
 Ala Ala Ala Val Ala Lys Lys Ala His Lys Glu Gly Cys Thr Leu Lys
 450 455 460
 Glu Ala Ala Leu Asn Leu Gly Val Leu Thr Ala Glu Glu Phe Asp Thr
 465 470 475 480
 Leu Val Val Pro Glu Lys Met Ile Gly Pro Ser Asp
 485 490

<210> 9769
 <211> 1500
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(1500)

<400> 9769
 atg gcc gct ttg aca atg cag ttt gaa gga gag aag aaa aac gta tcc 48
 Met Ala Ala Leu Thr Met Gln Phe Glu Gly Glu Lys Lys Asn Val Ser
 1 5 10 15
 gaa gtt gca gac gta acc ctc aag caa gaa gat gaa caa caa gaa cgt 96
 Glu Val Ala Asp Val Thr Leu Lys Gln Glu Asp Glu Gln Gln Glu Arg
 20 25 30
 aga tct tat tcg acg ccg ttt agg gaa gag aga gac acc ttt ggc ccg 144
 Arg Ser Tyr Ser Thr Pro Phe Arg Glu Glu Arg Asp Thr Phe Gly Pro
 35 40 45
 atc caa gtt cct tcc gat aaa tta tgg gga gca cag acg cag aga tcg 192
 Ile Gln Val Pro Ser Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser
 50 55 60
 ctt cag aac ttc gag att ggt ggt gac cgc gag cga atg ccc gaa cca 240
 485 490
 Seite 10264

PF59083SeqList PF59083.txt

Leu 65	Gln	Asn	Phe	Glu	Ile 70	Gly	Gly	Asp	Arg	Glu 75	Arg	Met	Pro	Glu	Pro 80	
atc	gtc	cga	gct	ttt	ggg	gtc	ttg	aag	aaa	tgt	gct	gcc	aag	gtt	aac	288
Ile	Val	Arg	Ala	Phe 85	Gly	Val	Leu	Lys	Lys 90	Cys	Ala	Ala	Lys	Val 95	Asn	
atg	gag	tat	ggg	ctt	gat	cca	atg	att	ggg	gaa	gcc	ata	atg	gaa	gct	336
Met	Glu	Tyr	Gly 100	Leu	Asp	Pro	Met	Ile 105	Gly	Glu	Ala	Ile	Met 110	Glu	Ala	
gca	caa	gaa	gta	gca	gaa	gga	aag	ctc	aat	gat	cat	ttc	cct	ctt	gtt	384
Ala	Gln 115	Glu	Val	Ala	Glu	Gly 120	Lys	Leu	Asn	Asp	His 125	Phe	Pro	Leu	Val	
gta	tgg	caa	act	ggg	agt	ggg	acg	cag	agt	aat	atg	aat	gct	aat	gag	432
Val	Trp 130	Gln	Thr	Gly	Ser	Gly 135	Thr	Gln	Ser	Asn	Met 140	Asn	Ala	Asn	Glu	
gtc	att	gcc	aat	aga	gca	gct	gag	att	ctt	ggg	cac	aaa	cgt	ggg	gaa	480
Val 145	Ile	Ala	Asn	Arg	Ala 150	Ala	Glu	Ile	Leu	Gly 155	His	Lys	Arg	Gly	Glu 160	
aaa	att	gtg	cac	cca	aat	gac	cat	gtg	aac	aga	tca	caa	tct	tct	aat	528
Lys	Ile	Val	His	Pro 165	Asn	Asp	His	Val	Asn 170	Arg	Ser	Gln	Ser	Ser 175	Asn	
gac	act	ttt	cca	act	gtc	atg	cac	att	gca	gct	gca	acc	gag	att	act	576
Asp	Thr	Phe 180	Pro	Thr	Val	Met	His 185	Ile	Ala	Ala	Ala	Thr	Glu 190	Ile	Thr	
tcg	agg	cta	atc	cct	agt	ttg	aaa	aat	ttg	cat	agc	tct	ttg	gaa	tct	624
Ser	Arg	Leu 195	Ile	Pro	Ser	Leu	Lys 200	Asn	Leu	His	Ser	Ser 205	Leu	Glu	Ser	
aag	tcc	ttc	gag	ttt	aaa	gat	ata	gtg	aaa	atc	gga	aga	act	cat	act	672
Lys	Ser 210	Phe	Glu	Phe	Lys	Asp 215	Ile	Val	Lys	Ile	Gly 220	Arg	Thr	His	Thr	
caa	gat	gct	aca	cct	ttg	aca	tta	gga	caa	gaa	ttt	ggg	ggc	tat	gct	720
Gln 225	Asp	Ala	Thr	Pro	Leu 230	Thr	Leu	Gly	Gln	Glu 235	Phe	Gly	Gly	Tyr	Ala 240	
act	caa	gtt	gag	tat	gga	ctt	aat	aga	gtc	gca	tgt	act	cta	ccc	cgc	768
Thr	Gln	Val	Glu	Tyr 245	Gly	Leu	Asn	Arg	Val 250	Ala	Cys	Thr	Leu	Pro 255	Arg	
atc	tat	cag	ctt	gca	caa	ggg	gga	act	gct	gtt	ggg	acc	gga	tta	aac	816
Ile	Tyr	Gln 260	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly 270	Leu	Asn	
act	aag	aaa	ggg	ttt	gat	gta	aag	atc	gct	gct	gca	gta	gct	gaa	gaa	864
Thr	Lys	Lys 275	Gly	Phe	Asp	Val	Lys 280	Ile	Ala	Ala	Ala	Val	Ala	Glu	Glu	
aca	aac	ttg	cca	ttc	gtc	acc	gca	gaa	aac	aag	ttt	gaa	gct	ctg	gct	912
Thr	Asn 290	Leu	Pro	Phe	Val	Thr 295	Ala	Glu	Asn	Lys	Phe 300	Glu	Ala	Leu	Ala	
gca	cac	gat	gct	tgt	gtt	gaa	aca	agt	gga	tct	ctt	aac	aca	atc	gcc	960
Ala 305	His	Asp	Ala	Cys	Val 310	Glu	Thr	Ser	Gly	Ser 315	Leu	Asn	Thr	Ile	Ala 320	
aca	tca	ttg	atg	aag	att	gcc	aat	gat	ata	cgt	ttt	ctt	gga	agt	ggg	1008
Thr	Ser	Leu	Met	Lys 325	Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser 335	Gly	
cca	aga	tgt	ggg	ctt	ggg	gaa	ctt	tct	ctg	cct	gag	aat	gaa	cca	gga	1056
Pro	Arg	Cys 340	Gly	Leu	Gly	Glu	Leu	Ser 345	Leu	Pro	Glu	Asn	Glu	Pro	Gly	
agc	agt	att	atg	cct	gga	aag	gta	aat	cct	aca	cag	tgt	gag	gcc	ttg	1104
Ser	Ser	Ile 355	Met	Pro	Gly	Lys	Val 360	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	
act	atg	gtt	tgt	gct	caa	gtt	atg	gga	aac	cat	gta	gcc	gtg	aca	att	1152
Thr	Met 370	Val	Cys	Ala	Gln	Val 375	Met	Gly	Asn	His	Val 380	Ala	Val	Thr	Ile	
ggg	ggg	tcg	aat	ggg	cat	ttt	gaa	ttg	aat	gta	ttc	aag	ccg	gtt	atc	1200
Gly 385	Gly	Ser	Asn	Gly	His 390	Phe	Glu	Leu	Asn	Val 395	Phe	Lys	Pro	Val	Ile 400	
gca	agc	gct	ctc	tta	cat	tcc	att	aga	cta	ata	gca	gat	gct	tca	gct	1248
Ala	Ser	Ala	Leu	His 405	Ser	Ser	Ile	Arg	Leu	Ile 410	Ala	Asp	Ala	Ser	Ala	
tca	ttt	gag	aaa	aac	tgt	gtt	aga	ggc	att	gag	gcc	aac	aga	gaa	agg	1296
Ser	Phe	Glu	Lys 420	Asn	Cys	Val	Arg	Gly 425	Ile	Glu	Ala	Asn	Arg	Glu	Arg	
atc	tca	aag	cta	ttg	cac	gag	tct	ctt	atg	ctt	gtg	aca	tca	ttg	aat	1344

PF59083SeqList PF59083.txt

Ile	Ser	Lys	Leu	Leu	His	Glu	Ser	Leu	Met	Leu	Val	Thr	Ser	Leu	Asn	
		435					440					445				
cct	aaa	att	ggc	tat	gac	aat	gct	gca	gca	gta	gcc	aaa	aga	gct	cac	1392
Pro	Lys	Ile	Gly	Tyr	Asp	Asn	Ala	Ala	Ala	Val	Ala	Lys	Arg	Ala	His	
	450					455					460					
aaa	gaa	gga	tgc	aca	tta	aag	cac	gca	gct	atg	aag	tta	ggg	gtt	ctt	1440
Lys	Glu	Gly	Cys	Thr	Leu	Lys	His	Ala	Ala	Met	Lys	Leu	Gly	Val	Leu	
465					470					475					480	
act	tcg	gaa	gag	ttt	gat	act	ctt	gtt	gtt	ccc	gag	aag	atg	att	ggg	1488
Thr	Ser	Glu	Glu	Phe	Asp	Thr	Leu	Val	Val	Pro	Glu	Lys	Met	Ile	Gly	
				485					490					495		
cca	tct	gat	taa													1500
Pro	Ser	Asp														

<210> 9770

<211> 499

<212> PRT

<213> Arabidopsis thaliana

<400> 9770

Met	Ala	Ala	Leu	Thr	Met	Gln	Phe	Glu	Gly	Glu	Lys	Lys	Asn	Val	Ser	
1				5					10					15		
Glu	Val	Ala	Asp	Val	Thr	Leu	Lys	Gln	Glu	Asp	Glu	Gln	Gln	Glu	Arg	
			20					25					30			
Arg	Ser	Tyr	Ser	Thr	Pro	Phe	Arg	Glu	Glu	Arg	Asp	Thr	Phe	Gly	Pro	
		35				40					45					
Ile	Gln	Val	Pro	Ser	Asp	Lys	Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	
	50					55				60						
Leu	Gln	Asn	Phe	Glu	Ile	Gly	Gly	Asp	Arg	Glu	Arg	Met	Pro	Glu	Pro	
65					70				75						80	
Ile	Val	Arg	Ala	Phe	Gly	Val	Leu	Lys	Lys	Cys	Ala	Ala	Lys	Val	Asn	
				85					90					95		
Met	Glu	Tyr	Gly	Leu	Asp	Pro	Met	Ile	Gly	Glu	Ala	Ile	Met	Glu	Ala	
			100					105					110			
Ala	Gln	Glu	Val	Ala	Glu	Gly	Lys	Leu	Asn	Asp	His	Phe	Pro	Leu	Val	
		115					120					125				
Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	
	130					135					140					
Val	Ile	Ala	Asn	Arg	Ala	Glu	Ile	Leu	Gly	His	Lys	Arg	Gly	Glu		
145					150				155					160		
Lys	Ile	Val	His	Pro	Asn	Asp	His	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	
				165					170					175		
Asp	Thr	Phe	Pro	Thr	Val	Met	His	Ile	Ala	Ala	Ala	Thr	Glu	Ile	Thr	
			180					185					190			
Ser	Arg	Leu	Ile	Pro	Ser	Leu	Lys	Asn	Leu	His	Ser	Ser	Leu	Glu	Ser	
		195					200					205				
Lys	Ser	Phe	Glu	Phe	Lys	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Thr	
	210					215					220					
Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	
225					230					235					240	
Thr	Gln	Val	Glu	Tyr	Gly	Leu	Asn	Arg	Val	Ala	Cys	Thr	Leu	Pro	Arg	
				245					250					255		
Ile	Tyr	Gln	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	
		260						265					270			
Thr	Lys	Lys	Gly	Phe	Asp	Val	Lys	Ile	Ala	Ala	Ala	Val	Ala	Glu	Glu	
		275					280					285				
Thr	Asn	Leu	Pro	Phe	Val	Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	
	290					295					300					
Ala	His	Asp	Ala	Cys	Val	Glu	Thr	Ser	Gly	Ser	Leu	Asn	Thr	Ile	Ala	
305					310					315					320	
Thr	Ser	Leu	Met	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	
				325					330					335		
Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	
			340					345					350			
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	
		355					360					365				
Thr	Met	Val	Cys	Ala	Gln	Val	Met	Gly	Asn	His	Val	Ala	Val	Thr	Ile	
	370					375					380					

PF59083SeqList PF59083.txt

Gly Gly Ser Asn Gly His Phe Glu Leu Asn Val Phe Lys Pro Val Ile
 385 390 395 400
 Ala Ser Ala Leu Leu His Ser Ile Arg Leu Ile Ala Asp Ala Ser Ala
 405 410 415
 Ser Phe Glu Lys Asn Cys Val Arg Gly Ile Glu Ala Asn Arg Glu Arg
 420 425 430
 Ile Ser Lys Leu Leu His Glu Ser Leu Met Leu Val Thr Ser Leu Asn
 435 440 445
 Pro Lys Ile Gly Tyr Asp Asn Ala Ala Ala Val Ala Lys Arg Ala His
 450 455 460
 Lys Glu Gly Cys Thr Leu Lys His Ala Ala Met Lys Leu Gly Val Leu
 465 470 475 480
 Thr Ser Glu Glu Phe Asp Thr Leu Val Val Pro Glu Lys Met Ile Gly
 485 490 495
 Pro Ser Asp

<210> 9771
 <211> 1467
 <212> DNA
 <213> Bradyrhizobium japonicum

<220>
 <221> CDS
 <222> (46)..(1467)
 <223> transl_table=11

<400> 9771
 atgaagaggc cgcgcgggcat ttcgcgcggc ggaatggatg tgctc atg gcc aaa tct 57
 Met Ala Lys Ser
 1
 gca cgc acg aag acc gct cgc ccc gcg acc cgc acc gag acc gac agt 105
 Ala Arg Thr Lys Thr Ala Arg Pro Ala Thr Arg Thr Glu Thr Asp Ser
 5 10 15 20
 ttc ggt ccc atc gag gtc ccc tcc gat cgc tat tgg ggc gcg cag acc 153
 Phe Gly Pro Ile Glu Val Pro Ser Asp Arg Tyr Trp Gly Ala Gln Thr
 25 30 35
 gaa cgt tcg cgg cag aat ttc cgc atc ggc acg gat cgc atg ccg atc 201
 Glu Arg Ser Arg Gln Asn Phe Arg Ile Gly Thr Asp Arg Met Pro Ile
 40 45 50
 tcg ctc gtg cat gcg ctc ggc atc gtc aag ctc gcc gcg gcg cag tcc 249
 Ser Leu Val His Ala Leu Gly Ile Val Lys Leu Ala Ala Ala Gln Ser
 55 60 65
 aac cgc gag ctc ggc ctg ctc gac cag cgc cgc gcc agt gcc atc atc 297
 Asn Arg Glu Leu Gly Leu Asp Gln Arg Arg Ala Ser Ala Ile Ile
 70 75 80
 cgc gcc gcg cgc gag gtg atc gac ggc agc ctc gac gat cat ttc ccg 345
 Arg Ala Ala Arg Glu Val Ile Asp Gly Ser Leu Asp Asp His Phe Pro
 85 90 95 100
 ctc gtc gtg tgg cag acc ggc tcg ggc acg cag acc aac atg aac ctc 393
 Leu Val Val Trp Gln Thr Gly Ser Gly Thr Gln Thr Asn Met Asn Leu
 105 110 115
 aac gag gtg atc gcc aac cgc gcc aat gag ctg ctc ggc ggc gag ctc 441
 Asn Glu Val Ile Ala Asn Arg Ala Asn Glu Leu Leu Gly Gly Glu Leu
 120 125 130
 ggc gcc aag aag ccg gtg cat ccg aac gat cac gtc aac atg agc cag 489
 Gly Ala Lys Lys Pro Val His Pro Asn Asp His Val Asn Met Ser Gln
 135 140 145
 tcg tcg aac gac tct ttt ccc acc gca atg cat atc gcg gcg gcg agc 537
 Ser Ser Asn Asp Ser Phe Pro Thr Ala Met His Ile Ala Ala Ala Ser
 150 155 160
 cgc atc acc gcc gat ctc gtt cct gcc ctt ggc gaa ctg ctc cgc gcg 585
 Arg Ile Thr Ala Asp Leu Val Pro Ala Leu Gly Glu Leu Leu Arg Ala
 165 170 175 180
 ctg cgc aag aag gag aag gag ttc gcc aag atc gtc aag atc ggc cgc 633
 Leu Arg Lys Lys Glu Lys Glu Phe Ala Lys Ile Val Lys Ile Gly Arg
 185 190 195
 acc cac acc cag gac gcg acg ccg ctg acg ctc ggc cag gaa ttc tcc 681
 Thr His Thr Gln Asp Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Ser

PF59083SeqList PF59083.txt

										200					205					210					
ggc	tat	gcc	gcg	cag	gtc	gaa	agc	ggg	atc	gcg	cga	ctg	aag	gtc	gcg	729									
Gly	Tyr	Ala	Ala	Gln	Val	Glu	Ser	Gly	Ile	Ala	Arg	Leu	Lys	Val	Ala										
gtg	aag	gag	ctc	tat	ccg	ctg	gcg	cag	ggc	ggc	acc	gcc	gtc	ggc	acc	777									
Val	Lys	Glu	Leu	Tyr	Pro	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr										
ggc	ctc	aac	gcg	aag	ccg	cgc	ttt	gca	aga	ctg	ttc	gca	aag	cac	gtt	825									
Gly	Leu	Asn	Ala	Lys	Pro	Arg	Phe	Ala	Arg	Leu	Phe	Ala	Lys	His	Val										
245																260									
gcc	gga	atc	acc	aaa	ctg	ccc	ttc	acc	agc	gcc	aac	aaa	ttc	gag		873									
Ala	Gly	Ile	Thr	Lys	Leu	Pro	Phe	Thr	Ser	Ala	Ala	Asn	Lys	Phe	Glu										
gcg	ctg	gcc	tgc	aac	gat	gct	tat	gtg	ctg	gcg	cac	ggc	gcc	atc	agt	921									
Ala	Leu	Ala	Ser	Asn	Asp	Ala	Tyr	Val	Leu	Ala	His	Gly	Ala	Ile	Ser										
tcg	gtc	gcg	aca	ggc	ctg	ttc	aag	atc	gcc	aac	gac	atc	cgc	ctg	ctc	969									
Ser	Val	Ala	Thr	Gly	Leu	Phe	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	Leu										
gga	tcg	ggt	ccg	cgc	tca	ggg	ctc	ggc	gag	ctg	atc	ctg	ccg	gag	aac	1017									
Gly	Ser	Gly	Pro	Arg	Ser	Gly	Leu	Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn										
310																320									
gaa	ccg	ggc	tgc	tgc	atc	atg	ccg	ggc	aag	gtc	aat	ccg	acg	cag	tgc	1065									
Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys										
325																340									
gag	gcg	atg	acc	atg	gtg	tgc	tgc	cag	gtg	ttc	ggc	aat	cac	acc	gcg	1113									
Glu	Ala	Met	Thr	Met	Val	Cys	Cys	Gln	Val	Phe	Gly	Asn	His	Thr	Ala										
atc	acg	gtc	gcc	ggc	agc	cag	ggc	cat	ttc	gag	ctc	aac	gtc	tac	aag	1161									
Ile	Thr	Val	Ala	Gly	Ser	Gln	Gly	His	Phe	Glu	Leu	Asn	Val	Tyr	Lys										
ccc	gtg	ctg	gcc	tac	aac	atg	ctg	cac	tcg	atc	cgc	ctg	atg	gcc	gat	1209									
Pro	Val	Leu	Ala	Tyr	Asn	Met	Leu	His	Ser	Ile	Arg	Leu	Met	Ala	Asp										
gcc	gcg	cgc	tcc	ttc	acc	gaa	cat	tgc	gtc	agc	ggc	atc	cgc	gcc	gac	1257									
Ala	Ala	Arg	Ser	Phe	Thr	Glu	His	Cys	Val	Ser	Gly	Ile	Arg	Ala	Asp										
390																400									
gaa	aag	cgc	ata	agt	gag	ctg	atg	cag	cgc	tcg	ctg	atg	ctg	gtg	acc	1305									
Glu	Lys	Arg	Ile	Ser	Glu	Leu	Met	Gln	Arg	Ser	Leu	Met	Leu	Val	Thr										
405																420									
gcg	ctc	gca	ccg	aag	atc	ggc	tac	gac	aac	gcc	gcc	aag	gtc	gcg	aag	1353									
Ala	Leu	Ala	Pro	Lys	Ile	Gly	Tyr	Asp	Asn	Ala	Ala	Lys	Val	Ala	Lys										
acg	gcg	cat	gcc	aac	ggc	acc	acg	ctg	aag	gag	gaa	gcg	ctg	cgg	ctc	1401									
Thr	Ala	His	Ala	Asn	Gly	Thr	Thr	Leu	Lys	Glu	Glu	Ala	Leu	Arg	Leu										
ggc	ttc	gtc	aca	gcg	gac	gag	ttc	gac	cgt	ttg	gtg	cag	ccg	gag	aag	1449									
Gly	Phe	Val	Thr	Ala	Asp	Glu	Phe	Asp	Arg	Leu	Val	Gln	Pro	Glu	Lys										
atg	acg	aaa	ccg	ggg	taa											1467									
Met	Thr	Lys	Pro	Gly																					
470																									

<210> 9772

<211> 473

<212> PRT

<213> Bradyrhizobium japonicum

<400> 9772

Met	Ala	Lys	Ser	Ala	Arg	Thr	Lys	Thr	Ala	Arg	Pro	Ala	Thr	Arg	Thr	
1	Glu	Thr	Asp	Ser	Phe	Gly	Pro	Ile	Glu	Val	Pro	Ser	Asp	Arg	Trp	
Gly	Ala	Gln	Thr	Glu	Arg	Ser	Arg	Gln	Asn	Phe	Arg	Ile	Gly	Thr	Asp	
Arg	Met	Pro	Ile	Ser	Leu	Val	His	Ala	Leu	Gly	Ile	Val	Lys	Leu	Ala	
Ala	Ala	Gln	Ser	Asn	Arg	Glu	Leu	Gly	Leu	Leu	Asp	Gln	Arg	Arg	Ala	
65																80

PF59083SeqList PF59083.txt

Ser Ala Ile Ile Arg Ala Ala Arg Glu Val Ile Asp Gly Ser Leu Asp
 85 90 95
 Asp His Phe Pro Leu Val Val Trp Gln Thr Gly Ser Gly Thr Gln Thr
 100 105 110
 Asn Met Asn Leu Asn Glu Val Ile Ala Asn Arg Ala Asn Glu Leu Leu
 115 120 125
 Gly Gly Glu Leu Gly Ala Lys Lys Pro Val His Pro Asn Asp His Val
 130 135 140
 Asn Met Ser Gln Ser Ser Asn Asp Ser Phe Pro Thr Ala Met His Ile
 145 150 155 160
 Ala Ala Ala Ser Arg Ile Thr Ala Asp Leu Val Pro Ala Leu Gly Glu
 165 170 175
 Leu Leu Arg Ala Leu Arg Lys Lys Glu Lys Glu Phe Ala Lys Ile Val
 180 185 190
 Lys Ile Gly Arg Thr His Thr Gln Asp Ala Thr Pro Leu Thr Leu Gly
 195 200 205
 Gln Glu Phe Ser Gly Tyr Ala Ala Gln Val Glu Ser Gly Ile Ala Arg
 210 215 220
 Leu Lys Val Ala Val Lys Glu Leu Tyr Pro Leu Ala Gln Gly Gly Thr
 225 230 235 240
 Ala Val Gly Thr Gly Leu Asn Ala Lys Pro Arg Phe Ala Arg Leu Phe
 245 250 255
 Ala Lys His Val Ala Gly Ile Thr Lys Leu Pro Phe Thr Ser Ala Ala
 260 265 270
 Asn Lys Phe Glu Ala Leu Ala Ser Asn Asp Ala Tyr Val Leu Ala His
 275 280 285
 Gly Ala Ile Ser Ser Val Ala Thr Gly Leu Phe Lys Ile Ala Asn Asp
 290 295 300
 Ile Arg Leu Leu Gly Ser Gly Pro Arg Ser Gly Leu Gly Glu Leu Ile
 305 310 315 320
 Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn
 325 330 335
 Pro Thr Gln Cys Glu Ala Met Thr Met Val Cys Cys Gln Val Phe Gly
 340 345 350
 Asn His Thr Ala Ile Thr Val Ala Gly Ser Gln Gly His Phe Glu Leu
 355 360 365
 Asn Val Tyr Lys Pro Val Leu Ala Tyr Asn Met Leu His Ser Ile Arg
 370 375 380
 Leu Met Ala Asp Ala Ala Arg Ser Phe Thr Glu His Cys Val Ser Gly
 385 390 395 400
 Ile Arg Ala Asp Glu Lys Arg Ile Ser Glu Leu Met Gln Arg Ser Leu
 405 410 415
 Met Leu Val Thr Ala Leu Ala Pro Lys Ile Gly Tyr Asp Asn Ala Ala
 420 425 430
 Lys Val Ala Lys Thr Ala His Ala Asn Gly Thr Thr Leu Lys Glu Glu
 435 440 445
 Ala Leu Arg Leu Gly Phe Val Thr Ala Asp Glu Phe Asp Arg Leu Val
 450 455 460
 Gln Pro Glu Lys Met Thr Lys Pro Gly
 465 470

<210> 9773

<211> 1665

<212> DNA

<213> Bradyrhizobium japonicum

<220>

<221> CDS

<222> (229)..(1665)

<223> transl_table=11

<400> 9773

gtgcgttctc tggctctgcc ggcatcgaag ccatcaacat tggagccgtg cgattgtctg

60

agtgttccgc acgcgcaacg cgcgttcgct cgctgcaagc cgaggcgccc accatgccat

120

tcgaaaaaag gacgttcggt cgcggaagcg tgtgcgctgt gccgtccgta cactttaggt

180

PF59083SeqList PF59083.txt

cggcgcccga	agagtgtctc	cgacatcaac	tgccacgaga	ggcaaagg	atg	aac	gac	237
					Met	Asn	Asp	
					1			
ctc	cgc	aaa	gag	aca	gac	agc	ctg	285
Leu	Arg	Lys	Glu	Thr	Asp	Ser	Leu	
	5					10		
aag	ctc	tgg	ggc	gcg	cag	acg	cag	333
Lys	Leu	Trp	Gly	Ala	Gln	Thr	Gln	
	20				25			
ggc	cgg	gac	ctg	atg	ccg	cgc	gaa	381
Gly	Arg	Asp	Leu	Met	Pro	Arg	Glu	
				40			45	
aag	aaa	gcg	gcc	gcg	aat	gcg	aat	429
Lys	Lys	Ala	Ala	Ala	Asn	Ala	Asn	
			55				60	
aag	att	cac	aaa	ctg	atc	gtc	cac	477
Lys	Ile	His	Lys	Leu	Ile	Val	His	
		70					75	
cag	cat	cac	gac	atg	ttt	ccc	ctt	525
Gln	His	His	Asp	Met	Phe	Pro	Leu	
	85					90		
acg	cag	ttc	aac	atg	aac	gtg	aac	573
Thr	Gln	Phe	Asn	Met	Asn	Val	Asn	
	100				105			
cag	ctt	gct	ggc	acg	gcg	ctc	ggc	621
Gln	Leu	Ala	Gly	Thr	Ala	Leu	Gly	
				120			125	
gat	cac	gtc	aac	atg	tcg	cag	tcg	669
Asp	His	Val	Asn	Met	Ser	Gln	Ser	
			135				140	
atg	tac	atc	gcg	gcc	gcg	atg	aac	717
Met	Tyr	Ile	Ala	Ala	Ala	Met	Asn	
		150					155	
gtc	gaa	gct	ctg	cac	gat	gcg	atc	765
Val	Glu	Ala	Leu	His	Asp	Ala	Ile	
	165					170		
gac	atc	gtc	aag	atc	ggc	cga	acc	813
Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	
	180				185			
acg	ctc	ggg	cag	gag	tgg	tcc	ggc	861
Thr	Leu	Gly	Gln	Glu	Trp	Ser	Gly	
				200			205	
ctg	gcg	cgc	atc	gac	gac	cgc	ctc	909
Leu	Ala	Arg	Ile	Asp	Asp	Ala	Leu	
			215				220	
ggc	ggc	acc	gcc	gtg	ggc	acc	ggg	957
Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	
		230					235	
gaa	gcc	gtc	gca	gcc	gag	atc	gcg	1005
Glu	Ala	Val	Ala	Ala	Glu	Ile	Ala	
	245					250		
agt	gcg	ccg	aac	aag	ttc	gcc	gtg	1053
Ser	Ala	Pro	Asn	Lys	Phe	Ala	Val	
	260				265			
cag	ctc	tcc	ggc	aca	ctg	cgc	acg	1101
Gln	Leu	Ser	Gly	Thr	Leu	Arg	Thr	
				280			285	
gca	aac	gac	atc	cgc	ctt	ttg	tcc	1149
Ala	Asn	Asp	Ile	Arg	Leu	Leu	Ser	
			295				300	
gag	ttg	cgg	att	ccc	gag	aac	gag	1197
Glu	Leu	Arg	Ile	Pro	Glu	Asn	Glu	
		310					315	
aag	gtc	aat	ccg	acg	cag	gct	gag	1245
Lys	Val	Asn	Pro	Thr	Gln	Ala	Glu	
	325					330		
gtg	atg	gcg	aac	gac	gtc	gcc	gtc	1293
							ggg	

PF59083SeqList PF59083.txt

Val 340	Met	Ala	Asn	Asp	Val 345	Ala	Val	Gly	Phe	Gly 350	Gly	Ala	Gly	Gly	Tyr 355	
ctg	gag	atg	aac	gtc	tac	aag	ccg	ctg	atc	atc	cac	aac	atc	gcg	caa	1341
Leu	Glu	Met	Asn	Val 360	Tyr	Lys	Pro	Leu	Ile 365	Ile	His	Asn	Ile	Ala 370	Gln	
tcc	gtc	acc	atc	ctc	acc	gac	ggc	tgc	acg	aac	ttc	cgc	acc	ttt	ctg	1389
Ser	Val	Thr	Ile	Leu	Thr	Asp	Gly	Cys	Thr	Asn	Phe	Arg	Thr	Phe	Leu	
gtc	gag	ggt	acc	gag	ccg	aac	cgc	aag	aaa	atc	aag	gag	tat	gtc	gag	1437
Val	Glu	Gly 390	Thr	Glu	Pro	Asn	Arg 395	Lys	Lys	Ile	Lys	Glu	Tyr	Val	Glu	
cgg	tcg	ctg	atg	ctc	gtg	acc	gcc	ctg	gcg	ccg	gtg	atc	ggc	tac	gac	1485
Arg	Ser	Leu	Met	Leu	Val	Thr 410	Ala	Leu	Ala	Pro	Val 415	Ile	Gly	Tyr	Asp	
aag	gca	tcg	cgg	atc	gcg	cat	tac	gcg	atg	gac	aac	gat	ctc	acg	ctg	1533
Lys	Ala	Ser	Arg	Ile	Ala 425	His	Tyr	Ala	Met	Asp 430	Asn	Asp	Leu	Thr	Leu 435	
aag	tcg	gcg	gcg	ctg	aag	ctc	ggc	ttc	gtg	acc	gag	ccg	gag	ttc	gac	1581
Lys	Ser	Ala	Ala	Leu 440	Lys	Leu	Gly	Phe	Val 445	Thr	Glu	Pro	Glu	Phe 450	Asp	
cgc	atc	gtg	gat	ccc	gcc	aag	atg	gtc	ccc	tac	gtt	gcc	gag	atc		1629
Arg	Ile	Val	Asp 455	Pro	Ala	Lys	Met	Val 460	Lys	Pro	Tyr	Val	Ala 465	Glu	Ile	
aag	gtg	ccg	ctc	gca	atc	ggt	gcg	aaa	acc	ggt	tga					1665
Lys	Val	Pro 470	Leu	Ala	Ile	Gly	Ala 475	Lys	Thr	Gly						

<210> 9774

<211> 478

<212> PRT

<213> Bradyrhizobium japonicum

<400> 9774

Met	Asn	Asp	Leu	Arg 5	Lys	Glu	Thr	Asp	Ser 10	Leu	Gly	Glu	Val	Asn 15	Val	
Pro	Ala	Asp	Lys	Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Glu	His	
Phe	Ser	Ile 20	Gly	Arg	Asp	Leu	Met 25	Pro	Arg	Glu	Met	Ile 30	Gln	Ser	Tyr	
Ala	Ile 35	Leu	Lys	Lys	Ala	Ala	Asn 40	Ala	Asn	Tyr	Ala	Gly	Gly	Arg		
Leu	Asp	Gly	Lys	Ile	His 55	Lys	Leu	Ile	Val	His 60	Thr	Cys	Asp	Glu	Ile 65	
Leu	Ala	Gly	Gln	His 70	Asp	Met	Phe	Pro	Leu	His 75	Val	Trp	Met	Thr 80		
Gly	Ser	Gly	Thr	Gln 85	Phe	Asn	Met	Asn 90	Val	Asn	Glu	Val	Ile	Ser	Asn 95	
Arg	Cys	Cys 100	Gln	Leu	Ala	Gly	Thr 105	Ala	Leu	Gly	Ser	Lys 110	Leu	Pro	Val	
His	Pro	Asn 115	Asp	His	Val	Asn 120	Met	Ser	Gln	Ser	Ser 125	Asn	Asp	Ser	Phe	
Pro	Ser	Ala 130	Met	Tyr	Ile 135	Ala	Ala	Ala	Met	Asn 140	Val	Thr	Gln	Arg	Leu 145	
Val	Pro	Ala 150	Val	Glu	Ala	Leu	His	Asp 155	Ala	Ile	Ala	Ala	Lys	Ser 160	Asn	
Gln	Trp	Asp 165	Asp	Ile	Val	Lys	Ile	Gly 170	Arg	Thr	His	Met	Gln 175	Asp	Ala	
Thr	Pro	Leu 180	Thr	Leu	Gly	Gln	Glu 185	Trp	Ser	Gly	Tyr	Ala 190	Ala	Met	Leu	
Ala	Asp 195	Gly	Leu	Ala	Arg	Ile 200	Asp	Asp	Ala	Leu	Lys 205	Gly	Val	Phe	Arg	
Leu	Ala	Leu	Gly	Gly	Thr 210	Ala	Val	Gly	Thr	Gly 215	Ile	Asn	Ala	Ala	Pro 220	
Gly	Phe	Ala	Glu	Ala 225	Val	Ala	Ala	Glu	Ile 230	Ala	Arg	Leu	Thr	Gly 235	Leu	
Pro	Phe	Val	Ser	Ala 240	Pro	Asn	Lys	Phe	Ala 245	Val	Gln	Gly	Ala	His 250	Asp	
Ala	Leu	Val 255	Gln	Leu	Ser	Gly	Thr 260	Leu	Arg	Thr	Leu	Ala 265	Gly	Ser	Leu	

PF59083SeqList PF59083.txt

Tyr Lys Ile Ala Asn Asp Ile Arg Leu Leu Ser Cys Gly Pro Arg Ala
 290 295 300
 Gly Phe Ala Glu Leu Arg Ile Pro Glu Asn Glu Pro Gly Ser Ser Ile
 305 310 315 320
 Met Pro Gly Lys Val Asn Pro Thr Gln Ala Glu Ala Leu Thr Met Ile
 325 330 335
 Ala Val Gln Val Met Ala Asn Asp Val Ala Val Gly Phe Gly Gly Ala
 340 345 350
 Gly Gly Tyr Leu Glu Met Asn Val Tyr Lys Pro Leu Ile Ile His Asn
 355 360 365
 Ile Ala Gln Ser Val Thr Ile Leu Thr Asp Gly Cys Thr Asn Phe Arg
 370 375 380
 Thr Phe Leu Val Glu Gly Thr Glu Pro Asn Arg Lys Lys Ile Lys Glu
 385 390 395 400
 Tyr Val Glu Arg Ser Leu Met Leu Val Thr Ala Leu Ala Pro Val Ile
 405 410 415
 Gly Tyr Asp Lys Ala Ser Arg Ile Ala His Tyr Ala Met Asp Asn Asp
 420 425 430
 Leu Thr Leu Lys Ser Ala Ala Leu Lys Leu Gly Phe Val Thr Glu Pro
 435 440 445
 Glu Phe Asp Arg Ile Val Asp Pro Ala Lys Met Val Lys Pro Tyr Val
 450 455 460
 Ala Glu Ile Lys Val Pro Leu Ala Ile Gly Ala Lys Thr Gly
 465 470 475

<210> 9775

<211> 1389

<212> DNA

<213> Bacillus anthracis

<220>

<221> CDS

<222> (1)..(1389)

<223> transl_table=11

<400> 9775

atg gag tac aga att gaa aga gat aca tta gga gaa ata aaa gtt cca	48
Met Glu Tyr Arg Ile Glu Arg Asp Thr Leu Gly Glu Ile Lys Val Pro	
1 5 10 15	
gct gat aaa tta tgg gca gca caa aca caa cgt agt aaa gaa aac ttc	96
Ala Asp Lys Leu Trp Ala Ala Gln Thr Gln Arg Ser Lys Glu Asn Phe	
20 25 30	
ccg att gga aca gag caa atg ccg ctt gaa att gta aaa gca ttt gca	144
Pro Ile Gly Thr Glu Gln Met Pro Leu Glu Ile Val Lys Ala Phe Ala	
35 40 45	
att tta aag aag agt gca gcg ctt agc aat caa aaa tta gga aag cta	192
Ile Leu Lys Lys Ser Ala Ala Leu Ser Asn Gln Lys Leu Gly Lys Leu	
50 55 60	
tca gaa gaa aaa gca gaa gca att gtg gta gct gct gac gaa atc att	240
Ser Glu Glu Lys Ala Glu Ala Ile Val Val Ala Asp Glu Ile Ile	
65 70 75 80	
gca ggg aaa tgg aat gaa cat ttt ccg ctt gtc gtg tgg caa aca ggt	288
Ala Gly Lys Trp Asn Glu His Phe Pro Leu Val Val Trp Gln Thr Gly	
85 90 95	
agt ggt aca caa tca aac atg aat gtg aat gaa gta att gca aat cgt	336
Ser Gly Thr Gln Ser Asn Met Asn Val Asn Glu Val Ile Ala Asn Arg	
100 105 110	
ggg aat caa att ttg aaa gaa aag gga tct gac gta cat att cat ccg	384
Gly Asn Gln Ile Leu Lys Glu Lys Gly Ser Asp Val His Ile His Pro	
115 120 125	
aat gat gat gtg aac atg tcc caa agt tca aat gat aca ttt cca aca	432
Asn Asp Asp Val Asn Met Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr	
130 135 140	
gcg ctt cat gta gca tgt gta ctc gca gta gaa aat cac gta tta cca	480
Ala Leu His Val Ala Cys Val Leu Ala Val Glu Asn His Val Leu Pro	
145 150 155 160	
gct att acg aaa tta aaa gaa acg tta gca gaa aaa gta act gca ttt	528
Ala Ile Thr Lys Leu Lys Glu Thr Leu Ala Glu Lys Val Thr Ala Phe	
165 170 175	

PF59083SeqList PF59083.txt

gaa	cat	att	ata	aaa	att	ggt	cgt	aca	cat	tta	caa	gat	gcg	aca	ccg	576
Glu	His	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	
			180					185					190			
tta	aca	tta	gga	caa	gaa	att	agt	gga	tg	cac	cgt	atg	ctt	gaa	aaa	624
Leu	Thr	Leu	Gly	Gln	Glu	Ile	Ser	Gly	Trp	His	Arg	Met	Leu	Glu	Lys	
			195				200					205				
aca	gag	cgt	atg	att	gca	gag	agc	aat	aca	tat	atg	aaa	gag	ctt	gcg	672
Thr	Glu	Arg	Met	Ile	Ala	Glu	Ser	Asn	Thr	Tyr	Met	Lys	Glu	Leu	Ala	
			210			215					220					
att	ggt	ggt	aca	gca	ggt	gga	aca	ggt	att	aac	gct	cat	cct	aaa	ttt	720
Ile	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Ala	His	Pro	Lys	Phe	
					230					235					240	
ggt	gag	atg	gta	tca	gag	gaa	att	agc	caa	ttt	aca	ggt	aaa	caa	ttt	768
Gly	Glu	Met	Val	Ser	Glu	Glu	Ile	Ser	Gln	Phe	Thr	Gly	Lys	Gln	Phe	
				245					250					255		
att	tct	gca	cca	aat	aag	ttc	cat	gca	tta	acg	agc	cat	gat	gaa	ggt	816
Ile	Ser	Ala	Pro	Asn	Lys	Phe	His	Ala	Leu	Thr	Ser	His	Asp	Glu	Val	
			260					265					270			
gta	tat	act	cac	ggt	gca	tta	aaa	gca	tta	gct	gcg	gat	tta	atg	aaa	864
Val	Tyr	Thr	His	Gly	Ala	Leu	Lys	Ala	Leu	Ala	Ala	Asp	Leu	Met	Lys	
			275				280					285				
atc	gct	aac	gat	gta	cgt	tg	ctg	gca	agt	ggt	cca	cgt	agt	ggt	tta	912
Ile	Ala	Asn	Asp	Val	Arg	Trp	Leu	Ala	Ser	Gly	Pro	Arg	Ser	Gly	Leu	
			290		295						300					
gga	gaa	att	att	att	ccg	gcg	aat	gag	cca	gga	agc	tct	att	atg	cca	960
Gly	Glu	Ile	Ile	Ile	Pro	Ala	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
					310					315					320	
ggt	aaa	gta	aat	cca	acg	caa	agt	gaa	gcg	tta	acg	atg	ggt	gta	gcg	1008
Gly	Lys	Val	Asn	Pro	Thr	Gln	Ser	Glu	Ala	Leu	Thr	Met	Val	Val	Ala	
				325					330					335		
caa	gtg	atg	gga	aat	gac	gca	aca	atc	gga	ttt	gct	gcg	agt	caa	ggt	1056
Gln	Val	Met	Gly	Asn	Asp	Ala	Thr	Ile	Gly	Phe	Ala	Ala	Ser	Gln	Gly	
			340					345					350			
aat	ttt	gag	tta	aac	gta	ttt	aaa	cct	ggt	att	gcg	tat	aac	ttc	tta	1104
Asn	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Ile	Ala	Tyr	Asn	Phe	Leu	
			355				360					365				
caa	tcc	gct	cac	tta	tta	gca	gat	gca	att	ggt	tca	ttt	aat	gat	aat	1152
Gln	Ser	Ala	His	Leu	Leu	Ala	Asp	Ala	Ile	Val	Ser	Phe	Asn	Asp	Asn	
			370			375					380					
tgt	gca	ggt	ggt	att	gaa	gct	gat	gaa	gaa	atc	att	aaa	gag	aat	gtg	1200
Cys	Ala	Val	Gly	Ile	Glu	Ala	Asp	Glu	Glu	Ile	Ile	Lys	Glu	Asn	Val	
					390					395					400	
aat	cgt	tca	tta	atg	ctt	ggt	aca	gca	tta	aac	ccg	cat	atc	gga	tat	1248
Asn	Arg	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	
				405					410					415		
gaa	aat	gca	gca	aaa	att	gcg	aag	cat	gct	cat	aaa	gaa	ggg	tta	act	1296
Glu	Asn	Ala	Ala	Lys	Ile	Ala	Lys	His	Ala	His	Lys	Glu	Gly	Leu	Thr	
				420				425					430			
tta	aaa	gaa	gca	gca	ttg	caa	tct	gga	cta	cta	aca	gaa	gag	caa	ttt	1344
Leu	Lys	Glu	Ala	Ala	Leu	Gln	Ser	Gly	Leu	Leu	Thr	Glu	Glu	Gln	Phe	
			435				440					445				
aat	gaa	att	gtc	gat	ccg	aaa	aaa	atg	att	gct	ccg	aaa	gag	taa		1389
Asn	Glu	Ile	Val	Asp	Pro	Lys	Lys	Met	Ile	Ala	Pro	Lys	Glu			
			450			455					460					

<210> 9776

<211> 462

<212> PRT

<213> Bacillus anthracis

<400> 9776

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

PF59083SeqList PF59083.txt

Ser Glu Glu Lys Ala Glu Ala Ile Val Val Ala Ala Asp Glu Ile Ile
65 70 75 80
Ala Gly Lys Trp Asn Glu His Phe Pro Leu Val Val Trp Gln Thr Gly
85 90 95
Ser Gly Thr Gln Ser Asn Met Asn Val Asn Glu Val Ile Ala Asn Arg
100 105 110
Gly Asn Gln Ile Leu Lys Glu Lys Gly Ser Asp Val His Ile His Pro
115 120 125
Asn Asp Asp Val Asn Met Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr
130 135 140
Ala Leu His Val Ala Cys Val Leu Ala Val Glu Asn His Val Leu Pro
145 150 155 160
Ala Ile Thr Lys Leu Lys Glu Thr Leu Ala Glu Lys Val Thr Ala Phe
165 170 175
Glu His Ile Ile Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr Pro
180 185 190
Leu Thr Leu Gly Gln Glu Ile Ser Gly Trp His Arg Met Leu Glu Lys
195 200 205
Thr Glu Arg Met Ile Ala Glu Ser Asn Thr Tyr Met Lys Glu Leu Ala
210 215 220
Ile Gly Gly Thr Ala Val Gly Thr Gly Ile Asn Ala His Pro Lys Phe
225 230 235 240
Gly Glu Met Val Ser Glu Glu Ile Ser Gln Phe Thr Gly Lys Gln Phe
245 250 255
Ile Ser Ala Pro Asn Lys Phe His Ala Leu Thr Ser His Asp Glu Val
260 265 270
Val Tyr Thr His Gly Ala Leu Lys Ala Leu Ala Ala Asp Leu Met Lys
275 280 285
Ile Ala Asn Asp Val Arg Trp Leu Ala Ser Gly Pro Arg Ser Gly Leu
290 295 300
Gly Glu Ile Ile Ile Pro Ala Asn Glu Pro Gly Ser Ser Ile Met Pro
305 310 315 320
Gly Lys Val Asn Pro Thr Gln Ser Glu Ala Leu Thr Met Val Val Ala
325 330 335
Gln Val Met Gly Asn Asp Ala Thr Ile Gly Phe Ala Ala Ser Gln Gly
340 345 350
Asn Phe Glu Leu Asn Val Phe Lys Pro Val Ile Ala Tyr Asn Phe Leu
355 360 365
Gln Ser Ala His Leu Leu Ala Asp Ala Ile Val Ser Phe Asn Asp Asn
370 375 380
Cys Ala Val Gly Ile Glu Ala Asp Glu Glu Ile Ile Lys Glu Asn Val
385 390 395 400
Asn Arg Ser Leu Met Leu Val Thr Ala Leu Asn Pro His Ile Gly Tyr
405 410 415
Glu Asn Ala Ala Lys Ile Ala Lys His Ala His Lys Glu Gly Leu Thr
420 425 430
Leu Lys Glu Ala Ala Leu Gln Ser Gly Leu Leu Thr Glu Glu Gln Phe
435 440 445
Asn Glu Ile Val Asp Pro Lys Lys Met Ile Ala Pro Lys Glu
450 455 460

<210> 9777

<211> 1389

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1389)

<223> transl_table=11

<400> 9777

atg gaa tac aga att gaa cga gac acc atg gga gaa gta aaa gtt cct 48
Met Glu Tyr Arg Ile Glu Arg Asp Thr Met Gly Glu Val Lys Val Pro
1 5 10 15

gct gat aaa ttt tgg ggc gcc caa aca cag cga agc aag gag aac ttt 96
Ala Asp Lys Phe Trp Gly Ala Gln Thr Gln Arg Ser Lys Glu Asn Phe
20 25 30

aag atc ggt tct gaa aaa atg ccg atg cgt gtt gtg aag gcg ttt gca 144
Seite 10274

PF59083SeqList PF59083.txt																
Lys	Ile	Gly	Ser	Glu	Lys	Met	Pro	Met	Arg	Val	Val	Lys	Ala	Phe	Ala	
att	tta	aaa	cga	agc	act	gct	cta	gct	aat	aaa	cgc	ctc	ggc	aat	ctg	192
Ile	Leu	Lys	Arg	Ser	Thr	Ala	Leu	Ala	Asn	Lys	Arg	Leu	Gly	Asn	Leu	
gac	gct	gaa	aaa	gca	gaa	gcg	att	gca	gcg	gtt	tgt	gat	gat	gtg	ctc	240
Asp	Ala	Glu	Lys	Ala	Glu	Ala	Ile	Ala	Ala	Val	Cys	Asp	Asp	Val	Leu	
65					70					75					80	
aaa	ggc	aag	tac	gat	gac	aac	ttc	ccg	ctt	gtc	gta	tgg	cag	acc	gga	288
Lys	Gly	Lys	Tyr	Asp	Asp	Asn	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	
				85					90					95		
agc	ggc	aca	caa	agc	aat	atg	aac	atg	aac	gaa	gtg	gta	gcc	aac	cgt	336
Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Met	Asn	Glu	Val	Val	Ala	Asn	Arg	
			100				105						110			
gcg	act	gct	tta	tta	aaa	gag	aag	aac	tct	gat	caa	acg	att	cat	cca	384
Ala	Thr	Ala	Leu	Leu	Lys	Glu	Lys	Asn	Ser	Asp	Gln	Thr	Ile	His	Pro	
		115				120						125				
aat	gat	gac	gtg	aac	cga	agc	caa	agc	tca	aac	gac	aca	ttc	ccg	act	432
Asn	Asp	Asp	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	
	130					135					140					
gcg	atg	cat	gtt	gcc	gct	gtt	ttg	gct	gtt	tac	gag	cag	ctt	gtg	ccg	480
Ala	Met	His	Val	Ala	Ala	Val	Leu	Ala	Val	Tyr	Glu	Gln	Leu	Val	Pro	
145				150		155									160	
gcg	ctt	gat	cag	ctt	cgc	aat	aca	ctg	gat	gaa	aaa	gca	aaa	gca	tac	528
Ala	Leu	Asp	Gln	Leu	Arg	Asn	Thr	Leu	Asp	Glu	Lys	Ala	Lys	Ala	Tyr	
				165				170					175			
aat	gat	att	gtc	aaa	atc	gga	cgc	acg	cat	ctt	cag	gat	gct	acg	cca	576
Asn	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	
			180				185						190			
ctg	acc	ctc	gga	cag	gaa	atc	agc	gga	tgg	gtt	cac	atg	ctg	gac	cgt	624
Leu	Thr	Leu	Gly	Gln	Glu	Ile	Ser	Gly	Trp	Val	His	Met	Leu	Asp	Arg	
		195				200						205				
tcg	aag	gaa	atg	att	ttg	gaa	gcg	aca	gat	aaa	atg	cgt	gcg	ctt	gca	672
Ser	Lys	Glu	Met	Ile	Leu	Glu	Ala	Thr	Asp	Lys	Met	Arg	Ala	Leu	Ala	
	210				215						220					
att	ggt	gga	acg	gct	gtc	gga	acg	ggt	atc	aac	gcc	cac	cca	gag	ttt	720
Ile	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Ala	His	Pro	Glu	Phe	
225				230					235					240		
gga	gag	ctt	gtc	tca	gaa	gag	atc	act	aag	ctg	acc	ggc	caa	acg	ttc	768
Gly	Glu	Leu	Val	Ser	Glu	Glu	Ile	Thr	Lys	Leu	Thr	Gly	Gln	Thr	Phe	
				245				250					255			
agc	agc	tcg	ccg	aat	aaa	ttc	cac	gcg	ctg	aca	agc	cat	gac	gaa	atc	816
Ser	Ser	Ser	Pro	Asn	Lys	Phe	His	Ala	Leu	Thr	Ser	His	Asp	Glu	Ile	
			260				265						270			
act	tat	gcg	cat	ggc	gca	tta	aaa	gcg	ctt	gcg	gct	gac	tta	atg	aaa	864
Thr	Tyr	Ala	His	Gly	Ala	Leu	Lys	Ala	Leu	Ala	Ala	Asp	Leu	Met	Lys	
		275				280						285				
atc	gcg	aac	gat	gtc	aga	tgg	ctc	gca	agc	gga	ccc	cgc	tgc	ggc	atc	912
Ile	Ala	Asn	Asp	Val	Arg	Trp	Leu	Ala	Ser	Gly	Pro	Arg	Cys	Gly	Ile	
	290					295					300					
ggg	gag	atc	gtc	att	cct	gaa	aat	gag	ccg	gga	agc	tct	att	atg	cct	960
Gly	Glu	Ile	Val	Ile	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
305				310				315						320		
ggt	aaa	gtc	aat	ccg	aca	caa	agc	gaa	gcg	tta	aca	atg	atc	gca	gcg	1008
Gly	Lys	Val	Asn	Pro	Thr	Gln	Ser	Glu	Ala	Leu	Thr	Met	Ile	Ala	Ala	
				325				330						335		
caa	atc	atg	ggg	aac	gat	gcg	aca	atc	ggc	ttt	gcg	gcg	agt	cag	ggg	1056
Gln	Ile	Met	Gly	Asn	Asp	Ala	Thr	Ile	Gly	Phe	Ala	Ala	Ser	Gln	Gly	
			340				345						350			
aac	ttt	gaa	ctg	aac	gtg	ttt	aag	cct	gtt	att	att	tac	aac	ttc	ctg	1104
Asn	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Ile	Ile	Tyr	Asn	Phe	Leu	
		355				360						365				
caa	tct	gtg	cag	ctg	ctc	agt	gac	ggc	atg	aat	tca	ttc	cat	gat	aaa	1152
Gln	Ser	Val	Gln	Leu	Leu	Ser	Asp	Gly	Met	Asn	Phe	His	Asp	Lys		
	370				375						380					
tgt	gct	gtc	ggt	att	gag	cct	aat	aaa	gaa	acc	att	cag	gaa	aac	ctg	1200
Cys	Ala	Val	Gly	Ile	Glu	Pro	Asn	Lys	Glu	Thr	Ile	Gln	Glu	Asn	Leu	
385				390				395						400		
tca	aat	tca	tta	atg	ctt	gtt	acg	gcg	ctg	aac	ccg	cat	atc	ggt	tat	1248

PF59083SeqList PF59083.txt

Ser	Asn	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	
				405					410					415		
gaa	aac	gcg	gcg	aaa	atc	gcc	aag	ctt	gcc	cat	aaa	gag	gga	ttg	acg	1296
Glu	Asn	Ala	Ala	Lys	Ile	Ala	Lys	Leu	Ala	His	Lys	Glu	Gly	Leu	Thr	
			420					425					430			
ctc	aaa	gaa	gca	gct	ttg	aag	ctt	gaa	ttg	ctg	aca	gag	gag	caa	ttt	1344
Leu	Lys	Glu	Ala	Ala	Leu	Lys	Leu	Glu	Leu	Leu	Thr	Glu	Glu	Gln	Phe	
		435					440					445				
aac	gaa	atg	gtt	aag	ccg	gaa	gac	atg	gta	aaa	cca	aag	gcg	taa		1389
Asn	Glu	Met	Val	Lys	Pro	Glu	Asp	Met	Val	Lys	Pro	Lys	Ala			
	450					455					460					

<210> 9778

<211> 462

<212> PRT

<213> Bacillus subtilis

<400> 9778

Met	Glu	Tyr	Arg	Ile	Glu	Arg	Asp	Thr	Met	Gly	Glu	Val	Lys	Val	Pro	
1				5					10					15		
Ala	Asp	Lys	Phe	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Lys	Glu	Asn	Phe	
			20					25					30			
Lys	Ile	Gly	Ser	Glu	Lys	Met	Pro	Met	Arg	Val	Val	Lys	Ala	Phe	Ala	
		35					40					45				
Ile	Leu	Lys	Arg	Ser	Thr	Ala	Leu	Ala	Asn	Lys	Arg	Leu	Gly	Asn	Leu	
	50					55					60					
Asp	Ala	Glu	Lys	Ala	Glu	Ala	Ile	Ala	Ala	Val	Cys	Asp	Asp	Val	Leu	
65				70					75						80	
Lys	Gly	Lys	Tyr	Asp	Asn	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly		
			85				90						95			
Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Met	Asn	Glu	Val	Val	Ala	Asn	Arg	
			100				105						110			
Ala	Thr	Ala	Leu	Leu	Lys	Glu	Lys	Asn	Ser	Asp	Gln	Thr	Ile	His	Pro	
		115					120					125				
Asn	Asp	Asp	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	
	130					135					140					
Ala	Met	His	Val	Ala	Ala	Val	Leu	Ala	Val	Tyr	Glu	Gln	Leu	Val	Pro	
145				150					155						160	
Ala	Leu	Asp	Gln	Leu	Arg	Asn	Thr	Leu	Asp	Glu	Lys	Ala	Lys	Ala	Tyr	
			165					170					175			
Asn	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	
		180					185					190				
Leu	Thr	Leu	Gly	Gln	Glu	Ile	Ser	Gly	Trp	Val	His	Met	Leu	Asp	Arg	
		195					200					205				
Ser	Lys	Glu	Met	Ile	Leu	Glu	Ala	Thr	Asp	Lys	Met	Arg	Ala	Leu	Ala	
	210					215					220					
Ile	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Ala	His	Pro	Glu	Phe	
225				230					235					240		
Gly	Glu	Leu	Val	Ser	Glu	Glu	Ile	Thr	Lys	Leu	Thr	Gly	Gln	Thr	Phe	
			245					250					255			
Ser	Ser	Ser	Pro	Asn	Lys	Phe	His	Ala	Leu	Thr	Ser	His	Asp	Glu	Ile	
			260				265						270			
Thr	Tyr	Ala	His	Gly	Ala	Leu	Lys	Ala	Leu	Ala	Ala	Asp	Leu	Met	Lys	
		275					280					285				
Ile	Ala	Asn	Asp	Val	Arg	Trp	Leu	Ala	Ser	Gly	Pro	Arg	Cys	Gly	Ile	
	290					295					300					
Gly	Glu	Ile	Val	Ile	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
305					310					315					320	
Gly	Lys	Val	Asn	Pro	Thr	Gln	Ser	Glu	Ala	Leu	Thr	Met	Ile	Ala	Ala	
			325						330					335		
Gln	Ile	Met	Gly	Asn	Asp	Ala	Thr	Ile	Gly	Phe	Ala	Ala	Ser	Gln	Gly	
		340					345						350			
Asn	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Ile	Ile	Tyr	Asn	Phe	Leu	
	355					360						365				
Gln	Ser	Val	Gln	Leu	Leu	Ser	Asp	Gly	Met	Asn	Ser	Phe	His	Asp	Lys	
	370					375					380					
Cys	Ala	Val	Gly	Ile	Glu	Pro	Asn	Lys	Glu	Thr	Ile	Gln	Glu	Asn	Leu	
385				390					395						400	
Ser	Asn	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	

PF59083SeqList PF59083.txt

405 410 415
 Glu Asn Ala Ala Lys Ile Ala Lys Leu Ala His Lys Glu Gly Leu Thr
 420 425 430
 Leu Lys Glu Ala Ala Leu Lys Leu Glu Leu Leu Thr Glu Glu Gln Phe
 435 440 445
 Asn Glu Met Val Lys Pro Glu Asp Met Val Lys Pro Lys Ala
 450 455 460

<210> 9779
 <211> 1392
 <212> DNA
 <213> Bordetella pertussis

<220>
 <221> CDS
 <222> (1)..(1392)
 <223> transl_table=11

<400> 9779
 atg aaa acc cgc acc gaa aaa gac act ttc ggc ccg atc gag gtg ccc 48
 Met Lys Thr Arg Thr Glu Lys Asp Thr Phe Gly Pro Ile Glu Val Pro
 1 5 10 15
 gag cag cac ctg tgg ggc gcg cag acc cag ccg tcg ctg cat ttc ttc 96
 Glu Gln His Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu His Phe Phe
 20 25 30
 gcg atc tcg acc gag aag atg ccg gtg ccg ctg gtc gcc gcc atg gca 144
 Ala Ile Ser Thr Glu Lys Met Pro Val Pro Leu Val Ala Ala Met Ala
 35 40 45
 cgc ctg aag cgc gcc gcc gcc aag gtc aac gcc gag ctg ggc gag ctg 192
 Arg Leu Lys Arg Ala Ala Ala Lys Val Asn Ala Glu Leu Gly Glu Leu
 50 55 60
 gat ccg cag gtc gca gac gcc atc atg cgg gcc gcc gat gag gtg atc 240
 Asp Pro Gln Val Ala Asp Ala Ile Met Arg Ala Ala Asp Glu Val Ile
 65 70 75 80
 gcc ggc aag tgg ccc gac gag ttt ccg ctg tcg gtc tgg cag acc gcc 288
 Ala Gly Lys Trp Pro Asp Glu Phe Pro Leu Ser Val Trp Gln Thr Gly
 85 90 95
 tcg ggc acg cag agc aac atg aac atg aac gag gtg ctg gcc aac cgc 336
 Ser Gly Thr Gln Ser Asn Met Asn Met Asn Glu Val Leu Ala Asn Arg
 100 105 110
 gcc tcc gag ctg ctg gcc gcc gag cgc gcc gaa gcc cgc aag gtg cac 384
 Ala Ser Glu Leu Leu Gly Gly Glu Arg Gly Glu Gly Arg Lys Val His
 115 120 125
 ccc aac gac cac gtg aac cgg gcc cag tcg tcc aac gat acc ttt ccg 432
 Pro Asn Asp His Val Asn Arg Gly Gln Ser Ser Asn Asp Thr Phe Pro
 130 135 140
 acc gcc atg cac gtg gcc gcc gcg gtc gag gtc gag cac cgc gtg ctg 480
 Thr Ala Met His Val Ala Ala Ala Val Glu Val Glu His Arg Val Leu
 145 150 155 160
 ccc gcc ctg aag gcg ttg arg gcc acc ctg gcc aag agc gcg gcg 528
 Pro Ala Leu Lys Ala Leu Arg Gly Thr Leu Ala Lys Ser Ala Ala
 165 170 175
 ttc tac gac atc gtc aag atc ggt cgc acc cat ttg cag gac gcc acc 576
 Phe Tyr Asp Ile Val Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr
 180 185 190
 ccg ttg acg ctg gcc cag gag atc tcc gcc tac gtg gcc cag ctg gac 624
 Pro Leu Thr Leu Gly Gln Glu Ile Ser Gly Tyr Val Ala Gln Leu Asp
 195 200 205
 ctg gcc gag cag cag atc cgc gcg acg ctg gcc gcc ctg cac cag ctg 672
 Leu Ala Glu Gln Gln Ile Arg Ala Thr Leu Ala Gly Leu His Gln Leu
 210 215 220
 gcc atc gcc gcc acg gcg gtg gcc acc gcc ctg aac gcg cat ccg cag 720
 Ala Ile Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Ala His Pro Gln
 225 230 235 240
 ttc agc gcc aag gta tcg gcc gaa ctg gcc cat gac acg gcc agc gcg 768
 Phe Ser Ala Lys Val Ser Ala Glu Leu Ala His Asp Thr Gly Ser Ala
 245 250 255
 ttc gtg tcg gcg ccc aac aag ttc cag gcg ctg gct tcg cac gag gcg 816
 Phe Val Ser Ala Pro Asn Lys Phe Gln Ala Leu Ser His Glu Ala

PF59083SeqList PF59083.txt

ctg	ctg	ttc	gcg	cac	ggc	gcc	ttg	aag	acg	ctg	gcc	gcc	ggc	ctg	atg	864
Leu	Leu	Phe	Ala	His	Gly	Ala	Leu	Lys	Thr	Leu	Ala	Ala	Gly	Leu	Met	
		275					280					285				
aag	atc	gcc	aac	gat	gtg	cgc	tgg	ctg	gcc	agc	ggc	ccg	cgc	tcg	ggg	912
Lys	Ile	Ala	Asn	Asp	Val	Arg	Trp	Leu	Ala	Ser	Gly	Pro	Arg	Ser	Gly	
		290				295					300					
ctg	ggc	gaa	atc	agc	att	ccc	gag	aac	gag	ccg	ggc	agc	tcc	atc	atg	960
Leu	Gly	Glu	Ile	Ser	Ile	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	
		305			310					315					320	
ccg	ggc	aag	gtc	aac	ccg	acc	cag	tgc	gaa	gcc	gtc	acg	atg	ctg	gcc	1008
Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Val	Thr	Met	Leu	Ala	
				325					330						335	
gcg	cag	gtc	atg	ggc	aac	gac	gtg	gcc	atc	aat	gtc	ggc	ggg	gcc	agc	1056
Ala	Gln	Val	Met	Gly	Asn	Asp	Val	Ala	Ile	Asn	Val	Gly	Gly	Ala	Ser	
			340					345					350			
ggc	aac	ttc	gag	ctg	aac	gtc	ttc	aag	ccg	ctg	gtg	atc	cac	aat	ttc	1104
Gly	Asn	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Leu	Val	Ile	His	Asn	Phe	
		355					360					365				
ctg	cag	tcg	gtg	cgc	ctg	ctg	gcc	gac	ggc	atg	gtc	agc	ttc	gac	aag	1152
Leu	Gln	Ser	Val	Arg	Leu	Leu	Ala	Asp	Gly	Met	Val	Ser	Phe	Asp	Lys	
		370				375					380					
cac	tgc	gcg	gcc	ggc	atc	gag	ccc	aac	cgc	gag	cgc	atc	acc	gag	ctg	1200
His	Cys	Ala	Ala	Gly	Ile	Glu	Pro	Asn	Arg	Glu	Arg	Ile	Thr	Glu	Leu	
		385			390					395					400	
gtc	gag	cgt	tcg	ctg	atg	ctg	gtg	act	gcg	ctc	aac	ccg	cac	atc	ggc	1248
Val	Glu	Arg	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	
				405				410						415		
tac	gac	aag	gcc	gcg	cag	atc	gcc	aag	aag	gcg	cac	aag	gaa	aac	ctg	1296
Tyr	Asp	Lys	Ala	Ala	Gln	Ile	Ala	Lys	Lys	Ala	His	Lys	Glu	Asn	Leu	
			420					425					430			
tcg	ctg	aaa	gag	gcg	gcg	ctg	gcg	ctg	ggg	cac	ctg	acc	gag	gcg	cag	1344
Ser	Leu	Lys	Glu	Ala	Ala	Leu	Ala	Leu	Gly	His	Leu	Thr	Glu	Ala	Gln	
		435					440					445				
ttc	gcc	gag	tgg	gtg	gtg	ccg	ggc	gac	atg	acc	aac	gcg	cgc	cgc		1389
Phe	Ala	Glu	Trp	Val	Val	Pro	Gly	Asp	Met	Thr	Asn	Ala	Arg	Arg		
		450				455					460					
tag																1392

<210> 9780
 <211> 463
 <212> PRT
 <213> Bordetella pertussis

<400> 9780
 Met Lys Thr Arg Thr Glu Lys Asp Thr Phe Gly Pro Ile Glu Val Pro
 1 5 10 15
 Glu Gln His Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu His Phe Phe
 20 25 30
 Ala Ile Ser Thr Glu Lys Met Pro Val Pro Leu Val Ala Ala Met Ala
 35 40 45
 Arg Leu Lys Arg Ala Ala Lys Val Asn Ala Glu Leu Gly Glu Leu
 50 55 60
 Asp Pro Gln Val Ala Asp Ala Ile Met Arg Ala Ala Asp Glu Val Ile
 65 70 75 80
 Ala Gly Lys Trp Pro Asp Glu Phe Pro Leu Ser Val Trp Gln Thr Gly
 85 90 95
 Ser Gly Thr Gln Ser Asn Met Asn Met Asn Glu Val Leu Ala Asn Arg
 100 105 110
 Ala Ser Glu Leu Leu Gly Gly Glu Arg Gly Glu Gly Arg Lys Val His
 115 120 125
 Pro Asn Asp His Val Asn Arg Gly Gln Ser Ser Asn Asp Thr Phe Pro
 130 135 140
 Thr Ala Met His Val Ala Ala Ala Val Glu Val Glu His Arg Val Leu
 145 150 155 160
 Pro Ala Leu Lys Ala Leu Arg Gly Thr Leu Ala Ala Lys Ser Ala Ala
 165 170 175

PF59083SeqList PF59083.txt

Phe Tyr Asp Ile Val Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr
180 185 190
Pro Leu Thr Leu Gly Gln Glu Ile Ser Gly Tyr Val Ala Gln Leu Asp
195 200 205
Leu Ala Glu Gln Gln Ile Arg Ala Thr Leu Ala Gly Leu His Gln Leu
210 215 220
Ala Ile Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Ala His Pro Gln
225 230 235 240
Phe Ser Ala Lys Val Ser Ala Glu Leu Ala His Asp Thr Gly Ser Ala
245 250 255
Phe Val Ser Ala Pro Asn Lys Phe Gln Ala Leu Ala Ser His Glu Ala
260 265 270
Leu Leu Phe Ala His Gly Ala Leu Lys Thr Leu Ala Ala Gly Leu Met
275 280 285
Lys Ile Ala Asn Asp Val Arg Trp Leu Ala Ser Gly Pro Arg Ser Gly
290 295 300
Leu Gly Glu Ile Ser Ile Pro Glu Asn Glu Pro Gly Ser Ser Ile Met
305 310 315 320
Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Val Thr Met Leu Ala
325 330 335
Ala Gln Val Met Gly Asn Asp Val Ala Ile Asn Val Gly Gly Ala Ser
340 345 350
Gly Asn Phe Glu Leu Asn Val Phe Lys Pro Leu Val Ile His Asn Phe
355 360 365
Leu Gln Ser Val Arg Leu Leu Ala Asp Gly Met Val Ser Phe Asp Lys
370 375 380
His Cys Ala Ala Gly Ile Glu Pro Asn Arg Glu Arg Ile Thr Glu Leu
385 390 395 400
Val Glu Arg Ser Leu Met Leu Val Thr Ala Leu Asn Pro His Ile Gly
405 410 415
Tyr Asp Lys Ala Ala Gln Ile Ala Lys Lys Ala His Lys Glu Asn Leu
420 425 430
Ser Leu Lys Glu Ala Ala Leu Ala Leu Gly His Leu Thr Glu Ala Gln
435 440 445
Phe Ala Glu Trp Val Val Pro Gly Asp Met Thr Asn Ala Arg Arg
450 455 460

<210> 9781
<211> 1422
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1422)
<223> transl_table=11

<400> 9781
atg agt gat ttc atg acc gag cag gaa ttc cgt att gag cac gac acc 48
Met Ser Asp Phe Met Thr Glu Gln Glu Phe Arg Ile Glu His Asp Thr
1 5 10 15
atg ggt gaa gtg aag gtt cca gca aag gct ctg tgg cag gca cag acc 96
Met Gly Glu Val Lys Val Pro Ala Lys Ala Leu Trp Gln Ala Gln Thr
20 25 30
cag cgc gct gtt gag aac ttc cct atc tct ggt cgt ggt ctg gaa tcc 144
Gln Arg Ala Val Glu Asn Phe Pro Ile Ser Gly Arg Gly Leu Glu Ser
35 40 45
gca cag atc cgc gca atg ggt ctg ctg aag gca gct tgt gcg cag gta 192
Ala Gln Ile Arg Ala Met Gly Leu Leu Lys Ala Ala Cys Ala Gln Val
50 55 60
aac aag gac tcc ggt gcg ctg gat gca gag aag gca gat gcc atc att 240
Asn Lys Asp Ser Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile
65 70 75 80
gca gct ggt aag gag atc gcg tcc ggt aag cat gac gct gag ttc cca 288
Ala Ala Gly Lys Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro
85 90 95
att gat gtg ttc cag act ggt tcc ggt act tcc tcc aac atg aac acc 336
Ile Asp Val Phe Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr
100 105 110

PF59083SeqList PF59083.txt																
aat Asn	gag Glu	gtt Val 115	atc Ile	gct Ala	tcc Ser	atc Ile	gcg Ala 120	aag Lys	gct Ala	aac Asn	ggc Gly 125	gtt Val	gag Glu	gtt Val	cac His	384
cca Pro	aat Asn 130	gac Asp	cac His	gtc Val	aac Asn	atg Met 135	ggt Gly	cag Gln	tcc Ser	tcc Ser	aat Asn 140	gac Asp	acc Thr	ttc Phe	cct Pro	432
act Thr 145	gca Ala	act Thr	cac His	gtt Val	gct Ala 150	gca Ala	acc Thr	gaa Glu	gct Ala	gct Ala 155	gtc Val	aat Asn	gac Asp	ctc Leu	atc Ile 160	480
cca Pro	ggc Gly	ctg Leu	aag Lys	gtt Val 165	ctg Leu	cac His	gag Glu	tct Ser	ttg Leu 170	gcg Ala	aag Lys	aag Lys	gct Ala	aac Asn 175	gag Glu	528
tgg Trp	tct Ser	gag Glu 180	gtt Val	gtt Val	aag Lys	tcc Ser	ggc Gly 185	cgc Arg	acc Thr	cac His	ctg Leu	atg Met	gac Asp 190	gct Ala	gtt Val	576
cca Pro	gta Val 195	acc Thr	ctg Leu	ggc Gly	cag Gln	gag Glu	ttc Phe 200	ggt Gly	tac Tyr	gct Ala 205	cgc Arg	cag Gln	atc Ile	cag Gln		624
ctc Leu	ggc Gly 210	atc Ile	gag Glu	cgc Arg	gtt Val	gag Glu 215	gct Ala	act Thr	ctt Leu	cct Pro 220	cgc Arg	ctt Leu	ggt Gly	gag Glu	ctg Leu	672
gct Ala 225	att Ile	ggt Gly	ggc Gly	acc Thr	gct Ala 230	gct Ala	ggt Gly	acc Thr	ggt Gly	atc Ile 235	aac Asn	acc Thr	tcc Ser	gct Ala	gat Asp 240	720
ttc Phe	ggc Gly	ggc Gly	aag Lys	gtt Val 245	gtt Val	gct Ala	gaa Glu	ctg Leu	atc Ile 250	aac Asn	ttg Leu	acc Thr	gac Asp	gtc Val 255	aag Lys	768
gag Glu	ctc Leu	aag Lys 260	gaa Glu	gct Ala	gag Glu	aac Asn	cac His 265	ttc Phe	gag Glu	gct Ala	cag Gln	gct Ala	gca Ala 270	cgc Arg	gac Asp	816
gct Ala	ctt Leu 275	gtt Val	gag Glu	ttc Phe	tcc Ser	ggc Gly	gca Ala 280	atg Met	cgc Arg	gtt Val	atc Ile 285	gct Ala	gtc Val	tcc Ser	ttg Leu	864
tac Tyr	aag Lys 290	atc Ile	gct Ala	aac Asn	gat Asp	atc Ile 295	cgc Arg	ctc Leu	atg Met	ggc Gly	tcc Ser 300	ggc Gly	cca Pro	ctg Leu	acc Thr	912
ggt Gly 305	ctt Leu	ggc Gly	gag Glu	atc Ile	cgt Arg 310	ctc Leu	cca Pro	gac Asp	ctg Leu	cag Gln 315	cca Pro	ggt Gly	tcc Ser	tcc Ser	atc Ile 320	960
atg Met	cca Pro	ggc Gly	aag Lys	gtc Val 325	aac Asn	cca Pro	gtt Val	ctc Leu	tgt Cys 330	gag Glu	acc Thr	gct Ala	acc Thr	cag Gln 335	gtt Val	1008
tcc Ser	gct Ala	cag Gln 340	gtt Ile	atc Ile	ggc Gly	aac Asn	gac Asp	gca Ala 345	gct Ala	gtt Val	gcg Ala	ttc Phe 350	tcc Ser	ggc Gly	acc Thr	1056
cag Gln	ggc Gly 355	cag Gln	ttc Phe	gag Glu	ctc Leu	aac Asn	gtg Val 360	ttc Phe	atc Ile	cca Pro	gtg Val 365	atg Met	gct Ala	cgc Arg	aac Asn	1104
gtg Val 370	ctt Leu	gag Glu	tcc Ser	gct Ala	cgc Arg	ctg Leu 375	ctg Ala	gct Asn	aac Asn	act Thr	tcc Ser 380	cgc Arg	gtg Val	ttc Phe	gca Ala	1152
acc Thr 385	cgt Arg	ctc Leu	gtt Val	gat Asp	ggc Gly 390	att Ile	gag Glu	cca Pro	aac Asn	gag Glu 395	gca Ala	cac His	atg Met	aag Lys	gag Glu 400	1200
ctc Leu	gct Ala	gag Glu	tct Ser	tca Ser 405	cct Pro	tcc Ser	atc Ile	gtt Val	acc Thr 410	cca Pro	ctg Leu	aac Asn	tct Ser	gca Ala 415	atc Ile	1248
ggc Gly	tac Tyr	gaa Glu 420	gct Ala	gct Ala	gca Ala	aag Lys	gtg Val 425	gct Lys	aag Lys	act Thr	gct Ala	ttg Leu 430	gct Ala	gag Glu	ggc Gly	1296
aag Lys	acc Thr 435	atc Ile	cgc Arg	cag Gln	act Thr	gtc Val	atc Ile 440	gat Asp	ttg Leu	ggc Gly	ttg Leu	gtt Val 445	gat Asp	ggc Gly	gag Glu	1344
aag Lys	ctc Leu 450	acc Thr	gag Glu	gaa Glu	gag Glu	ctg Leu 455	gac Asp	aag Lys	cgc Arg	ctc Leu	gac Asp 460	gtt Val	ctt Leu	gct Ala	atg Met	1392
gct Ala 465	cac His	acc Thr	gag Glu	cgc Arg	gag Glu 470	aac Asn	aag Lys	ttc Phe	taa							1422

PF59083SeqList PF59083.txt

<210> 9782
 <211> 473
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 9782
 Met Ser Asp Phe Met Thr Glu Gln Glu Phe Arg Ile Glu His Asp Thr
 1 5 10 15
 Met Gly Glu Val Lys Val Pro Ala Lys Ala Leu Trp Gln Ala Gln Thr
 20 25 30
 Gln Arg Ala Val Glu Asn Phe Pro Ile Ser Gly Arg Gly Leu Glu Ser
 35 40 45
 Ala Gln Ile Arg Ala Met Gly Leu Leu Lys Ala Ala Cys Ala Gln Val
 50 55 60
 Asn Lys Asp Ser Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile
 65 70 75 80
 Ala Ala Gly Lys Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro
 85 90 95
 Ile Asp Val Phe Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr
 100 105 110
 Asn Glu Val Ile Ala Ser Ile Ala Lys Ala Asn Gly Val Glu Val His
 115 120 125
 Pro Asn Asp His Val Asn Met Gly Gln Ser Ser Asn Asp Thr Phe Pro
 130 135 140
 Thr Ala Thr His Val Ala Thr Glu Ala Ala Val Asn Asp Leu Ile
 145 150 155 160
 Pro Gly Leu Lys Val Leu His Glu Ser Leu Ala Lys Lys Ala Asn Glu
 165 170 175
 Trp Ser Glu Val Val Lys Ser Gly Arg Thr His Leu Met Asp Ala Val
 180 185 190
 Pro Val Thr Leu Gly Gln Glu Phe Gly Gly Tyr Ala Arg Gln Ile Gln
 195 200 205
 Leu Gly Ile Glu Arg Val Glu Ala Thr Leu Pro Arg Leu Gly Glu Leu
 210 215 220
 Ala Ile Gly Gly Thr Ala Ala Gly Thr Gly Ile Asn Thr Ser Ala Asp
 225 230 235 240
 Phe Gly Gly Lys Val Val Ala Glu Leu Ile Asn Leu Thr Asp Val Lys
 245 250 255
 Glu Leu Lys Glu Ala Glu Asn His Phe Glu Ala Gln Ala Ala Arg Asp
 260 265 270
 Ala Leu Val Glu Phe Ser Gly Ala Met Arg Val Ile Ala Val Ser Leu
 275 280 285
 Tyr Lys Ile Ala Asn Asp Ile Arg Leu Met Gly Ser Gly Pro Leu Thr
 290 295 300
 Gly Leu Gly Glu Ile Arg Leu Pro Asp Leu Gln Pro Gly Ser Ser Ile
 305 310 315 320
 Met Pro Gly Lys Val Asn Pro Val Leu Cys Glu Thr Ala Thr Gln Val
 325 330 335
 Ser Ala Gln Val Ile Gly Asn Asp Ala Val Ala Phe Ser Gly Thr
 340 345 350
 Gln Gly Gln Phe Glu Leu Asn Val Phe Ile Pro Val Met Ala Arg Asn
 355 360 365
 Val Leu Glu Ser Ala Arg Leu Leu Ala Asn Thr Ser Arg Val Phe Ala
 370 375 380
 Thr Arg Leu Val Asp Gly Ile Glu Pro Asn Glu Ala His Met Lys Glu
 385 390 395 400
 Leu Ala Glu Ser Ser Pro Ser Ile Val Thr Pro Leu Asn Ser Ala Ile
 405 410 415
 Gly Tyr Glu Ala Ala Lys Val Ala Lys Thr Ala Leu Ala Glu Gly
 420 425 430
 Lys Thr Ile Arg Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu
 435 440 445
 Lys Leu Thr Glu Glu Glu Leu Asp Lys Arg Leu Asp Val Leu Ala Met
 450 455 460
 Ala His Thr Glu Arg Glu Asn Lys Phe
 465 470

<210> 9783

PF59083SeqList PF59083.txt

<211> 1404
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1404)
<223> transl_table=11

<400> 9783

atg aat aca gta cgc agc gaa aaa gat tcg atg ggg gcg att gat gtc	48
Met Asn Thr Val Arg Ser Glu Lys Asp Ser Met Gly Ala Ile Asp Val	
1 5 10 15	
ccg gca gat aag ctg tgg ggc gca caa act caa cgc tcg ctg gag cat	96
Pro Ala Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu Glu His	
20 25 30	
ttc cgc att tcg acg gag aaa atg ccc acc tca ctg att cat gcg ctg	144
Phe Arg Ile Ser Thr Glu Lys Met Pro Thr Ser Leu Ile His Ala Leu	
35 40 45	
gcg cta acc aag cgt gca gcg gca aaa gtt aat gaa gat tta ggc ttg	192
Ala Leu Thr Lys Arg Ala Ala Lys Val Asn Glu Asp Leu Gly Leu	
50 55 60	
ttg tct gaa gag aaa gcg agc gcc att cgt cag gcg gcg gat gaa gta	240
Leu Ser Glu Glu Lys Ala Ser Ala Ile Arg Gln Ala Ala Asp Glu Val	
65 70 75 80	
ctg gca gga cag cat gac gac gaa ttc ccg ctg gct atc tgg cag acc	288
Leu Ala Gly Gln His Asp Asp Glu Phe Pro Leu Ala Ile Trp Gln Thr	
85 90 95	
ggc tcc ggc acg caa agt aac atg aac atg aac gaa gtg ctg gct aac	336
Gly Ser Gly Thr Gln Ser Asn Met Asn Met Asn Glu Val Leu Ala Asn	
100 105 110	
cgg gcc agt gaa tta ctc ggc ggt gtg cgc ggg atg gaa cgt aaa gtt	384
Arg Ala Ser Glu Leu Leu Gly Gly Val Arg Gly Met Glu Arg Lys Val	
115 120 125	
cac cct aac gac gac gtg aac aaa agc caa agt tcc aac gat gtc ttt	432
His Pro Asn Asp Asp Val Asn Lys Ser Gln Ser Ser Asn Asp Val Phe	
130 135 140	
ccg acg gcg atg cac gtt gcg gcg ctg ctg gcg ctg cgc aag caa ctc	480
Pro Thr Ala Met His Val Ala Ala Leu Leu Ala Leu Arg Lys Gln Leu	
145 150 155	
att cct cag ctt aaa acc ctg aca cag aca ctg aat gag aaa tcc cgt	528
Ile Pro Gln Leu Lys Thr Leu Thr Gln Thr Leu Asn Glu Lys Ser Arg	
160 165 170 175	
gct ttt gcc gat atc gtc aaa att ggt cgt act cac ttg cag gat gcc	576
Ala Phe Ala Asp Ile Val Lys Ile Gly Arg Thr His Leu Gln Asp Ala	
180 185 190	
acg ccg tta acg ctg ggg cag gag att tcc ggc tgg gta gcg atg ctc	624
Thr Pro Leu Thr Leu Gly Gln Glu Ile Ser Gly Trp Val Ala Met Leu	
195 200 205	
gag cat aat ctc aaa cat atc gaa tac agc ctg cct cac gta gcg gaa	672
Glu His Asn Leu Lys His Ile Glu Tyr Ser Leu Pro His Val Ala Glu	
210 215 220	
ctg gct ctt ggc ggt aca gcg gtg ggt act gga cta aat acc cat ccg	720
Leu Ala Leu Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr His Pro	
225 230 235 240	
gag tat gcg cgt cgc gta gca gat gaa ctg gca gtc att acc tgt gca	768
Glu Tyr Ala Arg Arg Val Ala Asp Glu Leu Ala Val Ile Thr Cys Ala	
245 250 255	
ccg ttt gtt acc gcg ccg aac aaa ttt gaa gcg ctg gcg acc tgt gat	816
Pro Phe Val Thr Ala Pro Asn Lys Phe Glu Ala Leu Ala Thr Cys Asp	
260 265 270	
gcc ctg gtt cag gcg cac ggc gcg ttg aaa ggg ttg gct gcg tca ctg	864
Ala Leu Val Gln Ala His Gly Ala Leu Lys Gly Leu Ala Ala Ser Leu	
275 280 285	
atg aaa atc gcc aat gat gtc cgc tgg ctg gcc tct ggc ccg cgc tgc	912
Met Lys Ile Ala Asn Asp Val Arg Trp Leu Ala Ser Gly Pro Arg Cys	
290 295 300	
gga att ggt gaa atc tca atc ccg gaa aat gag ccg ggc agc tca atc	960
Gly Ile Gly Glu Ile Ser Ile Pro Glu Asn Glu Pro Gly Ser Ser Ile	

PF59083SeqList PF59083.txt

305					310					315					320	
atg	ccg	ggg	aaa	gtg	aac	cca	aca	cag	tgt	gag	gca	tta	acc	atg	ctc	1008
Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Leu	
				325					330					335		
tgc	tgt	cag	gtg	atg	ggg	aac	gac	gtg	gcg	atc	aac	atg	ggg	ggc	gct	1056
Cys	Cys	Gln	Val	Met	Gly	Asn	Asp	Val	Ala	Ile	Asn	Met	Gly	Gly	Ala	
			340					345					350			
tcc	ggt	aac	ttt	gaa	ctg	aac	gtc	ttc	cgt	cca	atg	gtg	atc	cac	aat	1104
Ser	Gly	Asn	Phe	Glu	Leu	Asn	Val	Phe	Arg	Pro	Met	Val	Ile	His	Asn	
		355					360					365				
ttc	ctg	caa	tcg	gtg	cgc	ttg	ctg	gca	gat	ggc	atg	gaa	agt	ttt	aac	1152
Phe	Leu	Gln	Ser	Val	Arg	Leu	Leu	Ala	Asp	Gly	Met	Glu	Ser	Phe	Asn	
	370					375					380					
aaa	cac	tgc	gca	gtg	ggt	att	gaa	ccg	aat	cgt	gag	cga	atc	aat	caa	1200
Lys	His	Cys	Ala	Val	Gly	Ile	Glu	Pro	Asn	Arg	Glu	Arg	Ile	Asn	Gln	
	385				390					395					400	
tta	ctc	aat	gaa	tcg	ctg	atg	ctg	gtg	act	gcg	ctt	aac	acc	cac	att	1248
Leu	Leu	Asn	Glu	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Thr	His	Ile	
			405					410						415		
ggt	tat	gac	aaa	gcc	gac	gag	atc	gcc	aaa	aaa	gcg	cat	aaa	gaa	ggg	1296
Gly	Tyr	Asp	Lys	Ala	Ala	Glu	Ile	Ala	Lys	Lys	Ala	His	Lys	Glu	Gly	
			420					425					430			
ctg	acc	tta	aaa	gct	gcg	gcc	ctt	gcg	ctg	ggg	tat	ctt	agc	gaa	gcc	1344
Leu	Thr	Leu	Lys	Ala	Ala	Ala	Leu	Ala	Leu	Gly	Tyr	Leu	Ser	Glu	Ala	
		435					440					445				
gag	ttt	gac	agc	tgg	gta	cgg	cca	gaa	cag	atg	gtc	ggc	agt	atg	aaa	1392
Glu	Phe	Asp	Ser	Trp	Val	Arg	Pro	Glu	Gln	Met	Val	Gly	Ser	Met	Lys	
	450					455					460					
gcc	ggg	cgt	taa													1404
Ala	Gly	Arg														
465																

<210> 9784

<211> 467

<212> PRT

<213> Escherichia coli

<400> 9784

Met	Asn	Thr	Val	Arg	Ser	Glu	Lys	Asp	Ser	Met	Gly	Ala	Ile	Asp	Val
1				5					10					15	
Pro	Ala	Asp	Lys	Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Glu	His
			20					25					30		
Phe	Arg	Ile	Ser	Thr	Glu	Lys	Met	Pro	Thr	Ser	Leu	Ile	His	Ala	Leu
		35					40					45			
Ala	Leu	Thr	Lys	Arg	Ala	Ala	Lys	Val	Asn	Glu	Asp	Leu	Gly	Leu	
	50					55				60					
Leu	Ser	Glu	Glu	Lys	Ala	Ser	Ala	Ile	Arg	Gln	Ala	Ala	Asp	Glu	Val
65					70				75					80	
Leu	Ala	Gly	Gln	His	Asp	Asp	Glu	Phe	Pro	Leu	Ala	Ile	Trp	Gln	Thr
			85					90					95		
Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Met	Asn	Glu	Val	Leu	Ala	Asn
			100					105					110		
Arg	Ala	Ser	Glu	Leu	Leu	Gly	Gly	Val	Arg	Gly	Met	Glu	Arg	Lys	Val
		115				120					125				
His	Pro	Asn	Asp	Asp	Val	Asn	Lys	Ser	Gln	Ser	Ser	Asn	Asp	Val	Phe
	130					135					140				
Pro	Thr	Ala	Met	His	Val	Ala	Ala	Leu	Leu	Ala	Leu	Arg	Lys	Gln	Leu
145					150					155				160	
Ile	Pro	Gln	Leu	Lys	Thr	Leu	Thr	Gln	Thr	Leu	Asn	Glu	Lys	Ser	Arg
			165					170					175		
Ala	Phe	Ala	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala
		180						185					190		
Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Ile	Ser	Gly	Trp	Val	Ala	Met	Leu
		195					200					205			
Glu	His	Asn	Leu	Lys	His	Ile	Glu	Tyr	Ser	Leu	Pro	His	Val	Ala	Glu
	210					215					220				
Leu	Ala	Leu	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	His	Pro
225					230			235						240	
Glu	Tyr	Ala	Arg	Arg	Val	Ala	Asp	Glu	Leu	Ala	Val	Ile	Thr	Cys	Ala

PF59083SeqList PF59083.txt

```

                245                250                255
Pro Phe Val Thr Ala Pro Asn Lys Phe Glu Ala Leu Ala Thr Cys Asp
Ala Leu Val Gln Ala His Gly Ala Leu Lys Gly Leu Ala Ala Ser Leu
Met Lys 275 Ala Asn Asp Val 280 Trp Leu Ala Ser 285 Gly Pro Arg Cys
Gly Ile Gly Glu Ile Ser Ile Pro Glu Asn Glu Pro Gly Ser Ser Ile
305 Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Leu
Cys Cys Gln Val Met Gly Asn Asp Val Ala Ile Asn Met Gly Gly Ala
Ser Gly Asn Phe Glu Leu Asn Val Phe Arg Pro Met Val Ile His Asn
Phe Leu 370 Gln Ser Val Arg Leu 375 Leu Ala Asp Gly Met 380 Glu Ser Phe Asn
Lys His Cys Ala Val Gly Ile Glu Pro Asn Arg Glu Arg Ile Asn Gln
385 Leu Leu Asn Glu Ser 405 Leu Met Leu Val Thr 410 Ala Leu Asn Thr His Ile
Gly Tyr Asp Lys Ala Ala Glu Ile Ala Lys Lys Ala His Lys Glu Gly
Leu Thr Leu Lys Ala Ala Ala Leu 440 Ala Leu Gly Tyr Leu Ser Glu Ala
Glu Phe 450 Asp Ser Trp Val Arg 455 Pro Glu Gln Met Val 460 Gly Ser Met Lys
Ala Gly Arg
465

```

<210> 9785

<211> 1413

<212> DNA

<213> Halobacterium salinarium

<220>

<221> CDS

<222> (1)..(1413)

<223> transl_table=11

<400> 9785

```

atg agc gag gat tac cgc acg gag cag gac agc ctc ggc gag atg cag      48
Met Ser Glu Asp Tyr Arg Thr Glu Gln Asp Ser Leu Gly Glu Met Gln
1 5 10 15
gtt ccc gct gac gcc tac tgg ggg gca cag acc cag cgc gcg atc gag      96
Val Pro Ala Asp Ala Tyr Trp Gly Ala Gln Thr Gln Arg Ala Ile Glu
20 25 30
aac ttc ccg atc tcg ggg atc gcg ttc ggg cgg cgg ttc gtg cgc gcg      144
Asn Phe Pro Ile Ser Gly Ile Ala Phe Gly Arg Arg Phe Val Arg Ala
35 40 45
ctc ggc gtc gtc aag aag gcc gcc gcg cag gcg aac cgc gac ctc ggc      192
Leu Gly Val Val Lys Lys Ala Ala Ala Gln Ala Asn Arg Asp Leu Gly
50 55 60
ctc gtt gac gac gag cgc gcc gac gcc atc gtc gcg gcc gcc gac gag      240
Leu Val Asp Asp Glu Arg Ala Asp Ala Ile Val Ala Ala Asp Glu
65 70 75 80
gtc atc gcc ggc gag cac gac gac cag ttc ccg gtc gac gtc ttc cag      288
Val Ile Ala Gly Glu His Asp Asp Gln Phe Pro Val Asp Val Phe Gln
85 90 95
acc ggg tcc ggg acg tcc tcg aac atg aac gag gtc atc gcg      336
Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Ala Asn Glu Val Ile Ala
100 105 110
aac cgc gcc gcg gag ctc ctc ggc gag gag atc ggg gat cgc gtc gtg      384
Asn Arg Ala Ala Glu Leu Leu Gly Glu Glu Ile Gly Asp Arg Val Val
115 120 125
cac ccc aac gac cac gtg aac tat ggc cag tcc agc aac gac gtg atc      432
His Pro Asn Asp His Val Asn Tyr Gly Gln Ser Ser Asn Asp Val Ile
130 135 140
ccg acc gcg atg cac gtg gcg agc ctc gac gcg ctc gtc aac gac gtc      480

```

PF59083SeqList PF59083.txt

Pro 145	Thr	Ala	Met	His	Val 150	Ala	Ser	Leu	Asp	Ala 155	Leu	Val	Asn	Asp	Val 160	
aaa	ccc	ggc	ctg	gag	acg	ctg	gca	gcg	gaa	ctc	gac	gac	aaa	gcg	gac	528
Lys	Pro	Gly	Leu	Glu	Thr	Leu	Ala	Ala	Glu	Leu	Asp	Asp	Lys	Ala	Asp	
			165						170							
gcg	ttc	gac	ggc	gtc	gtg	aag	acc	ggg	cg	acg	cac	ttg	cag	gac	gac	576
Ala	Phe	Asp	Gly	Val	Val	Lys	Thr	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	
			180					185					190			
acg	ccg	gtg	cgg	ttg	ggc	cag	gag	ttc	ggc	ggc	tac	cg	acc	caa	gtc	624
Thr	Pro	Val	Arg	Leu	Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Arg	Thr	Gln	Val	
			195					200				205				
gag	aag	ggc	atc	gac	cg	atc	gag	gcc	gtt	gcc	ccg	cg	ctc	tcg	gag	672
Glu	Lys	Gly	Ile	Asp	Arg	Ile	Glu	Ala	Val	Ala	Pro	Arg	Leu	Ser	Glu	
			210			215					220					
ctc	gcg	ctc	ggc	ggc	acc	gcc	gtc	ggc	acc	ggg	ctg	aac	acc	cac	ccc	720
Leu	Ala	Leu	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	His	Pro	
225					230					235					240	
gag	ttc	ccg	gag	acg	gcg	gcc	ggc	tac	atc	agc	gag	gag	acc	ggc	gtt	768
Glu	Phe	Pro	Glu	Thr	Ala	Ala	Gly	Tyr	Ile	Ser	Glu	Glu	Thr	Gly	Val	
				245				250						255		
acg	ttc	cgt	gag	gcg	gac	aac	cac	ttc	gag	gcg	cag	gcc	gcc	cac	gac	816
Thr	Phe	Arg	Glu	Ala	Asp	Asn	His	Phe	Glu	Ala	Gln	Ala	Ala	His	Asp	
			260					265				270				
gcc	atg	aac	gag	gcc	cac	ggc	gcg	ctg	cg	acg	gtc	gcg	ggg	tcg	ctg	864
Ala	Met	Asn	Glu	Ala	His	Gly	Ala	Leu	Arg	Thr	Val	Ala	Gly	Ser	Leu	
			275			280						285				
aac	aag	atc	gcc	aac	gac	ctc	cg	ctg	ctt	gcc	tcc	ggc	ccc	cg	aac	912
Asn	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Leu	Leu	Ala	Ser	Gly	Pro	Arg	Asn	
			290			295					300					
ggg	ctg	ggg	gag	atc	gag	ccc	gag	aac	cag	ccc	ggc	tcc	tcg	atc		960
Gly	Leu	Gly	Glu	Ile	Glu	Gln	Pro	Glu	Asn	Gln	Pro	Gly	Ser	Ser	Ile	
305				310					315						320	
atg	ccc	ggg	aag	atc	aac	ccc	gtg	gtg	gcg	gag	gcg	gtc	aac	cag	gtc	1008
Met	Pro	Gly	Lys	Ile	Asn	Pro	Val	Val	Ala	Glu	Ala	Val	Asn	Gln	Val	
				325				330						335		
cac	aag	cag	gtc	gtg	ggc	aac	gac	gcc	gcc	atc	gcc	gcg	ggg	gcc	gcg	1056
His	Lys	Gln	Val	Val	Gly	Asn	Asp	Ala	Ala	Ile	Ala	Ala	Gly	Ala	Ala	
			340					345				350				
gag	ggg	cag	atc	gac	ttg	aac	ctc	tac	aag	ccc	gtg	ctg	gcg	cac	aac	1104
Glu	Gly	Gln	Ile	Asp	Leu	Asn	Leu	Tyr	Lys	Pro	Val	Leu	Ala	His	Asn	
			355				360					365				
ttc	ctg	cag	tcc	gcg	gac	atg	ctc	gcc	aac	gcg	agc	gct	gcc	ttc	ggc	1152
Phe	Leu	Gln	Ser	Ala	Asp	Met	Leu	Ala	Asn	Ala	Ser	Ala	Ala	Phe	Gly	
			370			375					380					
gag	aag	ttc	gtc	gcc	aag	ctc	gaa	gcc	aac	gag	gcc	gcc	tgc	gag	gcg	1200
Glu	Lys	Phe	Val	Ala	Lys	Leu	Glu	Ala	Asn	Glu	Ala	Ala	Cys	Glu	Ala	
				390						395					400	
cag	gtc	gag	cg	tcg	atg	gcg	ctg	gcg	acc	gcg	ctc	aac	ccc	acg	atc	1248
Gln	Val	Glu	Arg	Ser	Met	Ala	Leu	Ala	Thr	Ala	Leu	Asn	Pro	Thr	Ile	
				405				410						415		
ggc	tac	gac	aag	gcc	agc	gag	gtc	gcg	aag	gcc	gcg	ctg	aag	gag	ggg	1296
Gly	Tyr	Asp	Lys	Ala	Ser	Glu	Val	Ala	Lys	Ala	Ala	Leu	Lys	Glu	Gly	
			420				425						430			
aaa	aca	gtc	acg	gag	gtc	gtc	gtc	gag	aag	gga	tac	ctc	tcg	gag	gcg	1344
Lys	Thr	Val	Thr	Glu	Val	Val	Val	Glu	Lys	Gly	Tyr	Leu	Ser	Glu	Ala	
			435			440						445				
gag	gcc	gct	gac	gtg	ctc	gac	ccc	gag	ggg	atg	acc	cac	cg	ggc	atc	1392
Glu	Ala	Ala	Asp	Val	Leu	Asp	Pro	Glu	Gly	Met	Thr	His	Arg	Gly	Ile	
			450			455					460					
ctc	tcc	ggc	gac	gac	acg											1413
Leu	Ser	Gly	Asp	Asp	Thr	tag										
465					470											

<210> 9786

<211> 470

<212> PRT

<213> Halobacterium salinarium

<400> 9786

PF59083SeqList PF59083.txt

```

Met Ser Glu Asp Tyr Arg Thr Glu Gln Asp Ser Leu Gly Glu Met Gln
1      5      10      15
Val Pro Ala Asp Ala Tyr Trp Gly Ala Gln Thr Gln Arg Ala Ile Glu
      20      25      30
Asn Phe Pro Ile Ser Gly Ile Ala Phe Gly Arg Arg Phe Val Arg Ala
      35      40      45
Leu Gly Val Val Lys Lys Ala Ala Ala Gln Ala Asn Arg Asp Leu Gly
      50      55      60
Leu Val Asp Asp Glu Arg Ala Asp Ala Ile Val Ala Ala Ala Asp Glu
65      70      75      80
Val Ile Ala Gly Glu His Asp Asp Gln Phe Pro Val Asp Val Phe Gln
      85      90      95
Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Ala Asn Glu Val Ile Ala
      100      105      110
Asn Arg Ala Glu Leu Leu Gly Glu Glu Ile Gly Asp Arg Val Val
      115      120      125
His Pro Asn Asp His Val Asn Tyr Gly Gln Ser Ser Asn Asp Val Ile
      130      135      140
Pro Thr Ala Met His Val Ala Ser Leu Asp Ala Leu Val Asn Asp Val
145      150      155      160
Lys Pro Gly Leu Glu Thr Leu Ala Ala Glu Leu Asp Asp Lys Ala Asp
      165      170      175
Ala Phe Asp Gly Val Val Lys Thr Gly Arg Thr His Leu Gln Asp Ala
      180      185      190
Thr Pro Val Arg Leu Gly Gln Glu Phe Gly Gly Tyr Arg Thr Gln Val
      195      200      205
Glu Lys Gly Ile Asp Arg Ile Glu Ala Val Ala Pro Arg Leu Ser Glu
      210      215      220
Leu Ala Leu Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr His Pro
225      230      235      240
Glu Phe Pro Glu Thr Ala Ala Gly Tyr Ile Ser Glu Glu Thr Gly Val
      245      250      255
Thr Phe Arg Glu Ala Asp Asn His Phe Glu Ala Gln Ala Ala His Asp
      260      265      270
Ala Met Asn Glu Ala His Gly Ala Leu Arg Thr Val Ala Gly Ser Leu
      275      280      285
Asn Lys Ile Ala Asn Asp Leu Arg Leu Leu Ala Ser Gly Pro Arg Asn
      290      295      300
Gly Leu Gly Glu Ile Glu Gln Pro Glu Asn Gln Pro Gly Ser Ser Ile
305      310      315      320
Met Pro Gly Lys Ile Asn Pro Val Val Ala Glu Ala Val Asn Gln Val
      325      330      335
His Lys Gln Val Val Gly Asn Asp Ala Ala Ile Ala Ala Gly Ala Ala
      340      345      350
Glu Gly Gln Ile Asp Leu Asn Leu Tyr Lys Pro Val Leu Ala His Asn
      355      360      365
Phe Leu Gln Ser Ala Asp Met Leu Ala Asn Ala Ser Ala Ala Phe Gly
      370      375      380
Glu Lys Phe Val Ala Lys Leu Glu Ala Asn Glu Ala Ala Cys Glu Ala
385      390      395      400
Gln Val Glu Arg Ser Met Ala Leu Ala Thr Ala Leu Asn Pro Thr Ile
      405      410      415
Gly Tyr Asp Lys Ala Ser Glu Val Ala Lys Ala Ala Leu Lys Glu Gly
      420      425      430
Lys Thr Val Thr Glu Val Val Val Glu Lys Gly Tyr Leu Ser Glu Ala
      435      440      445
Glu Ala Ala Asp Val Leu Asp Pro Glu Gly Met Thr His Arg Gly Ile
      450      455      460
Leu Ser Gly Asp Asp Thr
465      470

```

<210> 9787

<211> 1419

<212> DNA

<213> Methylobacterium extorquens

<220>

<221> CDS

<222> (1)..(1419)

<223> transl_table=11

<400> 9787

atg	tcg	ccg	cac	gag	aac	cct	tcc	gtc	gag	acg	cgt	acc	gag	tcc	gac	48
Met	Ser	Pro	His	Glu	Asn	Pro	Ser	Val	Glu	Thr	Arg	Thr	Glu	Ser	Asp	
1				5					10					15		
acc	ttc	ggc	ccg	atc	gaa	gtg	ccc	gcc	cac	cgc	tac	tgg	ggc	gcc	cag	96
Thr	Phe	Gly	Pro	Ile	Glu	Val	Pro	Ala	His	Arg	Tyr	Trp	Gly	Ala	Gln	
			20					25					30			
acg	cag	cgc	tcg	atc	cag	aac	ttc	aag	atc	ggc	acc	gag	cgc	cag	ccg	144
Thr	Gln	Arg	Ser	Ile	Gln	Asn	Phe	Lys	Ile	Gly	Thr	Glu	Arg	Gln	Pro	
			35				40					45				
gcg	ccg	ctc	gtc	cat	gcg	ctc	ggc	atc	gtc	aag	cag	gcc	gcc	gcg	ctg	192
Ala	Pro	Leu	Val	His	Ala	Leu	Gly	Ile	Val	Lys	Gln	Ala	Ala	Ala	Leu	
	50					55					60					
gtg	aac	aag	gat	ctc	ggc	ggc	ctc	gat	ccg	aag	atc	gcc	gac	gcg	atc	240
Val	Asn	Lys	Asp	Leu	Gly	Gly	Leu	Asp	Pro	Lys	Ile	Ala	Asp	Ala	Ile	
	65				70					75					80	
gcc	gaa	tcc	gct	gcc	gaa	gtg	gtc	gcc	gga	aag	cac	gac	gac	gag	ttc	288
Ala	Glu	Ser	Ala	Ala	Glu	Val	Val	Ala	Gly	Lys	His	Asp	Asp	Glu	Phe	
				85					90					95		
ccg	ctg	gtg	gtg	tgg	cag	acg	ggc	tcg	ggc	acg	cag	tcc	aac	atg	aac	336
Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	
			100				105					110				
gcc	aac	gag	gtg	atc	gcg	agc	ctc	gca	aac	gag	cgg	ctc	ggg	ggc	aag	384
Ala	Asn	Glu	Val	Ile	Ala	Ser	Leu	Ala	Asn	Glu	Arg	Leu	Gly	Gly	Lys	
		115				120						125				
cgc	ggc	ggc	aag	tcg	ccg	gtc	cac	ccc	aac	gat	cat	tgc	aac	cgc	ggc	432
Arg	Gly	Gly	Lys	Ser	Pro	Val	His	Pro	Asn	Asp	His	Cys	Asn	Arg	Gly	
	130					135					140					
cag	tcc	tcg	aac	gac	acc	ttc	ccc	acc	gcc	atg	cac	atc	gcg	gtc	gcc	480
Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Met	His	Ile	Ala	Val	Ala	
	145				150				155						160	
cgc	gag	gtt	cag	gag	cgg	ctg	ctg	ccg	gcg	ctc	tcc	cac	ctg	cac	acc	528
Arg	Glu	Val	Gln	Glu	Arg	Leu	Leu	Pro	Ala	Leu	Ser	His	Leu	His	Thr	
			165						170					175		
gcg	ctc	gat	gcc	aag	gcg	aag	gag	ttc	gag	agc	atc	gtc	aag	atc	ggc	576
Ala	Leu	Asp	Ala	Lys	Ala	Lys	Glu	Phe	Glu	Ser	Ile	Val	Lys	Ile	Gly	
			180				185						190			
cgc	acg	cac	ttg	cag	gat	gcg	acg	ccg	gtc	tcg	ctc	ggc	cag	gaa	ttc	624
Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	Val	Ser	Leu	Gly	Gln	Glu	Phe	
		195				200						205				
tcc	ggt	tac	gcc	gcg	cag	gtc	gcg	ctc	ggt	ggc	gcg	cgc	atc	gcc	gcc	672
Ser	Gly	Tyr	Ala	Ala	Gln	Val	Ala	Leu	Gly	Gly	Ala	Arg	Ile	Ala	Ala	
	210				215						220					
acg	ctc	ccc	ggc	gtg	ctg	gcg	ctg	gcg	cag	ggc	ggc	acc	gcc	gtc	ggc	720
Thr	Leu	Pro	Gly	Val	Leu	Ala	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	
	225				230				235						240	
acc	ggc	ctc	aat	gcg	cat	ccg	gaa	ttc	gcg	gag	cgg	ttt	gcg	gcc	aag	768
Thr	Gly	Leu	Asn	Ala	His	Pro	Glu	Phe	Ala	Glu	Arg	Phe	Ala	Ala	Lys	
			245					250						255		
gtc	gcg	gag	ctg	acc	ggg	ctg	ccc	ttt	acc	tcg	gcc	gag	aac	aag	ttc	816
Val	Ala	Glu	Leu	Thr	Gly	Leu	Pro	Phe	Thr	Ser	Ala	Glu	Asn	Lys	Phe	
			260				265						270			
gag	gcg	ctg	gcc	acc	cac	gac	gcc	ctc	gtc	ttc	ctt	cag	ggc	gcg	ctg	864
Glu	Ala	Leu	Ala	Thr	His	Asp	Ala	Leu	Val	Phe	Leu	Gln	Gly	Ala	Leu	
		275				280						285				
acg	gct	ttg	gca	tcg	ggc	ctc	ttc	aag	atc	gcc	aac	gac	atc	cgc	ctg	912
Thr	Ala	Leu	Ala	Ser	Gly	Leu	Phe	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	
	290					295					300					
ctc	ggc	tcc	ggc	ccg	cgc	tcg	ggc	ctc	ggc	gaa	ttg	tcg	ctg	ccg	gag	960
Leu	Gly	Ser	Gly	Pro	Arg	Ser	Gly	Leu	Gly	Glu	Leu	Ser	Leu	Pro	Glu	
	305				310				315						320	
aac	gag	ccc	ggc	tcg	atc	atg	ccg	ggc	aag	gtc	aac	ccg	acc	cag		1008
Asn	Glu	Pro	Gly	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln		
				325				330					335			
tgc	gag	gcg	ctg	acg	atg	gtc	tgc	gcg	cag	gtg	gtc	ggc	aac	ggc	acc	1056
Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	Gln	Val	Val	Gly	Asn	Gly	Thr	
			340					345					350			

PF59083SeqList PF59083.txt

acg	gtg	agc	ttt	gcc	ggc	tca	cag	ggg	cat	ttc	gag	ctc	aac	gtg	ttc	1104
Thr	Val	Ser	Phe	Ala	Gly	Ser	Gln	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	
		355					360					365				
aag	ccg	gtg	atc	gcc	aac	gcg	gtg	ctg	caa	tcg	gtg	cgg	att	ctg	gcc	1152
Lys	Pro	Val	Ile	Ala	Asn	Ala	Val	Leu	Gln	Ser	Val	Arg	Ile	Leu	Ala	
	370					375					380					
gac	gcc	tca	gtc	agc	ttc	acc	gac	aat	tgc	gtc	gtc	ggc	atc	aag	gcc	1200
Asp	Ala	Ser	Val	Ser	Phe	Thr	Asp	Asn	Cys	Val	Val	Gly	Ile	Lys	Ala	
385					390					395					400	
aac	acc	gac	cgg	atc	agc	gac	ctg	atg	agc	cgc	tcg	ctc	atg	ctg	gtg	1248
Asn	Thr	Asp	Arg	Ile	Ser	Asp	Leu	Met	Ser	Arg	Ser	Leu	Met	Leu	Val	
			405					410						415		
acc	gcg	ctc	gcg	ccc	tcg	atc	ggc	tac	gac	aag	gcc	gcc	gag	atc	gcc	1296
Thr	Ala	Leu	Ala	Pro	Ser	Ile	Gly	Tyr	Asp	Lys	Ala	Ala	Glu	Ile	Ala	
			420					425					430			
aag	acc	gcg	cac	aag	aac	ggc	acc	acc	ctg	aag	gaa	gag	gcg	ctg	cgg	1344
Lys	Thr	Ala	His	Lys	Asn	Gly	Thr	Thr	Leu	Lys	Glu	Glu	Ala	Leu	Arg	
		435				440						445				
ctc	ggc	tac	gtc	acg	gac	gag	gag	ttc	gag	cgg	gtc	gta	cgc	ccc	gaa	1392
Leu	Gly	Tyr	Val	Thr	Asp	Glu	Glu	Phe	Glu	Arg	Val	Val	Arg	Pro	Glu	
	450					455					460					
acc	atg	ctg	gcg	ccg	agc	gcg	gaa	taa								1419
Thr	Met	Leu	Ala	Pro	Ser	Ala	Glu									
465					470											

<210> 9788

<211> 472

<212> PRT

<213> Methylobacterium extorquens

<400> 9788

Met	Ser	Pro	His	Glu	Asn	Pro	Ser	Val	Glu	Thr	Arg	Thr	Glu	Ser	Asp	
1				5					10					15		
Thr	Phe	Gly	Pro	Ile	Glu	Val	Pro	Ala	His	Arg	Tyr	Trp	Gly	Ala	Gln	
			20					25					30			
Thr	Gln	Arg	Ser	Ile	Gln	Asn	Phe	Lys	Ile	Gly	Thr	Glu	Arg	Gln	Pro	
		35				40						45				
Ala	Pro	Leu	Val	His	Ala	Leu	Gly	Ile	Val	Lys	Gln	Ala	Ala	Ala	Leu	
	50					55					60					
Val	Asn	Lys	Asp	Leu	Gly	Leu	Asp	Pro	Lys	Ile	Ala	Asp	Ala	Ile		
65					70				75					80		
Ala	Glu	Ser	Ala	Ala	Glu	Val	Val	Ala	Gly	Lys	His	Asp	Asp	Glu	Phe	
			85					90						95		
Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	
			100					105					110			
Ala	Asn	Glu	Val	Ile	Ala	Ser	Leu	Ala	Asn	Glu	Arg	Leu	Gly	Gly	Lys	
		115				120						125				
Arg	Gly	Gly	Lys	Ser	Pro	Val	His	Pro	Asn	Asp	His	Cys	Asn	Arg	Gly	
	130					135				140						
Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Met	His	Ile	Ala	Val	Ala	
145					150					155					160	
Arg	Glu	Val	Gln	Glu	Arg	Leu	Leu	Pro	Ala	Leu	Ser	His	Leu	His	Thr	
			165					170						175		
Ala	Leu	Asp	Ala	Lys	Ala	Lys	Glu	Phe	Glu	Ser	Ile	Val	Lys	Ile	Gly	
		180						185					190			
Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	Val	Ser	Leu	Gly	Gln	Glu	Phe	
		195				200						205				
Ser	Gly	Tyr	Ala	Ala	Gln	Val	Ala	Leu	Gly	Gly	Ala	Arg	Ile	Ala	Ala	
	210				215						220					
Thr	Leu	Pro	Gly	Val	Leu	Ala	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	
225					230					235					240	
Thr	Gly	Leu	Asn	Ala	His	Pro	Glu	Phe	Ala	Glu	Arg	Phe	Ala	Ala	Lys	
			245					250						255		
Val	Ala	Glu	Leu	Thr	Gly	Leu	Pro	Phe	Thr	Ser	Ala	Glu	Asn	Lys	Phe	
		260						265					270			
Glu	Ala	Leu	Ala	Thr	His	Asp	Ala	Leu	Val	Phe	Leu	Gln	Gly	Ala	Leu	
		275				280						285				
Thr	Ala	Leu	Ala	Ser	Gly	Leu	Phe	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	
	290					295					300					

PF59083SeqList PF59083.txt

Leu Gly Ser Gly Pro Arg Ser Gly Leu Gly Glu Leu Ser Leu Pro Glu
 305 310 315 320
 Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Thr Gln
 325 330 335
 Cys Glu Ala Leu Thr Met Val Cys Ala Gln Val Val Gly Asn Gly Thr
 340 345 350
 Thr Val Ser Phe Ala Gly Ser Gln Gly His Phe Glu Leu Asn Val Phe
 355 360 365
 Lys Pro Val Ile Ala Asn Ala Val Leu Gln Ser Val Arg Ile Leu Ala
 370 375 380
 Asp Ala Ser Val Ser Phe Thr Asp Asn Cys Val Val Gly Ile Lys Ala
 385 390 395 400
 Asn Thr Asp Arg Ile Ser Asp Leu Met Ser Arg Ser Leu Met Leu Val
 405 410 415
 Thr Ala Leu Ala Pro Ser Ile Gly Tyr Asp Lys Ala Ala Glu Ile Ala
 420 425 430
 Lys Thr Ala His Lys Asn Gly Thr Thr Leu Lys Glu Glu Ala Leu Arg
 435 440 445
 Leu Gly Tyr Val Thr Asp Glu Glu Phe Glu Arg Val Val Arg Pro Glu
 450 455 460
 Thr Met Leu Ala Pro Ser Ala Glu
 465 470

<210> 9789

<211> 1395

<212> DNA

<213> Pseudomonas putida

<220>

<221> CDS

<222> (1)..(1395)

<223> transl_table=11

<400> 9789

atg agc cgt atc gag aca gac agc ctg ggc ccg gtc gaa gtt ccg gag	48
Met Ser Arg Ile Glu Thr Asp Ser Leu Gly Pro Val Glu Val Pro Glu	
1 5 10 15	
gac gcc tac tgg ggt gcg cag acc cag cgt tcg ctg atc aac ttc gcc	96
Asp Ala Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Ile Asn Phe Ala	
20 25 30	
att ggc aag gaa cgc atg ccc ctc gcg gta ttg cac gcc ctg gca ctg	144
Ile Gly Lys Glu Arg Met Pro Leu Ala Val Leu His Ala Leu Ala Leu	
35 40 45	
atc aag aag gcc gcg gcg cgc gtc aac gac cgc aat ggc gac ctg ccg	192
Ile Lys Lys Ala Ala Ala Arg Val Asn Asp Arg Asn Gly Asp Leu Pro	
50 55 60	
gcc gac atc gcc cgg ttg atc gaa cag gcc gcc gat gaa gtg ctg gat	240
Ala Asp Ile Ala Arg Leu Ile Glu Gln Ala Ala Asp Glu Val Leu Asp	
65 70 75 80	
ggc cag cac gac gat cag ttc ccg ctc gtc gtc tgg cag acg ggc agt	288
Gly Gln His Asp Asp Gln Phe Pro Leu Val Val Trp Gln Thr Gly Ser	
85 90 95	
ggc acc caa agc aac atg aac gtc aac gag gtg atc gcc gga cgc gcc	336
Gly Thr Gln Ser Asn Met Asn Val Asn Glu Val Ile Ala Gly Arg Ala	
100 105 110	
aac gaa ctg gcc ggc aaa ggc cgt ggc ggc aag gcg cca gta cac ccc	384
Asn Glu Leu Ala Gly Lys Gly Arg Gly Gly Lys Ala Pro Val His Pro	
115 120 125	
aat gac cac gtc aac cgc tcg cag agc tcc aac gac tgc ttc ccc acc	432
Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp Cys Phe Pro Thr	
130 135 140	
gcc atg cac att gcc gca gcc cag gcg gtg cat gaa aag ctg ctg ccg	480
Ala Met His Ile Ala Ala Ala Gln Ala Val His Glu Lys Leu Leu Pro	
145 150 155 160	
gcc gtc act gaa ctg tct tcg ggg ctg gcc gag ctg tcg atg cgc cac	528
Ala Val Thr Glu Leu Ser Ser Gly Leu Ala Glu Leu Ser Met Arg His	
165 170 175	
cac aag ctg gta aaa acc ggc cgc acg cac atg atg gac gcc acg ccg	576
His Lys Leu Val Lys Thr Gly Arg Thr His Met Met Asp Ala Thr Pro	

PF59083SeqList PF59083.txt

180															185					190					
att	acc	ttc	ggc	cag	gaa	gtg	tcg	gct	ttc	gtc	gcc	cag	ctc	gat	tac	624									
Ile	Thr	Phe	Gly	Gln	Glu	Val	Ser	Ala	Phe	Val	Ala	Gln	Leu	Asp	Tyr										
															195	200	205								
gcc	cag	cgc	gct	atc	cgc	gcc	acc	ctg	ccg	gcg	gtg	tgc	gaa	ctg	gcc	672									
Ala	Gln	Arg	Ala	Ile	Arg	Ala	Thr	Leu	Pro	Ala	Val	Cys	Glu	Leu	Ala										
															210	215	220								
cag	ggc	ggc	act	gcc	gtg	ggg	acc	ggg	ctg	aac	gct	ccg	cag	ggg	ttt	720									
Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Ala	Pro	Gln	Gly	Phe										
															225	230	235	240							
gcc	gag	gcc	atc	gcg	gcc	gag	ctg	gcg	gcg	ctg	tcc	ggc	ctg	ccg	ttc	768									
Ala	Glu	Ala	Ile	Ala	Ala	Glu	Leu	Ala	Ala	Leu	Ser	Gly	Leu	Pro	Phe										
															245	250	255								
atc	act	gca	ccc	aac	aag	ttc	gcc	gcc	ctc	gcc	ggc	cac	gaa	ccg	ctg	816									
Ile	Thr	Ala	Pro	Asn	Lys	Phe	Ala	Ala	Leu	Ala	Gly	His	Glu	Pro	Leu										
															260	265	270								
acc	agc	ctg	gcg	gga	gcc	ctg	aag	acc	ctg	gcc	gtg	gcc	ctg	atg	aaa	864									
Thr	Ser	Leu	Ala	Gly	Ala	Leu	Lys	Thr	Leu	Ala	Val	Ala	Leu	Met	Lys										
															275	280	285								
atc	gcc	aac	gac	ctg	cgc	ctg	ctg	ggg	tcc	ggc	cct	cgc	gcc	ggg	ctt	912									
Ile	Ala	Asn	Asp	Leu	Arg	Leu	Leu	Gly	Ser	Gly	Pro	Arg	Ala	Gly	Leu										
															290	295	300								
gcc	gag	gtg	cgc	ctg	cca	gcc	aac	gag	ccg	ggc	agc	tcg	atc	atg	ccg	960									
Ala	Glu	Val	Arg	Leu	Pro	Ala	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro										
															305	310	315	320							
ggc	aag	gtc	aac	ccc	acc	cag	tgc	gag	gcg	ctg	tcg	atg	ctg	gcc	tgc	1008									
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Ser	Met	Leu	Ala	Cys										
															325	330	335								
cag	gta	ctg	ggc	aac	gac	gcg	gcc	atc	ggc	ttt	gcc	gcc	agc	cag	ggg	1056									
Gln	Val	Leu	Gly	Asn	Asp	Ala	Ala	Ile	Gly	Phe	Ala	Ala	Ser	Gln	Gly										
															340	345	350								
cat	ttg	cag	ttg	aat	gtg	ttc	aag	ccg	gtg	atc	att	cat	aac	ctg	ctg	1104									
His	Leu	Gln	Leu	Asn	Val	Phe	Lys	Pro	Val	Ile	Ile	His	Asn	Leu	Leu										
															355	360	365								
caa	tcc	atc	gag	ttg	ctg	gcc	gat	ggg	tgc	cgc	aac	ttc	cag	cag	cat	1152									
Gln	Ser	Ile	Glu	Leu	Leu	Ala	Asp	Gly	Cys	Arg	Asn	Phe	Gln	Gln	His										
															370	375	380								
tgc	gtg	gcg	ggg	atc	gag	ccg	gat	gcc	gag	cag	atg	gcc	gcg	cac	ctg	1200									
Cys	Val	Ala	Gly	Ile	Glu	Pro	Asp	Ala	Glu	Gln	Met	Ala	Ala	His	Leu										
															385	390	395	400							
gag	cgt	ggg	ttg	atg	ctg	gtg	acg	gcg	ctg	aac	ccg	cat	att	ggc	tat	1248									
Glu	Arg	Gly	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr										
															405	410	415								
gac	aag	gcg	gca	gaa	att	gcc	aag	aag	gct	tac	agc	gag	ggc	acg	acc	1296									
Asp	Lys	Ala	Ala	Glu	Ile	Ala	Lys	Lys	Ala	Tyr	Ser	Glu	Gly	Thr	Thr										
															420	425	430								
ttg	cgc	gag	gcg	gca	ttg	gcg	ttg	aag	tac	ctg	acc	aat	gaa	cag	ttc	1344									
Leu	Arg	Glu	Ala	Ala	Leu	Ala	Leu	Lys	Tyr	Leu	Thr	Asn	Glu	Gln	Phe										
															435	440	445								
gac	cag	tgg	gtg	cgg	ccg	gag	aac	atg	ctg	gcg	cct	ggg	ggc	aaa	ggc	1392									
Asp	Gln	Trp	Val	Arg	Pro	Glu	Asn	Met	Leu	Ala	Pro	Gly	Gly	Lys	Gly										
															450	455	460								
tag															1395										

<210> 9790

<211> 464

<212> PRT

<213> Pseudomonas putida

<400> 9790

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

PF59083SeqList PF59083.txt

50 55 60
 Ala Asp Ile Ala Arg Leu Ile Glu Gln Ala Ala Asp Glu Val Leu Asp
 65 70 75 80
 Gly Gln His Asp Asp Gln Phe Pro Leu Val Val Trp Gln Thr Gly Ser
 85 90 95
 Gly Thr Gln Ser Asn Met Asn Val Asn Glu Val Ile Ala Gly Arg Ala
 100 105 110
 Asn Glu Leu Ala Gly Lys Gly Arg Gly Gly Lys Ala Pro Val His Pro
 115 120 125
 Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp Cys Phe Pro Thr
 130 135 140
 Ala Met His Ile Ala Ala Ala Gln Ala Val His Glu Lys Leu Leu Pro
 145 150 155 160
 Ala Val Thr Glu Leu Ser Ser Gly Leu Ala Glu Leu Ser Met Arg His
 165 170 175
 His Lys Leu Val Lys Thr Gly Arg Thr His Met Met Asp Ala Thr Pro
 180 185 190
 Ile Thr Phe Gly Gln Glu Val Ser Ala Phe Val Ala Gln Leu Asp Tyr
 195 200 205
 Ala Gln Arg Ala Ile Arg Ala Thr Leu Pro Ala Val Cys Glu Leu Ala
 210 215 220
 Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Ala Pro Gln Gly Phe
 225 230 235 240
 Ala Glu Ala Ile Ala Glu Leu Ala Ala Leu Ser Gly Leu Pro Phe
 245 250 255
 Ile Thr Ala Pro Asn Lys Phe Ala Ala Leu Ala Gly His Glu Pro Leu
 260 265 270
 Thr Ser Leu Ala Gly Ala Leu Lys Thr Leu Ala Val Ala Leu Met Lys
 275 280 285
 Ile Ala Asn Asp Leu Arg Leu Leu Gly Ser Gly Pro Arg Ala Gly Leu
 290 295 300
 Ala Glu Val Arg Leu Pro Ala Asn Glu Pro Gly Ser Ser Ile Met Pro
 305 310 315 320
 Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Ser Met Leu Ala Cys
 325 330 335
 Gln Val Leu Gly Asn Asp Ala Ala Ile Gly Phe Ala Ala Ser Gln Gly
 340 345 350
 His Leu Gln Leu Asn Val Phe Lys Pro Val Ile Ile His Asn Leu Leu
 355 360 365
 Gln Ser Ile Glu Leu Leu Ala Asp Gly Cys Arg Asn Phe Gln Gln His
 370 375 380
 Cys Val Ala Gly Ile Glu Pro Asp Ala Glu Gln Met Ala Ala His Leu
 385 390 395 400
 Glu Arg Gly Leu Met Leu Val Thr Ala Leu Asn Pro His Ile Gly Tyr
 405 410 415
 Asp Lys Ala Ala Glu Ile Ala Lys Lys Ala Tyr Ser Glu Gly Thr Thr
 420 425 430
 Leu Arg Glu Ala Ala Leu Ala Leu Lys Tyr Leu Thr Asn Glu Gln Phe
 435 440 445
 Asp Gln Trp Val Arg Pro Glu Asn Met Leu Ala Pro Gly Gly Lys Gly
 450 455 460

<210> 9791

<211> 1494

<212> DNA

<213> Rhizobium meliloti

<220>

<221> CDS

<222> (103)..(1494)

<223> transl_table=11

<400> 9791

atggccaagg cagagaaatg cccggcagcg gggagtaaga tcggccttgg acccggtccc

60

cgccctcggct tcatgaaccg catgacgaaa gcaggtatca cg atg aca tcg acc
Met Thr Ser Thr

114

1

PF59083SeqList PF59083.txt																
cgc	acg	gaa	aca	gat	acg	ttc	ggc	ccc	atc	gaa	gtg	gcg	agc	gac	cgc	162
Arg	Thr	Glu	Thr	Asp	Thr	Phe	Gly	Pro	Ile	Glu	Val	Ala	Ser	Asp	Arg	
5					10					15					20	
tat	tgg	ggc	gcc	cag	gcg	cag	cga	tcg	ctg	ggc	aat	ttc	aaa	atc	ggc	210
Tyr	Trp	Gly	Ala	Gln	Ala	Gln	Arg	Ser	Leu	Gly	Asn	Phe	Lys	Ile	Gly	
				25					30					35		
tgg	gaa	aag	cag	cct	ctg	gca	atc	gtg	cg	gca	ctc	ggc	atc	gtc	aaa	258
Trp	Glu	Lys	Gln	Pro	Leu	Ala	Ile	Val	Arg	Ala	Leu	Gly	Ile	Val	Lys	
			40					45					50			
cag	gcg	gct	gcc	cg	gcc	aac	atg	gcg	ctc	ggc	cg	ctc	gac	ccg	gcg	306
Gln	Ala	Ala	Ala	Arg	Ala	Asn	Met	Ala	Leu	Gly	Arg	Leu	Asp	Pro	Ala	
			55				60					65				
atc	ggc	gac	gcc	atc	gtc	aag	gcc	gca	cag	gag	gtg	atc	gac	ggc	aag	354
Ile	Gly	Asp	Ala	Ile	Val	Lys	Ala	Ala	Gln	Glu	Val	Ile	Asp	Gly	Lys	
	70					75				80						
ctt	gac	gag	cac	ttc	cct	ctc	gtc	gtg	tgg	cag	acg	ggc	tcc	gga	acc	402
Leu	Asp	Glu	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr	
					90					95					100	
cag	tcg	aac	atg	aat	gcg	aac	gag	gtc	gtt	tcc	aac	cg	gcg	atc	gag	450
Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Val	Ser	Asn	Arg	Ala	Ile	Glu	
				105				110						115		
ctg	ctc	ggc	ggc	gtc	atg	ggt	tcg	aag	aag	ccg	gtt	cac	ccg	aac	gat	498
Leu	Leu	Gly	Gly	Val	Met	Gly	Ser	Lys	Lys	Pro	Val	His	Pro	Asn	Asp	
			120					125					130			
cac	gtc	aat	atg	agc	cag	tcg	tcg	aac	gac	acc	tat	ccc	acg	gcc	atg	546
His	Val	Asn	Met	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Tyr	Pro	Thr	Ala	Met	
			135				140					145				
cac	atc	gcc	tgt	gcg	gag	cg	gtg	atc	cac	gat	ctg	ctg	ccg	gcg	ctc	594
His	Ile	Ala	Cys	Ala	Glu	Arg	Val	Ile	His	Asp	Leu	Leu	Pro	Ala	Leu	
	150					155					160					
aag	cac	ctg	cac	aag	gcg	ctc	gaa	gag	aag	gtg	aag	gct	ttc	gat	cac	642
Lys	His	Leu	His	Lys	Ala	Leu	Glu	Glu	Lys	Val	Lys	Ala	Phe	Asp	His	
					170					175					180	
atc	atc	aag	atc	ggc	cg	acc	cac	acg	cag	gac	gca	acg	ccc	ctg	acg	690
Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	Leu	Thr	
				185				190						195		
ctg	ggg	cag	gag	ttt	tcc	ggc	tat	gcg	gcg	cag	gtc	gcc	tcc	tcg	atc	738
Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Ala	Ala	Gln	Val	Ala	Ser	Ser	Ile	
			200					205					210			
aaa	cg	atc	gag	atg	acg	ctc	ccc	ggc	ctt	tgc	gag	ctc	gcc	cag	ggg	786
Lys	Arg	Ile	Glu	Met	Thr	Leu	Pro	Gly	Leu	Cys	Glu	Leu	Ala	Gln	Gly	
			215				220					225				
ggg	acc	gcg	gtc	ggc	acc	ggg	ctc	aat	gcg	ccg	gtc	gga	ttt	gcc	gag	834
Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Ala	Pro	Val	Gly	Phe	Ala	Glu	
			230			235					240					
aag	gtc	gcc	gag	gaa	atc	gct	gcc	atc	acc	ggc	atc	ggc	ttc	act	tcc	882
Lys	Val	Ala	Glu	Glu	Ile	Ala	Ala	Ile	Thr	Gly	Ile	Gly	Phe	Thr	Ser	
					250					255					260	
gcg	ccg	aac	aag	ttc	gaa	gcg	ctg	gcc	gcc	cac	gac	tcg	atg	gtc	ttc	930
Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ser	Met	Val	Phe	
				265				270						275		
agc	cac	ggg	gca	atc	aac	gcc	acc	gcc	gcc	gcg	ctc	ttc	aag	atc	gcc	978
Ser	His	Gly	Ala	Ile	Asn	Ala	Thr	Ala	Ala	Ala	Leu	Phe	Lys	Ile	Ala	
			280					285					290			
aac	gac	atc	cg	ttc	ctc	ggc	tcc	ggc	ccc	cg	tcc	ggc	ctc	ggc	gag	1026
Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Ser	Gly	Leu	Gly	Glu	
			295				300					305				
ctt	tca	ctg	ccg	gaa	aac	gag	ccg	ggc	tcg	tcc	atc	atg	ccg	ggc	aag	1074
Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	
			310			315						320				
gtc	aac	ccg	act	cag	tgc	gag	gcg	ctc	acc	cag	gtc	tgc	gtc	cag	gtc	1122
Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Gln	Val	Cys	Val	Gln	Val	
				330						335					340	
ttc	ggc	aat	cat	gcg	gcg	ctg	acc	ttt	gcc	ggc	agc	cag	ggc	cac	ttc	1170
Phe	Gly	Asn	His	Ala	Ala	Leu	Thr	Phe	Ala	Gly	Ser	Gln	Gly	His	Phe	
				345				350						355		
gag	ctc	aac	gtc	tac	aat	ccg	ctg	atg	gcg	tac	aac	ttc	ctg	cag	tcg	1218
Glu	Leu	Asn	Val	Tyr	Asn	Pro	Leu	Met	Ala	Tyr	Asn	Phe	Leu	Gln	Ser	
			360					365					370			

PF59083SeqList PF59083.txt

gtg	caa	ctg	ctc	gcc	gat	gcg	gct	atc	tcc	ttc	acc	gac	aat	tgc	gtc	1266
Val	Gln	Leu	Leu	Ala	Asp	Ala	Ala	Ile	Ser	Phe	Thr	Asp	Asn	Cys	Val	
		375					380					385				
gtc	ggg	atc	gag	gcg	cgg	gag	gac	aac	atc	aag	gcg	gcg	ctc	gac	cgt	1314
Val	Gly	Ile	Glu	Ala	Arg	Glu	Asp	Asn	Ile	Lys	Ala	Ala	Leu	Asp	Arg	
	390					395					400					
tcg	ctc	atg	ctg	gtg	act	gcg	ctt	gcg	ccg	aag	atc	ggc	tac	gac	aac	1362
Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Ala	Pro	Lys	Ile	Gly	Tyr	Asp	Asn	
405					410					415					420	
gcg	gcc	aag	atc	gcc	aag	acc	gcc	cac	aag	aac	ggc	acc	acg	ctt	cgc	1410
Ala	Ala	Lys	Ile	Ala	Lys	Thr	Ala	His	Lys	Asn	Gly	Thr	Thr	Leu	Arg	
				425					430					435		
gag	gag	gcc	gtc	ggc	ggc	ggc	tac	gtc	acg	gac	gag	gag	ttc	gac	gcc	1458
Glu	Glu	Ala	Val	Gly	Gly	Gly	Tyr	Val	Thr	Asp	Glu	Glu	Phe	Asp	Ala	
			440					445					450			
gtc	gtc	cgc	ccc	gaa	acc	atg	atc	ggc	ccg	gcc	tga					1494
Val	Val	Arg	Pro	Glu	Thr	Met	Ile	Gly	Pro	Ala						
		455					460									

<210> 9792

<211> 463

<212> PRT

<213> Rhizobium meliloti

<400> 9792

Met	Thr	Ser	Thr	Arg	Thr	Glu	Thr	Asp	Thr	Phe	Gly	Pro	Ile	Glu	Val	
1				5					10					15		
Ala	Ser	Asp	Arg	Tyr	Trp	Gly	Ala	Gln	Ala	Gln	Arg	Ser	Leu	Gly	Asn	
			20					25					30			
Phe	Lys	Ile	Gly	Trp	Glu	Lys	Gln	Pro	Leu	Ala	Ile	Val	Arg	Ala	Leu	
		35					40					45				
Gly	Ile	Val	Lys	Gln	Ala	Ala	Ala	Arg	Ala	Asn	Met	Ala	Leu	Gly	Arg	
	50				55					60						
Leu	Asp	Pro	Ala	Ile	Gly	Asp	Ala	Ile	Val	Lys	Ala	Ala	Gln	Glu	Val	
65				70						75				80		
Ile	Asp	Gly	Lys	Leu	Asp	Glu	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	
			85					90					95			
Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Val	Ser	Asn	
			100					105					110			
Arg	Ala	Ile	Glu	Leu	Leu	Gly	Gly	Val	Met	Gly	Ser	Lys	Lys	Pro	Val	
		115				120						125				
His	Pro	Asn	Asp	His	Val	Asn	Met	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Tyr	
	130				135					140						
Pro	Thr	Ala	Met	His	Ile	Ala	Cys	Ala	Glu	Arg	Val	Ile	His	Asp	Leu	
145				150						155					160	
Leu	Pro	Ala	Leu	Lys	His	Leu	His	Lys	Ala	Leu	Glu	Glu	Lys	Val	Lys	
			165					170						175		
Ala	Phe	Asp	His	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	
		180						185					190			
Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Ala	Ala	Gln	Val	
		195					200					205				
Ala	Ser	Ser	Ile	Lys	Arg	Ile	Glu	Met	Thr	Leu	Pro	Gly	Leu	Cys	Glu	
	210				215						220					
Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Ala	Pro	Val	
225					230					235					240	
Gly	Phe	Ala	Glu	Lys	Val	Ala	Glu	Glu	Ile	Ala	Ala	Ile	Thr	Gly	Ile	
			245					250					255			
Gly	Phe	Thr	Ser	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	
		260						265					270			
Ser	Met	Val	Phe	Ser	His	Gly	Ala	Ile	Asn	Ala	Thr	Ala	Ala	Ala	Leu	
		275				280						285				
Phe	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Ser	
	290				295					300						
Gly	Leu	Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	
305					310					315					320	
Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Gln	Val	
			325					330						335		
Cys	Val	Gln	Val	Phe	Gly	Asn	His	Ala	Ala	Leu	Thr	Phe	Ala	Gly	Ser	
			340					345					350			

PF59083SeqList PF59083.txt

Gln Gly His Phe Glu Leu Asn Val Tyr Asn Pro Leu Met Ala Tyr Asn
 355 360 365
 Phe Leu Gln Ser Val Gln Leu Leu Ala Asp Ala Ala Ile Ser Phe Thr
 370 375 380
 Asp Asn Cys Val Val Gly Ile Glu Ala Arg Glu Asp Asn Ile Lys Ala
 385 390 395 400
 Ala Leu Asp Arg Ser Leu Met Leu Val Thr Ala Leu Ala Pro Lys Ile
 405 410 415
 Gly Tyr Asp Asn Ala Ala Lys Ile Ala Lys Thr Ala His Lys Asn Gly
 420 425 430
 Thr Thr Leu Arg Glu Glu Ala Val Gly Gly Gly Tyr Val Thr Asp Glu
 435 440 445
 Glu Phe Asp Ala Val Val Arg Pro Glu Thr Met Ile Gly Pro Ala
 450 455 460

<210> 9793
 <211> 1404
 <212> DNA
 <213> Salmonella typhimurium

<220>
 <221> CDS
 <222> (1)..(1404)
 <223> transl_table=11

<400> 9793
 atg gta acg gta cgc cgc gag aaa gat tca atg ggc gcg att gaa gtc 48
 Met Val Thr Val Arg Arg Glu Lys Asp Ser Met Gly Ala Ile Glu Val
 1 5 10 15
 ccg gca gat aaa ctg tgg ggg gcg cag act caa cgt tcg ctg gag cat 96
 Pro Ala Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu Glu His
 20 25 30
 ttt cgg att tcc acg gag aaa atg ccc gtc tcg ctc att cac gct ctg 144
 Phe Arg Ile Ser Thr Glu Lys Met Pro Val Ser Leu Ile His Ala Leu
 35 40 45
 gcg ttg acc aag cgc gcc gct gcg aag gtc aac cag gac tta ggg ttg 192
 Ala Leu Thr Lys Arg Ala Ala Lys Val Asn Gln Asp Leu Gly Leu
 50 55 60
 ttg gcg gcg gaa aaa gcc agc gcg att atc cag gcg gct gat gaa gtg 240
 Leu Ala Ala Glu Lys Ala Ser Ala Ile Ile Gln Ala Ala Asp Glu Val
 65 70 75 80
 ctg gcg gga aaa cat gct gat gag ttt ccg ctg gcg att tgg cag acc 288
 Leu Ala Gly Lys His Ala Asp Glu Phe Pro Leu Ala Ile Trp Gln Thr
 85 90 95
 ggg tcc ggt acg caa agc aac atg aat atg aat gaa gtg tta gcg aac 336
 Gly Ser Gly Thr Gln Ser Asn Met Asn Met Asn Glu Val Leu Ala Asn
 100 105 110
 cgc gcc agt gaa att ttg ggc ggc gtt cgc ggt atg gaa cgc aag gtg 384
 Arg Ala Ser Glu Ile Leu Gly Gly Val Arg Gly Met Glu Arg Lys Val
 115 120 125
 cat ccc aat gat gac gtc aat aag agt caa agc tca aac gat gtt ttc 432
 His Pro Asn Asp Asp Val Asn Lys Ser Gln Ser Ser Asn Asp Val Phe
 130 135 140
 cca acc gcc atg cac gtg gcg gcg tta ctg gcg tta cgc gaa cac ctt 480
 Pro Thr Ala Met His Val Ala Ala Leu Leu Ala Leu Arg Glu His Leu
 145 150 155 160
 atc ccg caa tta tcc gca tta acg gat acg ctt cgc gat aaa tcc cac 528
 Ile Pro Gln Leu Ser Ala Leu Thr Asp Thr Leu Arg Asp Lys Ser His
 165 170 175
 gct ttc gcc gat att gtc aaa att ggc cgt act cac ctg cag gac gcg 576
 Ala Phe Ala Asp Ile Val Lys Ile Gly Arg Thr His Leu Gln Asp Ala
 180 185 190
 acg ccg ctc acc tta ggc cag gag att tcc ggt tgg gta gcc atg ctg 624
 Thr Pro Leu Thr Leu Gly Gln Glu Ile Ser Gly Trp Val Ala Met Leu
 195 200 205
 gaa cat aac ctc aga cac att gag cac agt tta ccg cac gtc gcg gaa 672
 Glu His Asn Leu Arg His Ile Glu His Ser Leu Pro His Val Ala Glu
 210 215 220
 ctg gcg ctc ggc gga acc gca gta ggg aca ggg ctt aat acc cat ccg 720

PF59083SeqList PF59083.txt

Leu 225	Ala	Leu	Gly	Gly	Thr 230	Ala	Val	Gly	Thr	Gly 235	Leu	Asn	Thr	His	Pro 240	
gaa	tat	gcc	cgg	cgc	gtg	gcc	gag	gaa	ctg	gcg	acg	att	acc	gcg	gcg	768
Glu	Tyr	Ala	Arg	Arg 245	Val	Ala	Glu	Glu	Leu 250	Ala	Thr	Ile	Thr	Ala 255	Ala	
ccg	ttt	gtt	acc	gcc	ccc	aat	aaa	ttc	gaa	gcg	ctg	gcg	acc	tgt	gac	816
Pro	Phe	Val	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Thr	Cys	Asp	
gcg	ttg	gta	cag	gcg	cat	ggc	gca	tta	aaa	gga	ctg	gcg	gcc	tcg	ctg	864
Ala	Leu	Val 275	Gln	Ala	His	Gly	Ala	Leu	Lys	Gly	Leu	Ala	Ala	Ser	Leu	
atg	aaa	atc	gcc	aac	gat	gtt	cgc	tgg	ctg	gcg	tcc	ggc	ccg	cg	tgc	912
Met	Lys	Ile	Ala	Asn	Asp	Val 295	Arg	Trp	Leu	Ala	Ser	Gly	Pro	Arg	Cys	
ggc	att	ggc	gag	att	gct	atc	ccg	gag	aat	gag	cca	ggc	agt	tcc	att	960
Gly	Ile	Gly	Glu	Ile	Ala 310	Ile	Pro	Glu	Asn	Glu 315	Pro	Gly	Ser	Ser	Ile 320	
atg	cct	ggt	aaa	gtg	aac	ccg	acc	cag	tgt	gaa	gcg	gta	acg	atg	cta	1008
Met	Pro	Gly	Lys	Val 325	Asn	Pro	Thr	Gln	Cys 330	Glu	Ala	Val	Thr	Met 335	Leu	
tgt	tgc	cag	gtg	atg	ggt	aac	gat	gtg	gcc	atc	aat	atg	ggg	ggc	gca	1056
Cys	Cys	Gln	Val	Met	Gly	Asn	Asp	Val 345	Ala	Ile	Asn	Met	Gly 350	Gly	Ala	
tcg	ggc	aac	ttt	gag	ctc	aac	gtc	tat	cgt	ccg	atg	ggt	att	cat	aat	1104
Ser	Gly	Asn	Phe	Glu	Leu	Asn	Val 360	Tyr	Arg	Pro	Met	Val 365	Ile	His	Asn	
ttt	ctg	caa	acg	gtg	cgc	ctg	ctg	gcc	gat	ggc	atg	gag	agt	ttt	aat	1152
Phe	Leu	Gln	Thr	Val	Arg	Leu 375	Leu	Ala	Asp	Gly 380	Met	Glu	Ser	Phe	Asn	
aaa	cac	tgt	gcg	tca	gga	atc	gag	cca	aac	cgc	gag	cg	att	acg	cag	1200
Lys	His	Cys	Ala	Ser	Gly 390	Ile	Glu	Pro	Asn	Arg 395	Glu	Arg	Ile	Thr	Gln 400	
ttg	ctg	aat	gag	tcg	ctg	atg	ctg	gtc	act	gcg	ctg	aat	acg	cac	atc	1248
Leu	Leu	Asn	Glu	Ser 405	Leu	Met	Leu	Val	Thr 410	Ala	Leu	Asn	Thr	His 415	Ile	
ggt	tac	gat	aaa	gcg	gcg	gag	att	gcg	aag	aag	gcg	cat	aaa	gaa	ggg	1296
Gly	Tyr	Asp	Lys	Ala	Ala	Glu	Ile	Ala	Lys	Lys	Ala	His	Lys 430	Glu	Gly	
ctg	acg	ctc	aaa	gcc	tca	gcc	gtg	gca	tta	gga	tac	ctt	agc	gac	gag	1344
Leu	Thr	Leu 435	Lys	Ala	Ser	Ala	Val 440	Ala	Leu	Gly	Tyr	Leu 445	Ser	Asp	Glu	
gag	ttc	gac	gcc	tgg	gta	cgt	ccg	gag	ttg	atg	gtt	ggc	agt	atg	acg	1392
Glu	Phe	Asp	Ala	Trp	Val	Arg 455	Pro	Glu	Leu	Met	Val 460	Gly	Ser	Met	Thr	
ccg	gga	cg	taa													1404
Pro	Gly	Arg														
465																

<210> 9794

<211> 467

<212> PRT

<213> Salmonella typhimurium

<400> 9794

Met	Val	Thr	Val	Arg	Arg	Glu	Lys	Asp	Ser	Met	Gly	Ala	Ile	Glu	Val
1				5					10					15	
Pro	Ala	Asp	Lys	Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Glu	His
			20					25					30		
Phe	Arg	Ile	Ser	Thr	Glu	Lys	Met	Pro	Val	Ser	Leu	Ile	His	Ala	Leu
		35					40					45			
Ala	Leu	Thr	Lys	Arg	Ala	Ala	Ala	Lys	Val	Asn	Gln	Asp	Leu	Gly	Leu
	50				55					60					
Leu	Ala	Ala	Glu	Lys	Ala	Ser	Ala	Ile	Ile	Gln	Ala	Ala	Asp	Glu	Val
65				70					75					80	
Leu	Ala	Gly	Lys	His	Ala	Asp	Glu	Phe	Pro	Leu	Ala	Ile	Trp	Gln	Thr
			85					90					95		
Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Met	Asn	Glu	Val	Leu	Ala	Asn
			100				105					110			
Arg	Ala	Ser	Glu	Ile	Leu	Gly	Gly	Val	Arg	Gly	Met	Glu	Arg	Lys	Val

PF59083SeqList PF59083.txt

```

      115
His Pro Asn Asp Asp Val Asn 120 125
      130
Pro Thr Ala Met His Val 135
145 Ile Pro Gln Leu Ser 150
      165
Ala Phe Ala Asp Ile Val Lys Ile Gly Arg Thr His Leu Gln Asp Ala
      180
Thr Pro Leu Thr Leu Gly Gln Glu Ile Ser Gly Trp Val Ala Met Leu
      195
Glu His Asn Leu Arg His Ile Glu His Ser Leu Pro His Val Ala Glu
      210
Leu Ala Leu Gly Gly Thr 215
225 Glu Tyr Ala Arg Arg Val Ala Glu Glu Leu 235
      245
Pro Phe Val Thr Ala Pro Asn Lys Phe Glu Ala Leu Ala Thr Cys Asp
      260
Ala Leu Val Gln Ala His Gly Ala Leu Lys Gly Leu Ala Ser Leu
      275
Met Lys Ile Ala Asn Asp Val Arg Trp Leu Ala Ser Gly Pro Arg Cys
      290
Gly Ile Gly Glu Ile Ala Ile Pro Glu Asn Glu Pro Gly Ser Ser Ile
305 Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Val Thr Met Leu
      325
Cys Cys Gln Val Met Gly Asn Asp Val Ala Ile Asn Met Gly Gly Ala
      340
Ser Gly Asn Phe Glu Leu Asn Val Tyr Arg Pro Met Val Ile His Asn
      355
Phe Leu Gln Thr Val Arg Leu Leu Ala Asp Gly Met Glu Ser Phe Asn
      370
Lys His Cys Ala Ser Gly Ile Glu Pro Asn Arg Glu Arg Ile Thr Gln
385 Leu Leu Asn Glu Ser Leu Met Leu Val Thr Ala Leu Asn Thr His Ile
      405
Gly Tyr Asp Lys Ala Ala Glu Ile Ala Lys Lys Ala His Lys Glu Gly
      420
Leu Thr Leu Lys Ala Ser Ala Val Ala Leu Gly Tyr Leu Ser Asp Glu
      435
Glu Phe Asp Ala Trp Val Arg Pro Glu Leu Met Val Gly Ser Met Thr
      450
Pro Gly Arg
465

```

<210> 9795
 <211> 1404
 <212> DNA
 <213> Streptomyces avermitilis

<220>
 <221> CDS
 <222> (1)..(1404)
 <223> transl_table=11

```

<400> 9795
atg acc gac gag gac gac aag cag aac tac cgt gtc gag cac gac tcc      48
Met Thr Asp Glu Asp Asp Lys Gln Asn Tyr Arg Val Glu His Asp Ser
1
atg ggt gag gtc cgt gtc ccc gcg gac gcc aag tgg cgg gcc cag acc      96
Met Gly Glu Val Arg Val Pro Ala Asp Ala Lys Trp Arg Ala Gln Thr
20
cag cgt gcc gtg gag aac ttc ccc atc tcc ggg cag cgg ctc gag cgg      144
Gln Arg Ala Val Glu Asn Phe 40 Ile Ser Gly Gln Arg Leu Glu Arg
35
gcg cac atc gag gcc ctc gcc cgg atc aag gga gcc gcc gcc aag gtg      192
Ala His Ile Glu Ala Leu Ala Arg Ile Lys Gly Ala Ala Ala Lys Val
50

```


PF59083SeqList PF59083.txt

aac	gcc	gag	ttg	ggc	gtg	ctc	gac	aag	gac	gtc	gcc	gag	gcc	att	cag	240
Asn	Ala	Glu	Leu	Gly	Val	Leu	Asp	Lys	Asp	Val	Ala	Glu	Ala	Ile	Gln	
65				70					75						80	
gag	gcg	gcc	gcc	gag	gtc	gcg	gag	ggg	cgt	tgg	gac	gag	cac	ttc	ccc	288
Glu	Ala	Ala	Ala	Glu	Val	Ala	Glu	Gly	Arg	Trp	Asp	Glu	His	Phe	Pro	
				85					90					95		
gtg	gac	gtg	ttc	cag	acc	ggc	tcc	ggg	acc	tcg	tcc	aac	atg	aac	gcc	336
Val	Asp	Val	Phe	Gln	Thr	Gly	Ser	Gly	Thr	Ser	Ser	Asn	Met	Asn	Ala	
				100					105					110		
aac	gag	gtc	atc	gcc	acg	ctc	gcg	acc	gaa	cgg	ctc	ggc	agg	gac	gta	384
Asn	Glu	Val	Ile	Ala	Thr	Leu	Ala	Thr	Glu	Arg	Leu	Gly	Arg	Asp	Val	
				115					120					125		
cac	ccc	aat	gac	cac	gtg	aac	gcg	tcg	cag	tcg	tcg	aac	gac	gtg	ttc	432
His	Pro	Asn	Asp	His	Val	Asn	Ala	Ser	Gln	Ser	Ser	Asn	Asp	Val	Phe	
ccg	tcc	agc	att	cac	atc	gcc	acc	gcc	gcc	gtc	acc	cgc	gat	ctg		480
Pro	Ser	Ser	Ile	His	Ile	Ala	Ala	Thr	Ala	Ala	Val	Thr	Arg	Asp	Leu	
145															160	
gta	ccc	gcc	ctg	gag	cac	ctg	gcc	gcc	gcc	ctg	ggc	cgc	aag	tcc	gag	528
Val	Pro	Ala	Leu	Glu	His	Leu	Ala	Ala	Ala	Leu	Gly	Arg	Lys	Ser	Glu	
															175	
gag	ttc	gcg	gac	gtc	gtg	aag	gcc	ggg	cgt	acg	cat	ctc	atg	gac	gcg	576
Glu	Phe	Ala	Asp	Val	Val	Lys	Ala	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	
															190	
acg	ccc	gtg	acc	ctg	ggg	cag	gag	ttc	ggc	gga	tac	gcg	gcc	cag	gtg	624
Thr	Pro	Val	Thr	Leu	Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Ala	Gln	Val	
															205	
cgg	tac	ggc	gtc	gag	cgg	ctg	gcc	gcc	tcc	ctg	ccg	cgg	ctc	gcc	gaa	672
Arg	Tyr	Gly	Val	Glu	Arg	Leu	Ala	Ala	Ser	Leu	Pro	Arg	Leu	Ala	Glu	
															220	
ctg	ccc	ctc	ggg	ggc	acc	gcg	gtc	ggg	acc	ggg	atc	aac	acc	ccg	ccg	720
Leu	Pro	Leu	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Thr	Pro	Pro	
225															240	
ggc	ttc	tcc	gcc	gcc	gtc	atc	gcc	gag	gtc	gcc	cgc	gtc	acc	ggg	ctg	768
Gly	Phe	Ser	Ala	Ala	Val	Ile	Ala	Glu	Val	Ala	Arg	Val	Thr	Gly	Leu	
															255	
ccg	ctc	acc	gag	gag	cgc	gac	cac	ttc	gag	gag	cag	ggt	gag	cgg	gac	816
Pro	Leu	Thr	Glu	Ala	Arg	Asp	His	Phe	Glu	Ala	Gln	Gly	Ala	Arg	Asp	
															270	
ggg	atc	gtc	gag	acc	agc	ggg	cag	ttg	cgg	acc	atc	gcc	gta	gga	ctg	864
Gly	Ile	Val	Glu	Thr	Ser	Gly	Gln	Leu	Arg	Thr	Ile	Ala	Val	Gly	Leu	
															285	
acg	aag	atc	gag	aac	gat	ctg	cgg	tgg	atg	gct	tcg	ggg	ccg	cgt	acc	912
Thr	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Trp	Met	Ala	Ser	Gly	Pro	Arg	Thr	
															300	
ggg	ctc	tcc	gag	atc	agc	ctg	ccc	gac	ctt	cag	ccg	ggg	tcc	tcg	atc	960
Gly	Leu	Ser	Glu	Ile	Ser	Leu	Pro	Asp	Leu	Gln	Pro	Gly	Ser	Ser	Ile	
305															320	
atg	ccc	ggc	aag	gtg	aat	ccc	gtg	att	ccc	gag	gcc	gtg	ctg	atg	gtc	1008
Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Ala	Val	Leu	Met	Val	
															335	
gcc	gca	cag	gtg	acg	ggc	aac	gac	gag	acc	gtc	gcc	gcc	gcc	gga	gcc	1056
Ala	Ala	Gln	Val	Thr	Gly	Asn	Asp	Ala	Thr	Val	Ala	Ala	Ala	Gly	Ala	
															350	
gcc	ggc	aac	ttc	gaa	ctc	aat	gtg	atg	ctg	ccc	gtc	atc	gag	aag	aac	1104
Ala	Gly	Asn	Phe	Glu	Leu	Asn	Val	Met	Leu	Pro	Val	Ile	Ala	Lys	Asn	
															365	
gtg	ctg	gag	tcc	gtc	cgg	ctg	ctc	gcc	cat	gtc	tcc	cgg	ctg	ctg	gcc	1152
Val	Leu	Glu	Ser	Val	Arg	Leu	Leu	Ala	His	Val	Ser	Arg	Leu	Leu	Ala	
															380	
gac	cgc	acc	gtc	gac	ggg	atc	gtc	gcc	cat	cgc	gac	cgg	gcc	cgt	gag	1200
Asp	Arg	Thr	Val	Asp	Gly	Ile	Val	Ala	His	Arg	Asp	Arg	Ala	Arg	Glu	
385															400	
tac	gcc	gag	tcg	tca	ccg	tcc	gtc	gtc	acc	ccg	ctg	aac	aag	tac	atc	1248
Tyr	Ala	Glu	Ser	Ser	Pro	Ser	Val	Val	Thr	Pro	Leu	Asn	Lys	Tyr	Ile	
															415	
ggg	tac	gag	gag	gcc	gag	aag	gtc	gcc	aag	aag	gcc	ctc	gcc	gag	cgg	1296
Gly	Tyr	Glu	Glu	Ala	Ala	Lys	Val	Ala	Lys	Lys	Ala	Leu	Ala	Glu	Arg	
															430	

PF59083SeqList PF59083.txt

cag	acg	atc	cg	cag	gtc	gtc	ctg	gag	agc	gga	tac	gtg	gac	cg	ggc	1344
Gln	Thr	Ile	Arg	Gln	Val	Val	Leu	Glu	Ser	Gly	Tyr	Val	Asp	Arg	Gly	
		435					440					445				
gac	ctc	acc	ctg	gag	cag	ctc	gac	gag	gcg	ctc	gac	gtc	ctg	cgg	atg	1392
Asp	Leu	Thr	Leu	Glu	Gln	Leu	Asp	Glu	Ala	Leu	Asp	Val	Leu	Arg	Met	
	450					455					460					
acg	cac	ccc	tga													1404
Thr	His	Pro														
465																

<210> 9796

<211> 467

<212> PRT

<213> Streptomyces avermitilis

<400> 9796

Met	Thr	Asp	Glu	Asp	Asp	Lys	Gln	Asn	Tyr	Arg	Val	Glu	His	Asp	Ser	
1				5					10					15		
Met	Gly	Glu	Val	Arg	Val	Pro	Ala	Asp	Ala	Lys	Trp	Arg	Ala	Gln	Thr	
			20					25					30			
Gln	Arg	Ala	Val	Glu	Asn	Phe	Pro	Ile	Ser	Gly	Gln	Arg	Leu	Glu	Arg	
		35					40					45				
Ala	His	Ile	Glu	Ala	Leu	Ala	Arg	Ile	Lys	Gly	Ala	Ala	Ala	Lys	Val	
	50					55					60					
Asn	Ala	Glu	Leu	Gly	Val	Leu	Asp	Lys	Asp	Val	Ala	Glu	Ala	Ile	Gln	
65				70					75					80		
Glu	Ala	Ala	Ala	Glu	Val	Ala	Glu	Gly	Arg	Trp	Asp	Glu	His	Phe	Pro	
			85					90						95		
Val	Asp	Val	Phe	Gln	Thr	Gly	Ser	Gly	Thr	Ser	Ser	Asn	Met	Asn	Ala	
		100						105					110			
Asn	Glu	Val	Ile	Ala	Thr	Leu	Ala	Thr	Glu	Arg	Leu	Gly	Arg	Asp	Val	
		115					120					125				
His	Pro	Asn	Asp	His	Val	Asn	Ala	Ser	Gln	Ser	Ser	Asn	Asp	Val	Phe	
	130					135					140					
Pro	Ser	Ser	Ile	His	Ile	Ala	Ala	Thr	Ala	Ala	Val	Thr	Arg	Asp	Leu	
145				150					155						160	
Val	Pro	Ala	Leu	Glu	His	Leu	Ala	Ala	Ala	Leu	Gly	Arg	Lys	Ser	Glu	
			165					170						175		
Glu	Phe	Ala	Asp	Val	Val	Lys	Ala	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	
		180						185					190			
Thr	Pro	Val	Thr	Leu	Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Ala	Gln	Val	
		195					200					205				
Arg	Tyr	Gly	Val	Glu	Arg	Leu	Ala	Ala	Ser	Leu	Pro	Arg	Leu	Ala	Glu	
	210					215					220					
Leu	Pro	Leu	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Ile	Asn	Thr	Pro	Pro	
225				230				235							240	
Gly	Phe	Ser	Ala	Ala	Val	Ile	Ala	Glu	Val	Ala	Arg	Val	Thr	Gly	Leu	
			245					250						255		
Pro	Leu	Thr	Glu	Ala	Arg	Asp	His	Phe	Glu	Ala	Gln	Gly	Ala	Arg	Asp	
		260						265					270			
Gly	Ile	Val	Glu	Thr	Ser	Gly	Gln	Leu	Arg	Thr	Ile	Ala	Val	Gly	Leu	
		275					280					285				
Thr	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Trp	Met	Ala	Ser	Gly	Pro	Arg	Thr	
	290					295					300					
Gly	Leu	Ser	Glu	Ile	Ser	Leu	Pro	Asp	Leu	Gln	Pro	Gly	Ser	Ser	Ile	
305				310						315					320	
Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Ile	Pro	Glu	Ala	Val	Leu	Met	Val	
			325					330						335		
Ala	Ala	Gln	Val	Thr	Gly	Asn	Asp	Ala	Thr	Val	Ala	Ala	Ala	Gly	Ala	
		340						345					350			
Ala	Gly	Asn	Phe	Glu	Leu	Asn	Val	Met	Leu	Pro	Val	Ile	Ala	Lys	Asn	
		355					360					365				
Val	Leu	Glu	Ser	Val	Arg	Leu	Leu	Ala	His	Val	Ser	Arg	Leu	Leu	Ala	
	370					375					380					
Asp	Arg	Thr	Val	Asp	Gly	Ile	Val	Ala	His	Arg	Asp	Arg	Ala	Arg	Glu	
385					390					395					400	
Tyr	Ala	Glu	Ser	Ser	Pro	Ser	Val	Val	Thr	Pro	Leu	Asn	Lys	Tyr	Ile	
			405					410						415		
Gly	Tyr	Glu	Glu	Ala	Ala	Lys	Val	Ala	Lys	Lys	Ala	Leu	Ala	Glu	Arg	

PF59083SeqList PF59083.txt

420 425 430
Gln Thr Ile Arg Gln Val Val Leu Glu Ser Gly Tyr Val Asp Arg Gly
435 440 445
Asp Leu Thr Leu Glu Gln Leu Asp Glu Ala Leu Asp Val Leu Arg Met
450 455 460
Thr His Pro
465

<210> 9797
<211> 1386
<212> DNA
<213> Streptomyces coelicolor

<220>
<221> CDS
<222> (1)..(1386)
<223> transl_table=11

<400> 9797
atg agc gaa tac cgc atc gag cac gac tcc atg ggc gag gtc cgc gtc 48
Met Ser Glu Tyr Arg Ile Glu His Asp Ser Met Gly Glu Val Arg Val
1 5 10 15
ccc gcg gac gcc aag tgg cgc gcc cag acc cag cgc gcc gtc gag aac 96
Pro Ala Asp Ala Lys Trp Arg Ala Gln Thr Gln Arg Ala Val Glu Asn
20 25 30
ttc ccc gtc tcc ggg cag cgc atc gag cgc gcg cac atc gag gcg ctg 144
Phe Pro Val Ser Gly Gln Arg Ile Glu Arg Ala His Ile Glu Ala Leu
35 40 45
gcg cgg atc aag agc gcg gcg gcg aag gtc aac gcc gag ctg gga gtg 192
Ala Arg Ile Lys Ser Ala Ala Lys Val Asn Ala Glu Leu Gly Val
50 55 60
ctc gac gag gac gtc gcc ggc gcg atc cag gag gcg gcc ggt gag gtg 240
Leu Asp Glu Asp Val Ala Gly Ala Ile Gln Glu Ala Ala Gly Glu Val
65 70 75 80
gcc gag ggg aag tgg gag gag cac ttc ccc gtc gac gtg ttc cag acc 288
Ala Glu Gly Lys Trp Asp Glu His Phe Pro Val Asp Val Phe Gln Thr
85 90 95
ggg tcc ggg acc tcg tcc aac atg aac acc aac gag gtc gtc gcc acc 336
Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Val Ala Thr
100 105 110
ctg gcg act gaa cgg ctc ggc cgc gac gtg cat ccc aac gac cac gtc 384
Leu Ala Thr Glu Arg Leu Gly Arg Asp Val His Pro Asn Asp His Val
115 120 125
aac gcc tcc cag tcg tcc aac gac gtc ttc ccg tcc tcg atc cac atc 432
Asn Ala Ser Gln Ser Ser Asn Asp Val Phe Pro Ser Ile His Ile
130 135 140
gcc gcc acc gcc gcc gtc acc cgc gac ctg atc ccg gcc ctg gac cat 480
Ala Ala Thr Ala Ala Val Thr Arg Asp Leu Ile Pro Ala Leu Asp His
145 150 155 160
ctc gcc ggc gcc ctg gag cgc aag gcc ggg gag ttc gcc gac gtg gtg 528
Leu Ala Gly Ala Leu Glu Arg Lys Ala Gly Glu Phe Ala Asp Val Val
165 170 175
aag tcc ggg cgt acg cac ctc atg gac gcc acg ccc gtc acc ctg ggc 576
Lys Ser Gly Arg Thr His Leu Met Asp Ala Thr Pro Val Thr Leu Gly
180 185 190
cag gag ttc ggc ggt tac gcg gcc cag gtg cgg tac ggc atc gag cgg 624
Gln Glu Phe Gly Gly Tyr Ala Ala Gln Val Arg Tyr Gly Ile Glu Arg
195 200 205
ctt cag gcc tca ctg ccc cgg ctc gcc gag ctg ccg ctg ggc ggc acc 672
Leu Gln Ala Ser Leu Pro Arg Leu Ala Glu Leu Pro Leu Gly Gly Thr
210 215 220
gcg gtc ggc acc ggc atc aac acc ccg ccc ggc ttc tcc gcc gcc gtc 720
Ala Val Gly Thr Gly Ile Asn Thr Pro Pro Gly Phe Ser Ala Ala Val
225 230 235 240
atc gag gag gtg gcc cgc gcg acg ggg ctg ccg ctg acc gag gcg cgc 768
Ile Glu Glu Val Ala Arg Ala Thr Gly Leu Pro Leu Thr Glu Ala Arg
245 250 255
gac cac ttc gag gcg cag ggc gcc cgg gac ggc atc gtc gag acc agc 816
Asp His Phe Glu Ala Gln Gly Ala Arg Asp Gly Ile Val Glu Thr Ser

PF59083SeqList PF59083.txt

260	265	270	
ggg cag ctg cgg acc atc ggc gtc ggg ctc acg aag atc gcc aac gac	864		
Gly Gln Leu Arg Thr Ile Gly Val Gly Leu Thr Lys Ile Ala Asn Asp			
275	280	285	
ctg cgc tgg atg gcg tcc ggt ccg cgc acc ggg ctc gcg gag atc tcg	912		
Leu Arg Trp Met Ala Ser Gly Pro Arg Thr Gly Leu Ala Glu Ile Ser			
290	295	300	
ctg ccc gac ctc cag ccc ggg tcg tcc atc atg ccc ggc aag gtc aac	960		
Leu Pro Asp Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn			
305	310	315	
ccg gtg atc ccc gag gcg gtc ctc atg gtc gcc cag gtc acc ggc	1008		
Pro Val Ile Pro Glu Ala Val Leu Met Val Ala Ala Gln Val Thr Gly			
325	330	335	
aac gac gcg acg gtc gcc gcg gcg ggc gcg gcc ggc aac ttc gag ctg	1056		
Asn Asp Ala Thr Val Ala Ala Gly Ala Ala Gly Asn Phe Glu Leu			
340	345	350	
aac gtg atg ctg ccg gtc atc gcc aag aac gtg ctg gag tcg gtg cgg	1104		
Asn Val Met Leu Pro Val Ile Ala Lys Asn Val Leu Glu Ser Val Arg			
355	360	365	
ctg ctc gcc aac gtc tcc cgg ctg ctc gcc gac cgc acc gtg gac ggg	1152		
Leu Leu Ala Asn Val Ser cgg Leu Leu Ala Asp Arg Thr Val Asp Gly			
370	375	380	
atc gtg gcg cac ccc gag cgg gcc cgc gag tac gcc gag tcc tcg ccc	1200		
Ile Val Ala His Pro Glu Arg Ala Arg Glu Tyr Ala Glu Ser Ser Pro			
385	390	395	
tcc gtg gtc acg ccg ctc aac aag tac ctc ggg tac gag gag gcc gcc	1248		
Ser Val Val Thr Pro Leu Asn Lys Tyr Leu Gly Tyr Glu Glu Ala Ala			
405	410	415	
aag gtc gcc aag agg gcg ctg gcc gag cgg aag acg atc cgg cag acc	1296		
Lys Val Ala Lys Arg Ala Leu Ala Glu Arg Lys Thr Ile Arg Gln Thr			
420	425	430	
gtg ctg gag ggc ggc tac gtg gaa cgc ggc gac ctc acg cgg gag caa	1344		
Val Leu Glu Gly Gly Tyr Val Glu Arg Gly Asp Leu Thr Arg Glu Gln			
435	440	445	
ctg gac cag gcc ctg gac gtg cgg atg acc cgc ccg tga	1386		
Leu Asp Gln Ala Leu Asp Val Leu Arg Met Thr Arg Pro			
450	455	460	

<210> 9798

<211> 461

<212> PRT

<213> Streptomyces coelicolor

<400> 9798

Met Ser Glu Tyr Arg Ile Glu His Asp Ser Met Gly Glu Val Arg Val	
1 5 10 15	
Pro Ala Asp Ala Lys Trp Arg Ala Gln Thr Gln Arg Ala Val Glu Asn	
20 25 30	
Phe Pro Val Ser Gly Gln Arg Ile Glu Arg Ala His Ile Glu Ala Leu	
35 40 45	
Ala Arg Ile Lys Ser Ala Ala Ala Lys Val Asn Ala Glu Leu Gly Val	
50 55 60	
Leu Asp Glu Asp Val Ala Gly Ala Ile Gln Glu Ala Ala Gly Glu Val	
65 70 75 80	
Ala Glu Gly Lys Trp Asp Glu His Phe Pro Val Asp Val Phe Gln Thr	
85 90 95	
Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Val Ala Thr	
100 105 110	
Leu Ala Thr Glu Arg Leu Gly Arg Asp Val His Pro Asn Asp His Val	
115 120 125	
Asn Ala Ser Gln Ser Ser Asn Asp Val Phe Pro Ser Ser Ile His Ile	
130 135 140	
Ala Ala Thr Ala Ala Val Thr Arg Asp Leu Ile Pro Ala Leu Asp His	
145 150 155 160	
Leu Ala Gly Ala Leu Glu Arg Lys Ala Gly Glu Phe Ala Asp Val Val	
165 170 175	
Lys Ser Gly Arg Thr His Leu Met Asp Ala Thr Pro Val Thr Leu Gly	
180 185 190	
Gln Glu Phe Gly Gly Tyr Ala Ala Gln Val Arg Tyr Gly Ile Glu Arg	

PF59083SeqList PF59083.txt

Leu	Gln	Ala	Ser	Leu	Pro	Arg	Leu	Ala	Glu	Leu	Pro	Leu	Gly	Gly	Thr
210	210	210	210	210	210	210	200	200	200	200	200	205	205	205	205
Ala	Val	Gly	Thr	Gly	Ile	Asn	Thr	Pro	Pro	Gly	Phe	Ser	Ala	Ala	Val
225	225	225	225	225	230	230	215	215	215	235	220	220	220	220	240
Ile	Glu	Glu	Val	Ala	Arg	Ala	Thr	Gly	Leu	Pro	Leu	Thr	Glu	Ala	Arg
				245					250					255	
Asp	His	Phe	Glu	Ala	Gln	Gly	Ala	Arg	Asp	Gly	Ile	Val	Glu	Thr	Ser
			260					265					270		
Gly	Gln	Leu	Arg	Thr	Ile	Gly	Val	Gly	Leu	Thr	Lys	Ile	Ala	Asn	Asp
			275				280					285			
Leu	Arg	Trp	Met	Ala	Ser	Gly	Pro	Arg	Thr	Gly	Leu	Ala	Glu	Ile	Ser
	290					295					300				
Leu	Pro	Asp	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn
305					310					315					320
Pro	Val	Ile	Pro	Glu	Ala	Val	Leu	Met	Val	Ala	Ala	Gln	Val	Thr	Gly
				325					330					335	
Asn	Asp	Ala	Thr	Val	Ala	Ala	Ala	Gly	Ala	Ala	Gly	Asn	Phe	Glu	Leu
			340					345					350		
Asn	Val	Met	Leu	Pro	Val	Ile	Ala	Lys	Asn	Val	Leu	Glu	Ser	Val	Arg
		355					360					365			
Leu	Leu	Ala	Asn	Val	Ser	Arg	Leu	Leu	Ala	Asp	Arg	Thr	Val	Asp	Gly
	370					375					380				
Ile	Val	Ala	His	Pro	Glu	Arg	Ala	Arg	Glu	Tyr	Ala	Glu	Ser	Ser	Pro
385					390					395					400
Ser	Val	Val	Thr	Pro	Leu	Asn	Lys	Tyr	Leu	Gly	Tyr	Glu	Glu	Ala	Ala
				405					410					415	
Lys	Val	Ala	Lys	Arg	Ala	Leu	Ala	Glu	Arg	Lys	Thr	Ile	Arg	Gln	Thr
			420					425					430		
Val	Leu	Glu	Gly	Gly	Tyr	Val	Glu	Arg	Gly	Asp	Leu	Thr	Arg	Glu	Gln
		435					440					445			
Leu	Asp	Gln	Ala	Leu	Asp	Val	Leu	Arg	Met	Thr	Arg	Pro			
	450					455					460				

<210> 9799
 <211> 1485
 <212> DNA
 <213> Rhizopus oryzae

<220>
 <221> CDS
 <222> (1)..(1485)

<400> 9799	
atg ttg cga gct tct gct acc aga ttc tta agt caa gct aaa aac atg	48
Met Leu Arg Ala Ser Ala Thr Arg Phe Leu Ser Gln Ala Lys Asn Met	
1 5 10 15	
aac aac tct cct cgt ctt ttc agt agt gcc tct gct gct ttg caa aaa	96
Asn Asn Ser Pro Arg Leu Phe Ser Ser Ala Ser Ala Ala Leu Gln Lys	
20 25 30	
ttc cgt gct gag cgc gat act ttt ggt gat ctc caa gtt cct gct gat	144
Phe Arg Ala Glu Arg Asp Thr Phe Gly Asp Leu Gln Val Pro Ala Asp	
35 40 45	
aga tat tgg ggt gct caa acc caa agg tct ctt caa aat ttt gac att	192
Arg Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn Phe Asp Ile	
50 55 60	
ggt ggc cct act gaa cgt atg ccc gaa cct ttg atc cgt gcc ttt ggt	240
Gly Gly Pro Thr Glu Arg Met Pro Glu Pro Leu Ile Arg Ala Phe Gly	
65 70 75 80	
gtc ctc aaa aag gct gct gct act gtc aac atg act tat ggc ttg gat	288
Val Leu Lys Lys Ala Ala Ala Thr Val Asn Met Thr Tyr Gly Leu Asp	
85 90 95	
cct aaa gtt ggt gaa gct att caa aag gct gct gac gag gtc att gat	336
Pro Lys Val Gly Glu Ala Ile Gln Lys Ala Ala Asp Glu Val Ile Asp	
100 105 110	
gga agc ttg att gat cat ttc cct ctt gtt gtc tgg caa act ggt tcc	384
Gly Ser Leu Ile Asp His Phe Pro Leu Val Val Trp Gln Thr Gly Ser	
115 120 125	
ggt act caa acc aag atg aac gtt aac gaa gtt atc tcc aac cgt gct	432

PF59083SeqList PF59083.txt																
Gly	Thr	Gln	Thr	Lys	Met	Asn	Val	Asn	Glu	Val	Ile	Ser	Asn	Arg	Ala	
130	130					135					140					
att	gaa	ctt	ttg	ggt	ggt	gag	ctt	ggt	agt	aag	gct	cct	ggt	cat	ccc	480
Ile	Glu	Leu	Leu	Gly	Gly	Glu	Leu	Gly	Ser	Lys	Ala	Pro	Val	His	Pro	
145				150						155					160	
aac	gat	cat	gtc	aac	atg	agt	caa	tca	tcc	aat	gac	acg	ttc	cct	act	528
Asn	Asp	His	Val	Asn	Met	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	
				165					170					175		
gcc	atg	cac	gtt	gct	gct	gtt	gtt	gaa	att	cac	ggt	cga	ctt	att	cct	576
Ala	Met	His	Val	Ala	Ala	Val	Val	Glu	Ile	His	Gly	Arg	Leu	Ile	Pro	
			180					185					190			
gct	ttg	acc	act	ttg	cgt	gat	gcc	ctt	caa	gcc	aaa	tcc	gct	gag	ttt	624
Ala	Leu	Thr	Thr	Leu	Arg	Asp	Ala	Leu	Gln	Ala	Lys	Ser	Ala	Glu	Phe	
			195				200					205				
gaa	cac	atc	atc	aag	atc	ggt	cgt	act	cac	ttg	caa	gat	gca	act	cct	672
Glu	His	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Leu	Gln	Asp	Ala	Thr	Pro	
						215					220					
ttg	act	ctc	ggt	caa	gaa	ttc	tct	ggt	tat	act	caa	caa	ttg	act	tac	720
Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Thr	Gln	Gln	Leu	Thr	Tyr	
225				230						235					240	
ggt	att	gct	cgt	gta	caa	ggt	acc	ttg	gag	cgc	ctc	tat	aac	ctt	gct	768
Gly	Ile	Ala	Arg	Val	Gln	Gly	Thr	Leu	Glu	Arg	Leu	Tyr	Asn	Leu	Ala	
				245				250						255		
caa	ggt	ggt	act	gct	gtt	ggt	act	ggt	ctt	aac	acc	aga	aaa	ggt	ttc	816
Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Arg	Lys	Gly	Phe	
			260					265					270			
gat	gcc	aag	gta	gct	gaa	gct	att	gct	tct	att	acc	ggt	ctt	cct	ttc	864
Asp	Ala	Lys	Val	Ala	Glu	Ala	Ile	Ala	Ser	Ile	Thr	Gly	Leu	Pro	Phe	
			275				280					285				
aag	acc	gcc	cct	aat	aag	ttt	gaa	gcc	ctt	gct	gct	cac	gat	gct	ctc	912
Lys	Thr	Ala	Pro	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Leu	
						295					300					
gtt	gaa	gct	cac	gga	gct	ctc	aat	acc	gtt	gct	tgt	tct	ctt	atg	aag	960
Val	Glu	Ala	His	Gly	Ala	Leu	Asn	Thr	Val	Ala	Cys	Ser	Leu	Met	Lys	
305				310						315					320	
atc	gcc	aac	gat	atc	cgt	tat	ctt	ggt	tct	gga	cct	cgc	tgt	ggt	ctt	1008
Ile	Ala	Asn	Asp	Ile	Arg	Tyr	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	
				325				330						335		
ggt	gaa	ctt	tcc	ttg	cct	gaa	aac	gaa	ccc	gga	tct	tct	atc	atg	ccc	1056
Gly	Glu	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
			340					345					350			
ggt	aag	gtt	aat	cct	act	caa	tgt	gaa	gct	atg	acc	atg	gtc	tgt	gct	1104
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Met	Thr	Met	Val	Cys	Ala	
			355				360					365				
caa	gtc	atg	ggt	aac	aac	act	gct	att	tct	gtt	gct	ggt	tcc	aat	ggt	1152
Gln	Val	Met	Gly	Asn	Asn	Thr	Ala	Ile	Ser	Val	Ala	Gly	Ser	Asn	Gly	
			370			375					380					
caa	ttc	gag	ctt	aat	gtc	ttc	aaa	ccc	gtc	atg	atc	aag	aac	ttg	atc	1200
Gln	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Met	Ile	Lys	Asn	Leu	Ile	
385				390						395					400	
caa	tcc	att	cgt	ctt	att	tct	gat	gcc	tct	att	tca	ttc	acc	aaa	aac	1248
Gln	Ser	Ile	Arg	Leu	Ile	Ser	Asp	Ala	Ser	Ile	Ser	Phe	Thr	Lys	Asn	
				405				410						415		
tgt	gtt	gtt	ggt	att	gaa	gcc	aat	gaa	aag	aag	att	agc	agc	att	atg	1296
Cys	Val	Val	Gly	Ile	Glu	Ala	Asn	Glu	Lys	Lys	Ile	Ser	Ser	Ile	Met	
			420					425					430			
aat	gag	tca	ttg	atg	ttg	gtc	act	gct	ctt	aac	cct	cat	att	ggt	tac	1344
Asn	Glu	Ser	Leu	Met	Leu	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	
			435			440						445				
gat	aaa	gct	gct	aaa	tgt	gcc	aag	aag	gcc	cac	aag	gaa	ggc	acc	acc	1392
Asp	Lys	Ala	Ala	Lys	Cys	Ala	Lys	Lys	Ala	His	Lys	Glu	Gly	Thr	Thr	
			450			455					460					
ttg	aag	gaa	gct	gcc	ctt	tct	ctt	ggt	tac	ttg	act	tct	gaa	gaa	ttc	1440
Leu	Lys	Glu	Ala	Ala	Leu	Ser	Leu	Gly	Tyr	Leu	Thr	Ser	Glu	Glu	Phe	
465				470				475							480	
gac	cag	tgg	gtt	aga	ccc	gaa	gat	atg	atc	tct	gcc	aag	gat	taa		1485
Asp	Gln	Trp	Val	Arg	Pro	Glu	Asp	Met	Ile	Ser	Ala	Lys	Asp			
				485				490								

PF59083SeqList PF59083.txt

<210> 9800

<211> 494

<212> PRT

<213> *Rhizopus oryzae*

<400> 9800

```

Met Leu Arg Ala Ser Ala Thr Arg Phe Leu Ser Gln Ala Lys Asn Met
1      5      10      15
Asn Asn Ser Pro Arg Leu Phe Ser Ser Ala Ser Ala Ala Leu Gln Lys
      20      25      30
Phe Arg Ala Glu Arg Asp Thr Phe Gly Asp Leu Gln Val Pro Ala Asp
      35      40      45
Arg Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn Phe Asp Ile
      50      55      60
Gly Gly Pro Thr Glu Arg Met Pro Glu Pro Leu Ile Arg Ala Phe Gly
65      70      75      80
Val Leu Lys Lys Ala Ala Ala Thr Val Asn Met Thr Tyr Gly Leu Asp
      85      90      95
Pro Lys Val Gly Glu Ala Ile Gln Lys Ala Ala Asp Glu Val Ile Asp
      100      105      110
Gly Ser Leu Ile Asp His Phe Pro Leu Val Val Trp Gln Thr Gly Ser
      115      120      125
Gly Thr Gln Thr Lys Met Asn Val Asn Glu Val Ile Ser Asn Arg Ala
      130      135      140
Ile Glu Leu Leu Gly Gly Glu Leu Gly Ser Lys Ala Pro Val His Pro
145      150      155      160
Asn Asp His Val Asn Met Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr
      165      170      175
Ala Met His Val Ala Ala Val Val Glu Ile His Gly Arg Leu Ile Pro
      180      185      190
Ala Leu Thr Thr Leu Arg Asp Ala Leu Gln Ala Lys Ser Ala Glu Phe
      195      200      205
Glu His Ile Ile Lys Ile Gly Arg Thr His Leu Gln Asp Ala Thr Pro
      210      215      220
Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Thr Gln Gln Leu Thr Tyr
225      230      235      240
Gly Ile Ala Arg Val Gln Gly Thr Leu Glu Arg Leu Tyr Asn Leu Ala
      245      250      255
Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Arg Lys Gly Phe
      260      265      270
Asp Ala Lys Val Ala Glu Ala Ile Ala Ser Ile Thr Gly Leu Pro Phe
      275      280      285
Lys Thr Ala Pro Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Leu
      290      295      300
Val Glu Ala His Gly Ala Leu Asn Thr Val Ala Cys Ser Leu Met Lys
305      310      315      320
Ile Ala Asn Asp Ile Arg Tyr Leu Gly Ser Gly Pro Arg Cys Gly Leu
      325      330      335
Gly Glu Leu Ser Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro
      340      345      350
Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Met Thr Met Val Cys Ala
      355      360      365
Gln Val Met Gly Asn Asn Thr Ala Ile Ser Val Ala Gly Ser Asn Gly
      370      375      380
Gln Phe Glu Leu Asn Val Phe Lys Pro Val Met Ile Lys Asn Leu Ile
385      390      395      400
Gln Ser Ile Arg Leu Ile Ser Asp Ala Ser Ile Ser Phe Thr Lys Asn
      405      410      415
Cys Val Val Gly Ile Glu Ala Asn Glu Lys Lys Ile Ser Ser Ile Met
      420      425      430
Asn Glu Ser Leu Met Leu Val Thr Ala Leu Asn Pro His Ile Gly Tyr
      435      440      445
Asp Lys Ala Ala Lys Cys Ala Lys Lys Ala His Lys Glu Gly Thr Thr
450      455      460
Leu Lys Glu Ala Ala Leu Ser Leu Gly Tyr Leu Thr Ser Glu Glu Phe
465      470      475      480
Asp Gln Trp Val Arg Pro Glu Asp Met Ile Ser Ala Lys Asp
      485      490

```

PF59083SeqList PF59083.txt

<210> 9801
<211> 1449
<212> DNA
<213> Schizosaccharomyces pombe

<220>
<221> CDS
<222> (1)..(1449)

```

<400> 9801
atg aat tcc act act ccg act tat cat ctc att ccc aaa ggc ggt aag      48
Met Asn Ser Thr Thr Pro Thr Tyr His Leu Ile Pro Lys Gly Gly Lys
  1      5      10      15
cat ggc gag ttc cga cag gaa tct gac acc ttt ggt ccc ata caa gtc      96
His Gly Glu Phe Arg Gln Glu Ser Asp Thr Phe Gly Pro Ile Gln Val
      20      25
cct gca gaa aag tat tgg ggt gct caa act cag cgt tct ctt caa aac      144
Pro Ala Glu Lys Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn
      35      40      45
ttt cga att ggt ggt gaa aaa gag cga ctt cct ctt ccc tta gtt cgc      192
Phe Arg Ile Gly Gly Glu Lys Glu Arg Leu Pro Leu Pro Leu Val Arg
      50      55      60
gca ttt gga gtt tta aag cgt gcg gct gct tct gtt aat cgt gaa ttc      240
Ala Phe Gly Val Leu Lys Arg Ala Ala Ala Ser Val Asn Arg Glu Phe
      65      70      75      80
ggt ttg gat ccc aaa ctt gca gat gcc att gaa cag gct gcc caa gaa      288
Gly Leu Asp Pro Lys Leu Ala Asp Ala Ile Glu Gln Ala Ala Gln Glu
      85      90      95
gtc att gat ggt cgt ttg gat gat aac ttc ccc ttg gtt gtt ttc caa      336
Val Ile Asp Gly Arg Leu Asp Asp Asn Phe Pro Leu Val Val Phe Gln
      100      105      110
act ggc tcg ggc acc caa tcc aat atg aac agt aac gag gta atc gct      384
Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ser Asn Glu Val Ile Ala
      115      120      125
aat cgt gcc ata gaa atc ctt ggt acg tta ggt tcg aaa aag ccc      432
Asn Arg Ala Ile Glu Ile Leu Gly Gly Thr Leu Gly Ser Lys Lys Pro
      130      135      140
gtt cat cca aac gat cac gtt aac atg tct caa tct tct aac gac act      480
Val His Pro Asn Asp His Val Asn Met Ser Gln Ser Ser Asn Asp Thr
      145      150      155
ttc ccc act gtt atg cat att gcc tct gtt ttg caa att cac act cat      528
Phe Pro Thr Val Met His Ile Ala Ser Val Leu Gln Ile His Thr His
      160      165      170      175
tta ctt cct gcc atg aag cac ctc cac cgg gcc ttg aag ggt aag gaa      576
Leu Leu Pro Ala Met Lys His Leu His Arg Ala Leu Lys Gly Lys Glu
      180      185      190
gag gag ttt aag aac att atc aaa atc ggt cga acc cac atg caa gat      624
Glu Glu Phe Lys Asn Ile Ile Lys Ile Gly Arg Thr His Met Gln Asp
      195      200      205
gcc act cct ctt tct tta ggt caa gaa ttt tcc ggc tat gtt act cag      672
Ala Thr Pro Leu Ser Leu Gly Gln Glu Phe Ser Gly Tyr Val Thr Gln
      210      215      220
gtt ggt tat ggc att gag cgc ata aac aac gct ctt cct cgt ctt tgt      720
Val Gly Tyr Gly Ile Glu Arg Ile Asn Asn Ala Leu Pro Arg Leu Cys
      225      230      235      240
ctt ctc gct caa ggt ggt act gcc gtg ggt act gga cta aat act ttt      768
Leu Leu Ala Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Phe
      245      250      255
gaa gga ttt gac gtg aag gtt gct gag aag gtt tca aag ctt aca aat      816
Glu Gly Phe Asp Val Lys Val Ala Glu Lys Val Ser Lys Leu Thr Asn
      260      265      270
att gag ttt aag acc gcc cct aac aag ttt gag gct ctt gca gcc cat      864
Ile Glu Phe Lys Thr Ala Pro Asn Lys Phe Glu Ala Leu Ala Ala His
      275      280      285
gat gcg att gtg gag atg agt ggt gct tta aat gtt att gct tgt tct      912
Asp Ala Ile Val Glu Met Ser Gly Ala Leu Asn Val Ile Ala Cys Ser
      290      295      300
ctt atg aaa att gct aac gat att cgt caa ctt ggt tct ggc cct cgt      960
Leu Met Lys Ile Ala Asn Asp Ile Arg Gln Leu Gly Ser Gly Pro Arg

```


PF59083SeqList PF59083.txt

305		310		315		320	
tgt ggt tta ggc gaa ttg atc ctt cct gct aat gaa cct gga agt tca							1008
Cys Gly Leu Gly Glu Leu Ile Leu Pro Ala Asn Glu Pro Gly Ser Ser							
		325		330		335	
atc atg cca ggc aaa gta aac ccc acc caa tgt gaa gcc tta aca atg							1056
Ile Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met							
		340		345		350	
gtt tgt gct caa gta atg ggc aat cat gcc act att act gtc gct ggt							1104
Val Cys Ala Gln Val Met Gly Asn His Ala Thr Ile Thr Val Ala Gly							
		355		360		365	
gcc tcc gga cac tgt gaa ctc aat gtt ttt aaa cct ctt tta gca aag							1152
Ala Ser Gly His Cys Glu Leu Asn Val Phe Lys Pro Leu Leu Ala Lys							
		370		375		380	
aac att cta agc agt att cgt ctt tta ggg gat gct tgc gag tct ttt							1200
Asn Ile Leu Ser Ser Ile Arg Leu Leu Gly Asp Ala Cys Glu Ser Phe							
		385		390		400	
act gat cat tgc gtt gtc ggc att gag cca aat tac gaa ggt att gcc							1248
Thr Asp His Cys Val Val Gly Ile Glu Pro Asn Tyr Glu Gly Ile Ala							
		405		410		415	
cgt cat ctt cgt gat tcc ttg atg ctt gtt act gcg tta aat cct cac							1296
Arg His Leu Arg Asp Ser Leu Met Leu Val Thr Ala Leu Asn Pro His							
		420		425		430	
atc ggt tat gat aac tgt gcc aag att gcc aag act gct ctt aaa aat							1344
Ile Gly Tyr Asp Asn Cys Ala Lys Ile Ala Lys Thr Ala Leu Lys Asn							
		435		440		445	
aag agc act ctc aag cac gag ttt gtt act ttg ggt ttc ggt acc ccc							1392
Lys Ser Thr Leu Lys His Glu Phe Val Thr Leu Gly Phe Gly Thr Pro							
		450		455		460	
gag caa ttc gat gaa tgg gtt cgc cct gaa tta atg att tca gct aag							1440
Glu Gln Phe Asp Glu Trp Val Arg Pro Glu Leu Met Ile Ser Ala Lys							
		465		470		475	
aaa gta taa							1449
Lys Val							

<210> 9802

<211> 482

<212> PRT

<213> Schizosaccharomyces pombe

<400> 9802

Met Asn Ser Thr Thr Pro Thr Tyr His Leu Ile Pro Lys Gly Gly Lys	
1 5 10 15	
His Gly Glu Phe Arg Gln Glu Ser Asp Thr Phe Gly Pro Ile Gln Val	
20 25 30	
Pro Ala Glu Lys Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn	
35 40 45	
Phe Arg Ile Gly Gly Glu Lys Glu Arg Leu Pro Leu Pro Leu Val Arg	
50 55 60	
Ala Phe Gly Val Leu Lys Arg Ala Ala Ala Ser Val Asn Arg Glu Phe	
65 70 75 80	
Gly Leu Asp Pro Lys Leu Ala Asp Ala Ile Glu Gln Ala Ala Gln Glu	
85 90 95	
Val Ile Asp Gly Arg Leu Asp Asp Asn Phe Pro Leu Val Val Phe Gln	
100 105 110	
Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ser Asn Glu Val Ile Ala	
115 120 125	
Asn Arg Ala Ile Glu Ile Leu Gly Gly Thr Leu Gly Ser Lys Lys Pro	
130 135 140	
Val His Pro Asn Asp His Val Asn Met Ser Gln Ser Ser Asn Asp Thr	
145 150 155 160	
Phe Pro Thr Val Met His Ile Ala Ser Val Leu Gln Ile His Thr His	
165 170 175	
Leu Leu Pro Ala Met Lys His Leu His Arg Ala Leu Lys Gly Lys Glu	
180 185 190	
Glu Glu Phe Lys Asn Ile Ile Lys Ile Gly Arg Thr His Met Gln Asp	
195 200 205	
Ala Thr Pro Leu Ser Leu Gly Gln Glu Phe Ser Gly Tyr Val Thr Gln	
210 215 220	

PF59083SeqList PF59083.txt

Val 225	Gly	Tyr	Gly	Ile	Glu 230	Arg	Ile	Asn	Asn	Ala 235	Leu	Pro	Arg	Leu	Cys 240
Leu	Leu	Ala	Gln	Gly 245	Gly	Thr	Ala	Val	Gly 250	Thr	Gly	Leu	Asn	Thr 255	Phe
Glu	Gly	Phe	Asp	Val	Lys	Val	Ala	Glu 265	Lys	Val	Ser	Lys	Leu	Thr	Asn
Ile	Glu	Phe 275	Lys	Thr	Ala	Pro	Asn 280	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His
Asp	Ala 290	Ile	Val	Glu	Met	Ser 295	Gly	Ala	Leu	Asn	Val 300	Ile	Ala	Cys	Ser
Leu 305	Met	Lys	Ile	Ala	Asn 310	Asp	Ile	Arg	Gln	Leu 315	Gly	Ser	Gly	Pro	Arg 320
Cys	Gly	Leu	Gly	Glu 325	Leu	Ile	Leu	Pro	Ala 330	Asn	Glu	Pro	Gly	Ser 335	Ser
Ile	Met	Pro	Gly 340	Lys	Val	Asn	Pro	Thr 345	Gln	Cys	Glu	Ala	Leu	Thr	Met
Val	Cys	Ala 355	Gln	Val	Met	Gly	Asn 360	His	Ala	Thr	Ile	Thr	Val	Ala	Gly
Ala	Ser 370	Gly	His	Cys	Glu	Leu 375	Asn	Val	Phe	Lys	Pro 380	Leu	Leu	Ala	Lys
Asn 385	Ile	Leu	Ser	Ser	Ile 390	Arg	Leu	Leu	Gly	Asp 395	Ala	Cys	Glu	Ser	Phe 400
Thr	Asp	His	Cys	Val 405	Val	Gly	Ile	Glu	Pro 410	Asn	Tyr	Glu	Gly	Ile 415	Ala
Arg	His	Leu	Arg 420	Asp	Ser	Leu	Met 425	Leu	Val	Thr	Ala	Leu	Asn	Pro	His
Ile	Gly	Tyr 435	Asp	Asn	Cys	Ala	Lys 440	Ile	Ala	Lys	Thr	Ala	Leu	Lys	Asn
Lys	Ser 450	Thr	Leu	Lys	His	Glu 455	Phe	Val	Thr	Leu	Gly 460	Phe	Gly	Thr	Pro
Glu 465	Gln	Phe	Asp	Glu	Trp 470	Val	Arg	Pro	Glu	Leu 475	Met	Ile	Ser	Ala	Lys 480
Lys	Val														

<210> 9803

<211> 2489

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (830)..(2296)

<400> 9803

taatcacttc tacgagtcta gtagatctct tctccttcct ataagtggtt aatgtattct 60

tcgagaagct catcattttt ttttttcatt tttttttttt ttttcagttt tctacaattt 120

catcaaatca atgggttaaac cgggcagaaa aactaccaag cgttactttt actgatgtta 180

gtactactac cgcagttatt gcgactacta cattaactat aactatacaa gaaaaaaagt 240

aaagagggct cgtaaagcaa agcttggtat ctcctacata gtcaatacat agtagtgagt 300

cgcttatagc cattctgtaa tgccatttgt taagacgtgt ccttaaacc ttccgaatcg 360

ccgcgggcga catcataatg tcagtaccta ataatgggta ttattcgtac cctgtgggta 420

gagagctatg gaagctagca gtaaagtgtc ctagttcttg ctatcactac catattggag 480

PF59083SeqList PF59083.txt

aggcttcagg cccctcccct gagccgatcc tcggaatgac taccccgatt cccggaatgg 540

gcgttcgatg attggctctt tcctgtaaag cctttttgcg tttcttatag gctatatata 600

atcttcatca ctgttgtaga cgtaaaca gcaccaaca ggaggccgga ccgaacacac 660

gggggagtga ctctagctct ttcttctggg atattcatat cgtttctcca ttacatacag 720

tcattttttt gcatttttaa attcgtgact tttagtactg cagctgtttt ttttctcacg 780

tcaagaaatt ccataaagtc taactattaa acggataaga gatacaatc atg ttg aga 838
Met Leu Arg

ttt acc aat tgt agt tgc aag act ttc gta aaa tcg tca tat aag ctt 886
Phe Thr 5 Asn Cys Ser Cys Lys 10 Thr Phe Val Lys 15 Ser Ser Tyr Lys Leu

aat ata aga aga atg aac tcc tcg ttc aga act gaa acc gat gca ttt 934
Asn Ile Arg Arg Met Asn Ser Ser Phe Arg Thr Glu Thr Asp Ala Phe 20 25 30 35

ggg gag ata cac gtg cct gct gat aag tac tgg ggt gcc caa act caa 982
Gly Glu Ile His Val Pro Ala Asp Lys Tyr Trp Gly Ala Gln Thr Gln 40 45 50

aga tcc ttt caa aac ttc aag att ggt ggc gct cgt gaa aga atg cca 1030
Arg Ser Phe Gln Asn Phe Lys Ile Gly Gly Ala Arg Glu Arg Met Pro 55 60 65

ttg cct ttg gtg cat gca ttt ggt gtt ttg aag aaa tct gcc gcg att 1078
Leu Pro Leu Val His Ala Phe Gly Val Leu Lys Lys Ser Ala Ala Ile 70 75 80

gtg aat gag tct ctg ggg gga ttg gat ccc aag atc tcc aag gct att 1126
Val Asn 85 Glu Ser Leu Gly Gly 90 Leu Asp Pro Lys 95 Ile Ser Lys Ala Ile

caa cag gcc gct gac gaa gtg gct tct ggt aag cta gac gac cac ttt 1174
Gln Gln Ala Ala Asp Glu Val Ala Ser Gly Lys 110 Leu Asp Asp His Phe 100 105 115

cca ttg gtt gtt ttc caa acg ggt tcc ggt acc cag tct aac atg aat 1222
Pro Leu Val Val Phe Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn 120 125 130

gct aat gaa gtt att tcc aat cgt gcc att gag atc cta gga ggc aag 1270
Ala Asn Glu Val 135 Ile Ser Asn Arg Ala Ile Glu Ile Leu Gly Gly Lys 140 145

att gga tct aaa caa gtc cat cca aac aat cat tgc aac caa tct caa 1318
Ile Gly Ser Lys Gln Val His Pro Asn Asn His Cys Asn Gln Ser Gln 150 155 160

tca tcc aat gat act ttc ccc act gtc atg cat atc gct gcc agt ttg 1366
Ser Ser 165 Asn Asp Thr Phe Pro 170 Thr Val Met His 175 Ala Ala Ser Leu

caa att caa aac gag ttg ata cct gag ttg acc aat tta aag aac gcc 1414
Gln Ile Gln Asn Glu Leu 185 Ile Pro Glu Leu Thr Asn Leu Lys Asn Ala 180 190 195

ctt gaa gcc aaa tcc aag gaa ttt gac cat att gtg aag atc ggt aga 1462
Leu Glu Ala Lys Ser Lys Glu Phe Asp His Ile Val Lys Ile Gly Arg 200 205 210

aca cac ttg caa gat gcc acg cct ttg aca cta ggt caa gag ttt tcc 1510
Thr His Leu Gln Asp Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Ser 215 220 225

ggg tac gtg caa caa gtt gag aac ggt atc caa aga gtg gca cat tct 1558
Gly Tyr Val Gln Gln Val Glu Asn Gly Ile Gln Arg Val Ala His Ser 230 235 240

ttg aaa aca ttg agt ttc ctg gca caa ggt ggt act gcc gtt ggt aca 1606
Leu Lys 245 Thr Leu Ser Phe 250 Glu Ala Gln Gly Gly Thr 255 Ala Val Gly Thr

ggg ttg aac acc aag ccc gga ttc gat gtc aag ata gcc gag caa att 1654
Gly Leu Asn Thr Lys Pro Gly Phe Asp Val Lys 260 265 Ile Ala Glu Gln Ile 270 275

PF59083SeqList PF59083.txt

tcc	aaa	gaa	act	gga	cta	aag	ttt	caa	acc	gcc	cct	aat	aag	ttc	gag	1702
Ser	Lys	Glu	Thr	Gly	Leu	Lys	Phe	Gln	Thr	Ala	Pro	Asn	Lys	Phe	Glu	
				280					285						290	
gct	ttg	gct	gct	cac	gac	gcc	att	gtc	gaa	tgt	agc	ggg	gct	cta	aac	1750
Ala	Leu	Ala	Ala	His	Asp	Ala	Ile	Val	Glu	Cys	Ser	Gly	Ala	Leu	Asn	
				295				300					305			
acc	ctt	gct	tgt	tct	ctt	ttc	aaa	ata	gcg	caa	gat	ata	aga	tac	tta	1798
Thr	Leu	Ala	Cys	Ser	Leu	Phe	Lys	Ile	Ala	Gln	Asp	Ile	Arg	Tyr	Leu	
				310			315					320				
ggg	tcc	ggg	cca	cgt	tgc	ggc	tac	cat	gaa	cta	atg	ctg	cca	gag	aat	1846
Gly	Ser	Gly	Pro	Arg	Cys	Gly	Tyr	His	Glu	Leu	Met	Leu	Pro	Glu	Asn	
						330					335					
gaa	cca	ggg	tcc	tca	atc	atg	cct	ggg	aaa	gtt	aac	cca	acc	caa	aac	1894
Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Asn	
					345					350					355	
gag	gca	ttg	act	caa	gtg	tgt	gtg	caa	gtc	atg	ggg	aac	aat	gca	gct	1942
Glu	Ala	Leu	Thr	Gln	Val	Cys	Val	Gln	Val	Met	Gly	Asn	Asn	Ala	Ala	
				360					365						370	
atc	acg	ttt	gcc	ggc	tct	caa	ggg	caa	ttc	gag	tta	aat	gtc	ttc	aag	1990
Ile	Thr	Phe	Gly	Ser	Gln	Gly	Gln	Phe	Glu	Leu	Asn	Val	Phe	Lys		
				375				380					385			
cca	gtc	atg	atc	gcc	aat	cta	ttg	aat	tcg	atc	agg	tta	att	act	gat	2038
Pro	Val	Met	Ile	Ala	Asn	Leu	Leu	Asn	Ser	Ile	Arg	Leu	Ile	Thr	Asp	
				390			395					400				
gcc	gca	tat	tca	ttt	aga	gtg	cac	tgt	gtt	gaa	ggg	atc	aaa	gcc	aat	2086
Ala	Ala	Tyr	Ser	Phe	Arg	Val	His	Cys	Val	Glu	Gly	Ile	Lys	Ala	Asn	
				405		410					415					
gag	cct	cgt	att	cat	gag	ttg	ttg	act	aaa	tct	tta	atg	tta	gtc	acc	2134
Glu	Pro	Arg	Ile	His	Glu	Leu	Leu	Thr	Lys	Ser	Leu	Met	Leu	Val	Thr	
					425					430					435	
gct	ttg	aac	cct	aag	atc	ggg	tat	gat	gcc	gct	tcc	aag	gtc	gcc	aag	2182
Ala	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	Asp	Ala	Ala	Ser	Lys	Val	Ala	Lys	
				440				445						450		
aat	gct	cat	aag	aag	ggc	att	acc	ttg	aag	gaa	agt	gca	ttg	gaa	ttg	2230
Asn	Ala	His	Lys	Lys	Gly	Ile	Thr	Leu	Lys	Glu	Ser	Ala	Leu	Glu	Leu	
				455				460					465			
ggg	gta	ttg	act	gaa	aag	gaa	ttt	gat	gaa	tgg	gtt	gtt	cct	gaa	cac	2278
Gly	Val	Leu	Thr	Glu	Lys	Glu	Phe	Asp	Glu	Trp	Val	Val	Pro	Glu	His	
				470			475					480				
atg	cta	ggg	cct	aaa	taa	acg	agc	ct	aa	tac	ctaa	ta	ata	tac	aa	2333
Met	Leu	Gly	Pro	Lys												
				485												
tcttattata	tgaaggaaaa	taaggaagtg	gagagaattt	gtgattcagc	aatgggtccct											2393
ccgctaaggt	cccgctcttg	gccagttatg	tcagaagagg	agcataggca	tacattccat											2453
ttttgatggc	ttaatggggc	ccataaattt	acatca													2489

<210> 9804

<211> 488

<212> PRT

<213> Saccharomyces cerevisiae

<400> 9804

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

PF59083SeqList PF59083.txt

85 90 95
 Lys Ala Ile Gln Gln Ala Ala Asp Glu Val Ala Ser Gly Lys Leu Asp
 100 105 110
 Asp His Phe Pro Leu Val Val Phe Gln Thr Gly Ser Gly Thr Gln Ser
 115 120 125
 Asn Met Asn Ala Asn Glu Val Ile Ser Asn Arg Ala Ile Glu Ile Leu
 130 135 140
 Gly Gly Lys Ile Gly Ser Lys Gln Val His Pro Asn Asn His Cys Asn
 145 150 155 160
 Gln Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr Val Met His Ile Ala
 165 170 175
 Ala Ser Leu Gln Ile Gln Asn Glu Leu Ile Pro Glu Leu Thr Asn Leu
 180 185 190
 Lys Asn Ala Leu Glu Ala Lys Ser Lys Glu Phe Asp His Ile Val Lys
 195 200 205
 Ile Gly Arg Thr His Leu Gln Asp Ala Thr Pro Leu Thr Leu Gly Gln
 210 215 220
 Glu Phe Ser Gly Tyr Val Gln Gln Val Glu Asn Gly Ile Gln Arg Val
 225 230 235 240
 Ala His Ser Leu Lys Thr Leu Ser Phe Leu Ala Gln Gly Gly Thr Ala
 245 250 255
 Val Gly Thr Gly Leu Asn Thr Lys Pro Gly Phe Asp Val Lys Ile Ala
 260 265 270
 Glu Gln Ile Ser Lys Glu Thr Gly Leu Lys Phe Gln Thr Ala Pro Asn
 275 280 285
 Lys Phe Glu Ala Leu Ala Ala His Asp Ala Ile Val Glu Cys Ser Gly
 290 295 300
 Ala Leu Asn Thr Leu Ala Cys Ser Leu Phe Lys Ile Ala Gln Asp Ile
 305 310 315 320
 Arg Tyr Leu Gly Ser Gly Pro Arg Cys Gly Tyr His Glu Leu Met Leu
 325 330 335
 Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro
 340 345 350
 Thr Gln Asn Glu Ala Leu Thr Gln Val Cys Val Gln Val Met Gly Asn
 355 360 365
 Asn Ala Ala Ile Thr Phe Ala Gly Ser Gln Gly Gln Phe Glu Leu Asn
 370 375 380
 Val Phe Lys Pro Val Met Ile Ala Asn Leu Leu Asn Ser Ile Arg Leu
 385 390 395 400
 Ile Thr Asp Ala Ala Tyr Ser Phe Arg Val His Cys Val Glu Gly Ile
 405 410 415
 Lys Ala Asn Glu Pro Arg Ile His Glu Leu Leu Thr Lys Ser Leu Met
 420 425 430
 Leu Val Thr Ala Leu Asn Pro Lys Ile Gly Tyr Asp Ala Ser Lys
 435 440 445
 Val Ala Lys Asn Ala His Lys Lys Gly Ile Thr Leu Lys Glu Ser Ala
 450 455 460
 Leu Glu Leu Gly Val Leu Thr Glu Lys Glu Phe Asp Glu Trp Val Val
 465 470 475 480
 Pro Glu His Met Leu Gly Pro Lys
 485

<210> 9805
 <211> 1488
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(1488)

<400> 9805
 atg gcg ttg tac gtg ctc tcg cgt cgt tta tca gct gga tcc aac tca 48
 Met Ala Leu Tyr Val Leu Ser Arg Arg Leu Ser Ala Gly Ser Asn Ser
 1 5 10 15
 acc acg ctc ctc gcc ttg cgt ttt gtt tcc tct acc aga tcc tac tcc 96
 Thr Thr Leu Leu Ala Leu Arg Phe Val Ser Ser Thr Arg Ser Tyr Ser
 20 25 30
 tct tcc ttc agg gaa gaa aga gat acc ttt gga gcc att caa gtt ccc 144
 475
 Seite 10309

PF59083SeqList PF59083.txt

Ser	Ser	Phe	Arg	Glu	Glu	Arg	Asp	Thr	Phe	Gly	Ala	Ile	Gln	Val	Pro	
tcc	gag	aaa	tta	tgg	gga	gca	caa	act	caa	aga	tcg	ttg	cag	aac	ttc	192
Ser	Glu	Lys	Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	
gat	atc	ggg	ggg	ccc	cg	gaa	cg	atg	ccc	gaa	ccc	atc	att	cg	gcc	240
Asp	Ile	Gly	Gly	Pro	Arg	Glu	Arg	Met	Pro	Glu	Pro	Ile	Ile	Arg	Ala	
65					70				75						80	
ttt	ggc	gtc	ttg	aag	aaa	tgc	gct	gct	aag	gtg	aac	atg	gag	tat	ggt	288
Phe	Gly	Val	Leu	Lys	Lys	Cys	Ala	Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	
				85					90					95		
ctt	gat	ccc	gcc	ggt	gga	aaa	gcg	att	atg	caa	gcg	gca	caa	gaa	gtg	336
Leu	Asp	Pro	Ala	Val	Gly	Lys	Ala	Ile	Met	Gln	Ala	Ala	Gln	Glu	Val	
			100					105					110			
gcc	gag	gga	aaa	cta	aac	gac	cat	ttt	cct	ctc	gtt	gta	tgg	caa	act	384
Ala	Glu	Gly	Lys	Leu	Asn	Asp	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	
		115					120					125				
ggc	agt	ggc	act	caa	agt	aac	atg	aat	gct	aac	gag	ggt	att	gca	aac	432
Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	
	130					135					140					
cga	gca	gca	gag	att	ctt	ggc	cat	aag	cg	ggt	gag	aag	ttt	gtg	cac	480
Arg	Ala	Ala	Glu	Ile	Leu	Gly	His	Lys	Arg	Gly	Glu	Lys	Phe	Val	His	
145					150				155						160	
cca	aat	gac	cat	gtc	aat	aga	tca	cag	tct	tct	aat	gat	aca	ttc	cca	528
Pro	Asn	Asp	His	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	
			165					170						175		
act	gta	atg	cac	att	gca	gcc	gca	acg	gaa	ata	aac	tca	aga	ctg	atc	576
Thr	Val	Met	His	Ile	Ala	Ala	Ala	Thr	Glu	Ile	Asn	Ser	Arg	Leu	Ile	
			180					185					190			
ccc	agc	ctt	aaa	acg	tta	cac	gat	act	cta	aac	tca	aag	tca	ggt	gaa	624
Pro	Ser	Leu	Lys	Thr	Leu	His	Asp	Thr	Leu	Asn	Ser	Lys	Ser	Val	Glu	
		195					200					205				
ttt	aaa	gat	att	gtc	aag	att	gga	cg	act	cat	act	caa	gat	gca	aca	672
Phe	Lys	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	
	210					215					220					
cct	ttg	act	ctt	gga	caa	gag	ttt	agt	gga	tat	act	aca	caa	gtg	aag	720
Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Thr	Thr	Gln	Val	Lys	
225				230					235					240		
tac	ggt	att	gat	aga	gta	att	gac	act	ttg	cca	cac	atg	tat	cag	ctt	768
Tyr	Gly	Ile	Asp	Arg	Val	Ile	Asp	Thr	Leu	Pro	His	Met	Tyr	Gln	Leu	
			245					250						255		
gcc	cag	ggt	ggt	aca	gct	gta	ggg	act	gga	ttg	aat	aca	aag	aag	ggg	816
Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	
		260					265						270			
ttt	gat	gcc	aag	ata	gca	gca	gca	gta	gct	gag	gaa	aca	aat	ctg	cct	864
Phe	Asp	Ala	Lys	Ile	Ala	Ala	Ala	Val	Ala	Glu	Glu	Thr	Asn	Leu	Pro	
		275				280						285				
ttt	gtc	acg	gca	gaa	aat	aag	ttt	gag	gcc	ttg	gct	gcc	cat	gat	gct	912
Phe	Val	Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	
	290					295					300					
ttt	ggt	gaa	act	agt	gga	gcc	ctt	aac	act	gtt	gtg	gct	tca	ttg	atg	960
Phe	Val	Glu	Thr	Ser	Gly	Ala	Leu	Asn	Thr	Val	Val	Ala	Ser	Leu	Met	
305				310					315					320		
aag	att	gct	aat	gat	ata	cg	tta	ttg	gga	agt	ggt	cca	cg	tgc	ggt	1008
Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	
			325					330						335		
ctt	ggg	gag	ctc	att	ctt	cct	gaa	aac	gaa	cca	gga	agc	agt	att	atg	1056
Leu	Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	
			340				345						350			
cct	ggg	aag	ggt	aac	ccg	acc	cag	tgt	gag	gct	ttg	acg	atg	gtg	tgt	1104
Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	
		355				360						365				
gca	cag	gtc	atg	gga	aac	cat	gtt	gca	atc	aca	gtg	ggt	gga	tca	aat	1152
Ala	Gln	Val	Met	Gly	Asn	His	Val	Ala	Ile	Thr	Val	Gly	Gly	Ser	Asn	
	370					375					380					
ggt	cat	ttt	gag	ctc	aat	gtg	ttc	aag	cca	atg	att	gcc	aat	tgt	ctc	1200
Gly	His	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Met	Ile	Ala	Asn	Cys	Leu	
385				390					395					400		
ctg	cat	tcg	ctg	aga	ctg	ctt	gga	gat	tcg	tct	gct	tcc	ttt	gaa	aag	1248

PF59083SeqList PF59083.txt

Leu	His	Ser	Leu	Arg	Leu	Leu	Gly	Asp	Ser	Ser	Ala	Ser	Phe	Glu	Lys	
				405					410					415		
aat	tgt	ttg	aga	ggg	att	caa	gct	aat	agg	gaa	aga	att	tca	aaa	tta	1296
Asn	Cys	Leu	Arg	Gly	Ile	Gln	Ala	Asn	Arg	Glu	Arg	Ile	Ser	Lys	Leu	
			420					425					430			
ctg	cat	gag	tca	ctt	atg	ctt	gtc	aca	tcc	tta	aac	cca	aaa	atc	ggg	1344
Leu	His	Glu	Ser	Leu	Met	Leu	Val	Thr	Ser	Leu	Asn	Pro	Lys	Ile	Gly	
		435					440					445				
tat	gac	aag	gca	gca	aca	gtt	gcc	aag	aca	gct	cac	aaa	gag	ggg	act	1392
Tyr	Asp	Lys	Ala	Ala	Thr	Val	Ala	Lys	Thr	Ala	His	Lys	Glu	Gly	Thr	
	450					455					460					
act	ctt	aag	gaa	gct	gca	ttg	aaa	ctc	gga	gtg	ctc	tgc	tct	gaa	gat	1440
Thr	Leu	Lys	Glu	Ala	Ala	Leu	Lys	Leu	Gly	Val	Leu	Cys	Ser	Glu	Asp	
465					470				475						480	
ttt	gac	aag	ctt	gtg	gta	cct	gag	aaa	atg	ctt	gga	cca	tct	gat	tga	1488
Phe	Asp	Lys	Leu	Val	Val	Pro	Glu	Lys	Met	Leu	Gly	Pro	Ser	Asp		
				485					490					495		

<210> 9806

<211> 495

<212> PRT

<213> Glycine max

<400> 9806

Met	Ala	Leu	Tyr	Val	Leu	Ser	Arg	Arg	Leu	Ser	Ala	Gly	Ser	Asn	Ser	
1				5					10					15		
Thr	Thr	Leu	Leu	Ala	Leu	Arg	Phe	Val	Ser	Ser	Thr	Arg	Ser	Tyr	Ser	
			20					25					30			
Ser	Ser	Phe	Arg	Glu	Glu	Arg	Asp	Thr	Phe	Gly	Ala	Ile	Gln	Val	Pro	
		35					40					45				
Ser	Glu	Lys	Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	
	50					55				60						
Asp	Ile	Gly	Gly	Pro	Arg	Glu	Arg	Met	Pro	Glu	Pro	Ile	Ile	Arg	Ala	
65					70				75						80	
Phe	Gly	Val	Leu	Lys	Lys	Cys	Ala	Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	
			85						90					95		
Leu	Asp	Pro	Ala	Val	Gly	Lys	Ala	Ile	Met	Gln	Ala	Ala	Gln	Glu	Val	
			100					105					110			
Ala	Glu	Gly	Lys	Leu	Asn	Asp	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	
		115					120					125				
Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	
	130					135					140					
Arg	Ala	Ala	Glu	Ile	Leu	Gly	His	Lys	Arg	Gly	Glu	Lys	Phe	Val	His	
145					150				155						160	
Pro	Asn	Asp	His	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	
			165						170					175		
Thr	Val	Met	His	Ile	Ala	Ala	Ala	Thr	Glu	Ile	Asn	Ser	Arg	Leu	Ile	
			180					185						190		
Pro	Ser	Leu	Lys	Thr	Leu	His	Asp	Thr	Leu	Asn	Ser	Lys	Ser	Val	Glu	
		195					200					205				
Phe	Lys	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	
	210					215					220					
Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Thr	Thr	Gln	Val	Lys	
225					230					235					240	
Tyr	Gly	Ile	Asp	Arg	Val	Ile	Asp	Thr	Leu	Pro	His	Met	Tyr	Gln	Leu	
			245						250					255		
Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	
		260						265					270			
Phe	Asp	Ala	Lys	Ile	Ala	Ala	Ala	Val	Ala	Glu	Glu	Thr	Asn	Leu	Pro	
		275					280					285				
Phe	Val	Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	
	290					295					300					
Phe	Val	Glu	Thr	Ser	Gly	Ala	Leu	Asn	Thr	Val	Val	Ala	Ser	Leu	Met	
305					310					315					320	
Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	
			325						330					335		
Leu	Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	
			340					345					350			
Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	

PF59083SeqList PF59083.txt

355 360 365
 Ala Gln Val Met Gly Asn His Val Ala Ile Thr Val Gly Gly Ser Asn
 370 375 380
 Gly His Phe Glu Leu Asn Val Phe Lys Pro Met Ile Ala Asn Cys Leu
 385 390 395
 Leu His Ser Leu Arg Leu Leu Gly Asp Ser Ala Ser Phe Glu Lys
 405 410 415
 Asn Cys Leu Arg Gly Ile Gln Ala Asn Arg Glu Arg Ile Ser Lys Leu
 420 425 430
 Leu His Glu Ser Leu Met Leu Val Thr Ser Leu Asn Pro Lys Ile Gly
 435 440 445
 Tyr Asp Lys Ala Ala Thr Val Ala Lys Thr Ala His Lys Glu Gly Thr
 450 455 460
 Thr Leu Lys Glu Ala Ala Leu Lys Leu Gly Val Leu Cys Ser Glu Asp
 465 470 475 480
 Phe Asp Lys Leu Val Pro Glu Lys Met Leu Gly Pro Ser Asp
 485 490 495

<210> 9807
 <211> 1485
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(1485)

<400> 9807
 atg gcg atg gtt ctg cga cgc ctc gcg ggc gca tca ggc tcg ccg tcg 48
 Met Ala Met Val Leu Arg Arg Leu Ala Gly Ala Ser Gly Ser Pro Ser
 1 5 10 15
 gcg gct gca ctg ctg ctc cgt ccg gcg ctg acc cgc ccg atc tcc acc 96
 Ala Ala Ala Leu Leu Leu Arg Pro Ala Leu Thr Arg Pro Ile Ser Thr
 20 25 30
 gac ttc cgc gag gag cgc gac aca ttc ggc ccc atc cgc gta ccc aac 144
 Asp Phe Arg Glu Glu Arg Asp Thr Phe Gly Pro Ile Arg Val Pro Asn
 35 40 45
 gac aag ttg tgg ggc gcg cag aca cag aga tcg ctg caa aat ttt gac 192
 Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn Phe Asp
 50 55 60
 att ggc ggc gag cgc gag cgg atg ccc gtg cct atc atc cgc gcc ttt 240
 Ile Gly Gly Glu Arg Glu Arg Met Pro Val Pro Ile Ile Arg Ala Phe
 65 70 75 80
 ggc gtg cta aaa aag tgc gct gct aag gtg aat atg gag tat gga ctt 288
 Gly Val Leu Lys Lys Cys Ala Ala Lys Val Asn Met Glu Tyr Gly Leu
 85 90 95
 gat cca aca att ggg aag gca ata atg cag gcg gct gag gag gtt gca 336
 Asp Pro Thr Ile Gly Lys Ala Ile Met Gln Ala Ala Glu Glu Val Ala
 100 105 110
 gag gga aag ttg gat gat cac ttt ccg ctt gtt atc tgg caa act ggc 384
 Glu Gly Lys Leu Asp Asp His Phe Pro Leu Val Ile Trp Gln Thr Gly
 115 120 125
 agt ggc aca caa agc aac atg aat gcc aat gag gta att gca aac agg 432
 Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ala Asn Arg
 130 135 140
 gca gct gag ata ctt gga cat aag cgt ggt gac aag ttt gta cac cct 480
 Ala Ala Glu Ile Leu Gly His Lys Arg Gly Asp Lys Phe Val His Pro
 145 150 155 160
 aat gat cat gtg aac agg tca cag tcc tca aat gat aca ttt cca act 528
 Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr
 165 170 175
 gtt atg cac ata gca gca gct gta gag atc aat tca agg ttt atc cca 576
 Val Met His Ile Ala Ala Ala Val Glu Ile Asn Ser Arg Phe Ile Pro
 180 185 190
 agt ctg gag cag ttg cat aag tca ctt cat tca aag tct gat gaa ttt 624
 Ser Leu Glu Gln Leu His Lys Ser Leu His Ser Lys Ser Asp Glu Phe
 195 200 205
 aaa gac att att aaa att ggg cgt aca cat acc caa gat gcc acc cca 672
 Lys Asp Ile Ile Lys Ile Gly Arg Thr His Thr Asp Ala Thr Pro

PF59083SeqList PF59083.txt

210	ctg act ctt ggt caa gag	215	ttc agt ggt tat gct aca cag gtg aaa tat	720
Leu Thr Leu Gly Gln Glu	220	Phe Ser Gly Tyr Ala Thr Gln Val Lys Tyr		
225	gga att gac cga att gca tgc acc tta cca agg atg tat cag ctt gct	230	235	240
Gly Ile Asp Arg Ile Ala Cys Thr Leu Pro Arg Met Tyr Gln Leu Ala	245	250	255	
caa ggt ggg act gca gtc ggc act ggc ttg aac acg aag aaa gga ttt	260	265	270	816
Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Lys Lys Gly Phe	275	280	285	
gat ggc aaa att gca gct gct gtg gct gag gaa aca gaa cta cct ttc	290	295	300	864
Asp Gly Lys Ile Ala Ala Val Ala Glu Glu Thr Glu Leu Pro Phe	305	310	315	
gtg aca gca gag aac aag ttt gaa gct ttg gca gct cat gac gct ttt	320	325	330	912
Val Thr Ala Glu Asn Lys Phe Glu Ala Leu Ala His Asp Ala Phe	335	340	345	
gtt gag agc agt ggt gct gtg aac aca att tct gca tct ctt atg aag	350	355	360	960
Val Glu Ser Ser Gly Ala Val Asn Thr Ile Ser Ala Ser Leu Met Lys	365	370	375	
305	ata gca aat gac ata cgc ttg ctg gga agt ggc cct cgt tgt gga ctt	380	385	1008
Ile Ala Asn Asp Ile Arg Leu Leu Gly Ser Gly Pro Arg Cys Gly Leu	390	395	400	
ggg gaa ctt atc cta cca gaa aat gag cct ggg agc agc att atg cct	405	410	415	1056
Gly Glu Leu Ile Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro	420	425	430	
gga aag gtc aat cct acc cag tgt gaa gct ctg acc atg gtt tgt gct	435	440	445	1104
Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys Ala	445	450	455	
cag gtt atg ggt aat cat gtc ggt gtt aca ata ggt ggt tca aat ggg	460	465	470	1152
Gln Val Met Gly Asn His Gln Gly Val Thr Ile Gly Ser Asn Gly	470	475	480	
cat ttt gaa ctg aac gtt tat aag cca atg att gct gct gga ttg ctt	485	490	495	1200
His Phe Glu Leu Asn Val Tyr Lys Pro Met Ile Ala Ala Gly Leu Leu	500	505	510	
cga tca ttg aga tta tta ggg gat gca tct gta tcc ttt gag aaa aac	515	520	525	1248
Arg Ser Leu Arg Leu Leu Gly Asp Ala Ser Val Ser Phe Glu Lys Asn	530	535	540	
tgt gtc agg gga ata gaa gca aac cat aag aga att tca caa ttg ttg	545	550	555	1296
Cys Val Arg Gly Ile Glu Ala Asn His Lys Arg Ile Ser Gln Leu Leu	560	565	570	
cac gag tct ttg atg ttg gta aca tcg ttg aac ccc aaa att ggc tat	575	580	585	1344
His Glu Ser Leu Met Leu Val Thr Ser Leu Asn Pro Lys Ile Gly Tyr	590	595	600	
gac aat gct gca gct gtt gct aag aaa gct cac aaa gaa gga aca aca	605	610	615	1392
Asp Asn Ala Ala Val Val Lys Lys Ala His Lys Glu Gly Thr Thr	620	625	630	
ctg aag gaa gct gct tta agc ctc aga gtt ttg acg gaa aag gaa ttc	635	640	645	1440
Leu Lys Glu Ala Ala Leu Ser Leu Arg Val Leu Thr Glu Lys Glu Phe	650	655	660	
465	cat gaa ctc gtt gtt cca gag aaa atg att ggc cct tct gat taa	665	670	1485
His Glu Leu Val Val Pro Glu Lys Met Ile Gly Pro Ser Asp	675	680	685	

<210> 9808
 <211> 494
 <212> PRT
 <213> Hordeum vulgare

<400> 9808
 Met Ala Met Val Leu Arg Arg Leu Ala Gly Ala Ser Gly Ser Pro Ser
 1 5 10 15
 Ala Ala Ala Leu Leu Arg Pro Ala Leu Thr Arg Pro Ile Ser Thr
 20 25 30
 Asp Phe Arg Glu Glu Arg Asp Thr Phe Gly Pro Ile Arg Val Pro Asn
 35 40 45
 Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn Phe Asp
 50 55 60
 Ile Gly Gly Glu Arg Glu Arg Met Pro Val Pro Ile Ile Arg Ala Phe
 65 70 75 80

PF59083SeqList PF59083.txt

Gly Val Leu Lys Lys Cys Ala Ala Lys Val Asn Met Glu Tyr Gly Leu
 85 90 95
 Asp Pro Thr Ile Gly Lys Ala Ile Met Gln Ala Ala Glu Glu Val Ala
 100 105 110
 Glu Gly Lys Leu Asp Asp His Phe Pro Leu Val Ile Trp Gln Thr Gly
 115 120 125
 Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ala Asn Arg
 130 135 140
 Ala Ala Glu Ile Leu Gly His Lys Arg Gly Asp Lys Phe Val His Pro
 145 150 155 160
 Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr
 165 170 175
 Val Met His Ile Ala Ala Ala Val Glu Ile Asn Ser Arg Phe Ile Pro
 180 185 190
 Ser Leu Glu Gln Leu His Lys Ser Leu His Ser Lys Ser Asp Glu Phe
 195 200 205
 Lys Asp Ile Ile Lys Ile Gly Arg Thr His Thr Gln Asp Ala Thr Pro
 210 215 220
 Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Ala Thr Gln Val Lys Tyr
 225 230 235 240
 Gly Ile Asp Arg Ile Ala Cys Thr Leu Pro Arg Met Tyr Gln Leu Ala
 245 250 255
 Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Lys Lys Gly Phe
 260 265 270
 Asp Gly Lys Ile Ala Ala Ala Val Ala Glu Glu Thr Glu Leu Pro Phe
 275 280 285
 Val Thr Ala Glu Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Phe
 290 295 300
 Val Glu Ser Ser Gly Ala Val Asn Thr Ile Ser Ala Ser Leu Met Lys
 305 310 315 320
 Ile Ala Asn Asp Ile Arg Leu Leu Gly Ser Gly Pro Arg Cys Gly Leu
 325 330 335
 Gly Glu Leu Ile Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro
 340 345 350
 Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys Ala
 355 360 365
 Gln Val Met Gly Asn His Val Gly Val Thr Ile Gly Gly Ser Asn Gly
 370 375 380
 His Phe Glu Leu Asn Val Tyr Lys Pro Met Ile Ala Ala Gly Leu Leu
 385 390 395 400
 Arg Ser Leu Arg Leu Leu Gly Asp Ala Ser Val Ser Phe Glu Lys Asn
 405 410 415
 Cys Val Arg Gly Ile Glu Ala Asn His Lys Arg Ile Ser Gln Leu Leu
 420 425 430
 His Glu Ser Leu Met Leu Val Thr Ser Leu Asn Pro Lys Ile Gly Tyr
 435 440 445
 Asp Asn Ala Ala Ala Val Ala Lys Lys Ala His Lys Glu Gly Thr Thr
 450 455 460
 Leu Lys Glu Ala Ala Leu Ser Leu Arg Val Leu Thr Glu Lys Glu Phe
 465 470 475 480
 His Glu Leu Val Val Pro Glu Lys Met Ile Gly Pro Ser Asp
 485 490

<210> 9809

<211> 1485

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (1)..(1485)

<400> 9809

atg gcg atg gtt ctg cgg cgc ctc gcc ggc gca tca ggc tcg cct tcg
 Met Ala Met Val Leu Arg Arg Leu Ala Gly Ala Ser Gly Ser Pro Ser
 1 5 10 15
 gcg gct gca ctg ctg ctc cgg ccg gcg ctg acc cgc ccg atc tcc acc
 Ala Ala Ala Leu Leu Leu Arg Pro Ala Leu Thr Arg Pro Ile Ser Thr
 20 25 30

48

96

PF59083SeqList PF59083.txt																
ggc	ttc	cgc	gag	gag	cgc	gac	acg	ttc	ggc	ccc	atc	cgc	gtg	ccc	aac	144
Gly	Phe	Arg	Glu	Glu	Arg	Asp	Thr	Phe	Gly	Pro	Ile	Arg	Val	Pro	Asn	
		35					40					45				
gac	aag	ttg	tgg	ggc	gcg	cag	aca	cag	aga	tcg	ctg	caa	aat	ttc	gac	192
Asp	Lys	Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	Asp	
	50					55					60					
att	ggc	ggc	gag	cgc	gag	cgg	atg	cct	gtg	cct	atc	atc	cgc	gcc	ttt	240
Ile	Gly	Gly	Glu	Arg	Glu	Arg	Met	Pro	Val	Pro	Ile	Ile	Arg	Ala	Phe	
	65				70					75					80	
ggc	gtg	cta	aaa	aag	tgc	gcc	gct	aag	gtg	aat	atg	gag	tat	ggc	ctt	288
Gly	Val	Leu	Lys	Lys	Cys	Ala	Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	Leu	
				85					90					95		
gat	cca	aca	att	ggg	aag	gca	ata	atg	cag	gcg	gcc	gag	gag	gtt	gca	336
Asp	Pro	Thr	Ile	Gly	Lys	Ala	Ile	Met	Gln	Ala	Ala	Glu	Glu	Val	Ala	
			100					105						110		
gag	gga	aag	ttg	gat	gat	cac	ttt	ccg	ctt	gtt	atc	tgg	caa	act	ggc	384
Glu	Gly	Lys	Leu	Asp	Asp	His	Phe	Pro	Leu	Val	Ile	Trp	Gln	Thr	Gly	
		115					120					125				
agt	ggc	aca	caa	agc	aac	atg	aat	gcc	aat	gag	gta	att	gca	aat	agg	432
Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	
	130					135					140					
gcg	gct	gag	ata	ctt	gga	cat	aag	cgt	ggt	gac	aag	ttt	gta	cac	cct	480
Ala	Ala	Glu	Ile	Leu	Gly	His	Lys	Arg	Gly	Asp	Lys	Phe	Val	His	Pro	
	145				150					155					160	
aat	gac	cat	gtg	aac	agg	tca	cag	tcc	tcg	aat	gat	aca	ttt	ccc	act	528
Asn	Asp	His	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	
				165					170					175		
gtt	atg	cac	ata	gca	gca	gct	gta	gag	atc	aat	tca	agg	ttt	atc	cca	576
Val	Met	His	Ile	Ala	Ala	Ala	Val	Glu	Ile	Asn	Ser	Arg	Phe	Ile	Pro	
			180					185					190			
agt	ctg	gag	cag	ttg	cat	aag	tca	ctt	cat	tca	aag	tct	gat	gag	ttt	624
Ser	Leu	Glu	Gln	Leu	His	Lys	Ser	Leu	His	Ser	Lys	Ser	Asp	Glu	Phe	
		195					200					205				
aaa	gac	atc	att	aaa	att	ggg	cgt	aca	cat	acc	caa	gat	gcc	acc	cca	672
Lys	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	
	210					215					220					
ctg	act	ctt	ggt	caa	gag	ttc	agt	ggt	tat	gct	aca	cag	gtg	aaa	tat	720
Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Ala	Thr	Gln	Val	Lys	Tyr	
	225				230					235					240	
gga	att	gac	cga	att	gca	tgt	acc	tta	cca	agg	atg	tat	cag	ctt	gct	768
Gly	Ile	Asp	Arg	Ile	Ala	Cys	Thr	Leu	Pro	Arg	Met	Tyr	Gln	Leu	Ala	
				245					250					255		
caa	ggt	ggg	act	gca	gtt	ggt	act	ggc	ttg	aac	acg	aag	aaa	gga	ttt	816
Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	
			260					265					270			
gat	ggc	aaa	att	gca	gct	gct	gtg	gct	gag	gaa	aca	gaa	cta	cct	ttc	864
Asp	Gly	Lys	Ile	Ala	Ala	Ala	Val	Ala	Glu	Glu	Thr	Glu	Leu	Pro	Phe	
		275					280					285				
gtg	aca	gca	gag	aac	aag	ttt	gaa	gct	ttg	gca	gca	cat	gat	gct	ttt	912
Val	Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Phe	
	290					295					300					
gtt	gag	agc	agt	ggt	gct	gtg	aac	aca	att	tct	gca	tct	ctt	atg	aag	960
Val	Glu	Ser	Ser	Gly	Ala	Val	Asn	Thr	Ile	Ser	Ala	Ser	Leu	Met	Lys	
	305				310					315					320	
ata	gca	aat	gac	ata	cgc	ttg	ctg	gga	agt	ggc	cct	cgt	tgt	gga	ctt	1008
Ile	Ala	Asn	Asp	Ile	Arg	Leu	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	
				325					330					335		
ggt	gaa	ctt	atc	cta	cca	gaa	aat	gag	cct	ggg	agc	agc	att	atg	cct	1056
Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
			340					345					350			
gga	aag	gtt	aat	cct	acc	cag	tgt	gag	gct	ctg	acc	atg	gtt	tgt	gct	1104
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	
		355					360					365				
cag	gtt	atg	ggc	aat	cat	gtc	ggt	gtt	aca	ata	ggt	ggt	tca	aat	ggg	1152
Gln	Val	Met	Gly	Asn	His	Val	Gly	Val	Thr	Ile	Gly	Gly	Ser	Asn	Gly	
	370					375					380					
cat	ttt	gaa	ctg	aac	gtt	tat	aag	cca	atg	att	gct	gct	gga	ttg	ctt	1200
His	Phe	Glu	Leu	Asn	Val	Tyr	Lys	Pro	Met	Ile	Ala	Ala	Gly	Leu	Leu	
	385				390					395					400	

PF59083SeqList PF59083.txt

cga	tca	ttg	aga	tta	tta	ggg	gat	gca	tct	gta	tcc	ttt	gag	aaa	aac	1248
Arg	Ser	Leu	Arg	Leu	Leu	Gly	Asp	Ala	Ser	Val	Ser	Phe	Glu	Lys	Asn	
				405					410					415		
tgt	gtc	agg	gga	ata	gaa	gca	aac	cat	aag	aga	att	tca	caa	ttg	ttg	1296
Cys	Val	Arg	Gly	Ile	Glu	Ala	Asn	His	Lys	Arg	Ile	Ser	Gln	Leu	Leu	
			420					425					430			
cac	gag	tct	ttg	atg	ttg	gtg	aca	tcg	ttg	aac	ccc	aaa	att	ggc	tat	1344
His	Glu	Ser	Leu	Met	Leu	Val	Thr	Ser	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	
		435					440				445					
gac	aat	gct	gca	gcc	gtt	gct	aag	aaa	gct	cac	aaa	gaa	gga	aca	aca	1392
Asp	Asn	Ala	Ala	Ala	Val	Ala	Lys	Lys	Ala	His	Lys	Glu	Gly	Thr	Thr	
	450					455					460					
ctg	aag	gaa	gct	gct	tta	agc	ctt	gga	ggt	ttg	acg	gaa	aag	gaa	ttc	1440
Leu	Lys	Glu	Ala	Ala	Leu	Ser	Leu	Gly	Val	Leu	Thr	Glu	Lys	Glu	Phe	
465					470			475							480	
cat	gaa	ctc	ggt	ggt	cca	gag	aaa	atg	att	ggc	cct	tct	gat	taa		1485
His	Glu	Leu	Val	Val	Pro	Glu	Lys	Met	Ile	Gly	Pro	Ser	Asp			
				485				490								

<210> 9810

<211> 494

<212> PRT

<213> Triticum aestivum

<400> 9810

Met	Ala	Met	Val	Leu	Arg	Arg	Leu	Ala	Gly	Ala	Ser	Gly	Ser	Pro	Ser	
1				5					10					15		
Ala	Ala	Ala	Leu	Leu	Leu	Arg	Pro	Ala	Leu	Thr	Arg	Pro	Ile	Ser	Thr	
			20					25					30			
Gly	Phe	Arg	Glu	Glu	Arg	Asp	Thr	Phe	Gly	Pro	Ile	Arg	Val	Pro	Asn	
		35					40					45				
Asp	Lys	Leu	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	Asp	
	50				55					60						
Ile	Gly	Gly	Glu	Arg	Glu	Arg	Met	Pro	Val	Pro	Ile	Ile	Arg	Ala	Phe	
65					70				75						80	
Gly	Val	Leu	Lys	Lys	Cys	Ala	Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	Leu	
			85					90						95		
Asp	Pro	Thr	Ile	Gly	Lys	Ala	Ile	Met	Gln	Ala	Ala	Glu	Glu	Val	Ala	
			100					105					110			
Glu	Gly	Lys	Leu	Asp	Asp	His	Phe	Pro	Leu	Val	Ile	Trp	Gln	Thr	Gly	
		115					120					125				
Ser	Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	
	130				135					140						
Ala	Ala	Glu	Ile	Leu	Gly	His	Lys	Arg	Gly	Asp	Lys	Phe	Val	His	Pro	
145					150					155					160	
Asn	Asp	His	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	
			165					170						175		
Val	Met	His	Ile	Ala	Ala	Ala	Val	Glu	Ile	Asn	Ser	Arg	Phe	Ile	Pro	
			180					185					190			
Ser	Leu	Glu	Gln	Leu	His	Lys	Ser	Leu	His	Ser	Lys	Ser	Asp	Glu	Phe	
		195					200					205				
Lys	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	
	210				215					220						
Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Ala	Thr	Gln	Val	Lys	Tyr	
225					230					235					240	
Gly	Ile	Asp	Arg	Ile	Ala	Cys	Thr	Leu	Pro	Arg	Met	Tyr	Gln	Leu	Ala	
			245					250						255		
Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	
			260					265					270			
Asp	Gly	Lys	Ile	Ala	Ala	Ala	Val	Ala	Glu	Glu	Thr	Glu	Leu	Pro	Phe	
		275					280					285				
Val	Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Phe	
	290					295				300						
Val	Glu	Ser	Ser	Gly	Ala	Val	Asn	Thr	Ile	Ser	Ala	Ser	Leu	Met	Lys	
					310					315					320	
Ile	Ala	Asn	Asp	Ile	Arg	Leu	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	
			325					330						335		
Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
			340					345					350			

PF59083SeqList PF59083.txt

Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys Ala
 355 360 365
 Gln Val Met Gly Asn His Val Gly Val Thr Ile Gly Gly Ser Asn Gly
 370 375 380
 His Phe Glu Leu Asn Val Tyr Lys Pro Met Ile Ala Ala Gly Leu Leu
 385 390 395 400
 Arg Ser Leu Arg Leu Leu Gly Asp Ala Ser Val Ser Phe Glu Lys Asn
 405 410 415
 Cys Val Arg Gly Ile Glu Ala Asn His Lys Arg Ile Ser Gln Leu Leu
 420 425 430
 His Glu Ser Leu Met Leu Val Thr Ser Leu Asn Pro Lys Ile Gly Tyr
 435 440 445
 Asp Asn Ala Ala Ala Val Ala Lys Lys Ala His Lys Glu Gly Thr Thr
 450 455 460
 Leu Lys Glu Ala Ala Leu Ser Leu Gly Val Leu Thr Glu Lys Glu Phe
 465 470 475 480
 His Glu Leu Val Val Pro Glu Lys Met Ile Gly Pro Ser Asp
 485 490

<210> 9811
 <211> 1497
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(1497)

<400> 9811
 atg gcg atg gct ctg cgc cgc ctt gcg ggc gtg tcc gga tcg ccg tcg 48
 Met Ala Met Ala Leu Arg Arg Leu Ala Gly Val Ser Gly Ser Pro Ser
 1 5 10 15
 gcc tcc tct gcc gcg gcc acg gtg cta ctc cgg tcg gcg ctg acc cgc 96
 Ala Ser Ser Ala Ala Ala Thr Val Leu Leu Arg Ser Ala Leu Thr Arg
 20 25 30
 ccg atc tcc acc ggc ttc cgc gag gag cgc gac acc ttc ggt ccc atc 144
 Pro Ile Ser Thr Gly Phe Arg Glu Glu Arg Asp Thr Phe Gly Pro Ile
 35 40 45
 caa gtc ccc aac gac aag ctg tgg ggc gcg cag acg cag aga tcg ctg 192
 Gln Val Pro Asn Asp Lys Trp Gly Ala Gln Thr Gln Arg Ser Leu
 50 55 60
 cag aac ttt gac att ggc ggg gag cgt gag agg atg ccc gtt ccc atc 240
 Gln Asn Phe Asp Ile Gly Gly Glu Arg Glu Arg Met Pro Val Pro Ile
 65 70 75 80
 atc cgt gcc ttt ggc gtg cta aaa aag tgc gcc gct aag gtg aat atg 288
 Ile Arg Ala Phe Gly Val Leu Lys Lys Cys Ala Ala Lys Val Asn Met
 85 90 95
 gac tat ggc ctt gat cca aca ata ggg aag gcc ata ata cag gca gct 336
 Asp Tyr Gly Leu Asp Pro Thr Ile Gly Lys Ala Ile Ile Gln Ala Ala
 100 105 110
 gag gag gtc gca gag gga aag ttg gat gat cac ttc cca ctt gtt atc 384
 Glu Glu Val Ala Glu Gly Lys Leu Asp Asp His Phe Pro Leu Val Ile
 115 120 125
 tgg caa act ggc agt ggc aca caa agc aac atg aat gcc aat gag gta 432
 Trp Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu Val
 130 135 140
 att gca aat agg gca tct gag atc ctt gga cac aag cgc ggt gag aag 480
 Ile Ala Asn Arg Ala Ser Glu Ile Leu Gly His Lys Arg Gly Glu Lys
 145 150 155 160
 ttt gtg cac cca aat gac cat gtg aat agg tca caa tct tca aat gat 528
 Phe Val His Pro Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp
 165 170 175
 aca ttt ccc act gta atg cat ata gcg acg gcc gtt gag ata cat tcg 576
 Thr Phe Pro Thr Val Met His Ile Ala Thr Ala Val Glu Ile His Ser
 180 185 190
 agg ttt atc cca agt ttg caa cag ttg cat gat tca ctt cat tcg aaa 624
 Arg Phe Ile Pro Ser Leu Gln Gln Leu His Asp Ser Leu His Ser Lys
 195 200 205
 act att gag ttt aaa gac ata att aaa att gga cgt aca cat acc caa 672

PF59083SeqList PF59083.txt

Thr	Ile	Glu	Phe	Lys	Asp	Ile	Ile	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	
210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290
gat	gcc	acc	cca	ttg	act	ctt	ggc	caa	gaa	ttc	agt	ggc	tac	act	aca	720
Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Thr	Thr	
225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	
cag	gtc	aaa	tat	gga	att	gac	cgc	att	aat	tgt	aca	tta	cct	cgg	atg	768
Gln	Val	Lys	Tyr	Gly	Ile	Asp	Arg	Ile	Asn	Cys	Thr	Leu	Pro	Arg	Met	
245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	
tac	cag	ctt	gct	caa	ggt	gga	act	gca	ggt	gga	act	ggc	ttg	aac	acc	816
Tyr	Gln	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	
260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	
aag	aaa	gga	ttt	gat	gcc	aaa	ata	gct	gct	gca	gtg	gct	gag	gaa	aca	864
Lys	Lys	Gly	Phe	Asp	Ala	Lys	Ile	Ala	Ala	Ala	Val	Ala	Glu	Glu	Thr	
275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	
aac	cta	ccc	ttt	gtg	aca	gca	gag	aac	aag	ttt	gaa	gct	ttg	gca	gca	912
Asn	Leu	Pro	Phe	Val	Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	
290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	
cat	gac	gct	ttt	ggt	gag	agc	agt	ggg	gcc	gta	aat	aca	att	tct	gca	960
His	Asp	Ala	Phe	Val	Glu	Ser	Ser	Gly	Ala	Val	Asn	Thr	Ile	Ser	Ala	
305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	
tct	ctt	atg	aag	ata	gca	aac	gac	ata	cgt	ttg	cta	gga	agt	ggg	cct	1008
Ser	Leu	Met	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	Leu	Gly	Ser	Gly	Pro	
325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	
cgg	tgt	ggg	ctt	ggg	gaa	cta	atc	cta	cca	gaa	aat	gag	cct	ggg	agc	1056
Arg	Cys	Gly	Leu	Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	
340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	
agc	att	atg	cct	ggg	aaa	gtt	aat	cca	acc	cag	tgt	gag	gct	ctg	aca	1104
Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	
355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	
atg	gtt	tgt	gca	cag	gtc	atg	ggg	aat	cat	gtt	ggg	gtt	aca	gtt	ggg	1152
Met	Val	Cys	Ala	Gln	Val	Met	Gly	Asn	His	Val	Gly	Val	Thr	Val	Gly	
370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	
ggg	gcc	aat	ggg	cat	ttt	gaa	ctg	aat	gtt	ttt	aag	cca	atg	atc	gca	1200
Gly	Ala	Asn	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Met	Ile	Ala	
385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	
gcc	gga	tta	ctt	cga	tcg	ttg	agg	ttg	tta	ggg	gat	gca	tcc	gtg	tcc	1248
Ala	Gly	Leu	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Gly	Asp	Ala	Ser	Val	Ser	
405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	
ttc	gag	aaa	aat	tgt	gtc	agg	gga	att	caa	gca	aac	cac	aag	aga	att	1296
Phe	Glu	Lys	Asn	Cys	Val	Arg	Gly	Ile	Gln	Ala	Asn	His	Lys	Arg	Ile	
420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	
tca	caa	ctt	ttg	cat	gag	tct	ctg	atg	tta	gtg	aca	tct	ttg	aac	cct	1344
Ser	Gln	Leu	Leu	His	Glu	Ser	Leu	Met	Leu	Val	Thr	Ser	Leu	Asn	Pro	
435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	
aaa	att	ggc	tat	gac	aat	gct	gca	gct	gtt	gct	aag	aaa	gcc	cac	aaa	1392
Lys	Ile	Gly	Tyr	Asp	Asn	Ala	Ala	Ala	Val	Ala	Lys	Lys	Ala	His	Lys	
450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	
gaa	gga	acc	acg	ttg	aag	gag	gct	gca	tta	gac	ctt	gga	gta	tta	acg	1440
Glu	Gly	Thr	Thr	Leu	Lys	Glu	Ala	Ala	Leu	Asp	Leu	Gly	Val	Leu	Thr	
465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	
gag	caa	gaa	ttc	cat	gag	ctt	gtc	gtt	cca	gag	aaa	atg	att	ggg	cct	1488
Glu	Gln	Glu	Phe	His	Glu	Leu	Val	Val	Pro	Glu	Lys	Met	Ile	Gly	Pro	
485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	
tct	gat	tga														1497
Ser	Asp															

<210> 9812
 <211> 498
 <212> PRT
 <213> Zea mays

<400> 9812
 Met Ala Met Ala Leu Arg Arg Leu Ala Gly Val Ser Gly Ser Pro Ser
 1 5 10 15
 Ala Ser Ser Ala Ala Thr Val Leu Leu Arg Ser Ala Leu Thr Arg
 20 25 30
 Pro Ile Ser Thr Gly Phe Arg Glu Glu Arg Asp Thr Phe Gly Pro Ile
 35 40 45

PF59083SeqList PF59083.txt

Gln Val Pro Asn Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu
50 55 60
Gln Asn Phe Asp Ile Gly Gly Glu Arg Glu Arg Met Pro Val Pro Ile
65 70 75 80
Ile Arg Ala Phe Gly Val Leu Lys Lys Cys Ala Ala Lys Val Asn Met
85 90 95
Asp Tyr Gly Leu Asp Pro Thr Ile Gly Lys Ala Ile Ile Gln Ala Ala
100 105 110
Glu Glu Val Ala Glu Gly Lys Leu Asp Asp His Phe Pro Leu Val Ile
115 120 125
Trp Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu Val
130 135 140
Ile Ala Asn Arg Ala Ser Glu Ile Leu Gly His Lys Arg Gly Glu Lys
145 150 155 160
Phe Val His Pro Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp
165 170 175
Thr Phe Pro Thr Val Met His Ile Ala Thr Ala Val Glu Ile His Ser
180 185 190
Arg Phe Ile Pro Ser Leu Gln Gln Leu His Asp Ser Leu His Ser Lys
195 200 205
Thr Ile Glu Phe Lys Asp Ile Ile Lys Ile Gly Arg Thr His Thr Gln
210 215 220
Asp Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Thr Thr
225 230 235 240
Gln Val Lys Tyr Gly Ile Asp Arg Ile Asn Cys Thr Leu Pro Arg Met
245 250 255
Tyr Gln Leu Ala Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr
260 265 270
Lys Lys Gly Phe Asp Ala Lys Ile Ala Ala Ala Val Ala Glu Glu Thr
275 280 285
Asn Leu Pro Phe Val Thr Ala Glu Asn Lys Phe Glu Ala Leu Ala Ala
290 295 300
His Asp Ala Phe Val Glu Ser Ser Gly Ala Val Asn Thr Ile Ser Ala
305 310 315 320
Ser Leu Met Lys Ile Ala Asn Asp Ile Arg Leu Leu Gly Ser Gly Pro
325 330 335
Arg Cys Gly Leu Gly Glu Leu Ile Leu Pro Glu Asn Glu Pro Gly Ser
340 345 350
Ser Ile Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr
355 360 365
Met Val Cys Ala Gln Val Met Gly Asn His Val Gly Val Thr Val Gly
370 375 380
Gly Ala Asn Gly His Phe Glu Leu Asn Val Phe Lys Pro Met Ile Ala
385 390 395 400
Ala Gly Leu Leu Arg Ser Leu Arg Leu Leu Gly Asp Ala Ser Val Ser
405 410 415
Phe Glu Lys Asn Cys Val Arg Gly Ile Gln Ala Asn His Lys Arg Ile
420 425 430
Ser Gln Leu Leu His Glu Ser Leu Met Leu Val Thr Ser Leu Asn Pro
435 440 445
Lys Ile Gly Tyr Asp Asn Ala Ala Ala Val Ala Lys Lys Ala His Lys
450 455 460
Glu Gly Thr Thr Leu Lys Glu Ala Ala Leu Asp Leu Gly Val Leu Thr
465 470 475 480
Glu Gln Glu Phe His Glu Leu Val Val Pro Glu Lys Met Ile Gly Pro
485 490 495
Ser Asp

<210> 9813

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 9813

atgtgttttaa agcaaatacat tggcag

<210> 9814
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 9814
 ttactgttcg ctttcacag tatag

25

<210> 9815
 <211> 461
 <212> PRT
 <213> Artificial sequence

<220>
 <223> consensus sequence

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is any amino acid

<220>
 <221> Variant
 <222> (4)..(4)
 <223> Xaa in position 4 is any amino acid

<220>
 <221> Variant
 <222> (5)..(10)
 <223> Xaa in position 5 to 10 is any or no amino acid

<220>
 <221> Variant
 <222> (12)..(13)
 <223> Xaa in position 12 to 13 is any amino acid

<220>
 <221> Variant
 <222> (15)..(17)
 <223> Xaa in position 15 to 17 is any amino acid

<220>
 <221> Variant
 <222> (20)..(24)
 <223> Xaa in position 20 to 24 is any amino acid

<220>
 <221> Variant
 <222> (26)..(27)
 <223> Xaa in position 26 to 27 is any amino acid

<220>
 <221> Variant
 <222> (29)..(29)
 <223> Xaa in position 29 is any amino acid

<220>
 <221> Variant
 <222> (31)..(33)
 <223> Xaa in position 31 to 33 is any amino acid

<220>
 <221> Variant
 <222> (36)..(36)

<223> Xaa in position 36 is any amino acid

<220>
<221> Variant
<222> (38)..(53)
<223> Xaa in position 38 to 53 is any amino acid

<220>
<221> Variant
<222> (54)..(55)
<223> Xaa in position 54 to 55 is any or no amino acid

<220>
<221> Variant
<222> (57)..(57)
<223> Xaa in position 57 is any amino acid

<220>
<221> Variant
<222> (61)..(62)
<223> Xaa in position 61 to 62 is any amino acid

<220>
<221> Variant
<222> (64)..(75)
<223> Xaa in position 64 to 75 is any amino acid

<220>
<221> Variant
<222> (76)..(76)
<223> Xaa in position 76 is any or no amino acid

<220>
<221> Variant
<222> (78)..(79)
<223> Xaa in position 78 to 79 is any amino acid

<220>
<221> Variant
<222> (81)..(92)
<223> Xaa in position 81 to 92 is any amino acid

<220>
<221> Variant
<222> (93)..(94)
<223> Xaa in position 93 to 94 is any or no amino acid

<220>
<221> Variant
<222> (96)..(100)
<223> Xaa in position 96 to 100 is any amino acid

<220>
<221> Variant
<222> (102)..(102)
<223> Xaa in position 102 is any amino acid

<220>
<221> Variant
<222> (104)..(104)
<223> Xaa in position 104 is any amino acid

<220>
<221> Variant
<222> (107)..(108)
<223> Xaa in position 107 to 108 is any amino acid

<220>
<221> Variant

<222> (112)..(112)
<223> Xaa in position 112 is any amino acid

<220>
<221> Variant
<222> (116)..(117)
<223> Xaa in position 116 to 117 is any amino acid

<220>
<221> Variant
<222> (119)..(119)
<223> Xaa in position 119 is any amino acid

<220>
<221> Variant
<222> (121)..(121)
<223> Xaa in position 121 is any amino acid

<220>
<221> Variant
<222> (123)..(123)
<223> Xaa in position 123 is any amino acid

<220>
<221> Variant
<222> (124)..(124)
<223> Xaa in position 124 is any or no amino acid

<220>
<221> Variant
<222> (126)..(127)
<223> Xaa in position 126 to 127 is any amino acid

<220>
<221> Variant
<222> (128)..(129)
<223> Xaa in position 128 to 129 is any or no amino acid

<220>
<221> Variant
<222> (131)..(132)
<223> Xaa in position 131 to 132 is any amino acid

<220>
<221> Variant
<222> (133)..(136)
<223> Xaa in position 133 to 136 is any or no amino acid

<220>
<221> Variant
<222> (139)..(139)
<223> Xaa in position 139 is any amino acid

<220>
<221> Variant
<222> (143)..(144)
<223> Xaa in position 143 to 144 is any amino acid

<220>
<221> Variant
<222> (147)..(147)
<223> Xaa in position 147 is any amino acid

<220>
<221> Variant
<222> (150)..(151)
<223> Xaa in position 150 to 151 is any amino acid

<220>

```

<221> Variant
<222> (154)..(157)
<223> Xaa in position 154 to 157 is any amino acid

<220>
<221> Variant
<222> (159)..(165)
<223> Xaa in position 159 to 165 is any amino acid

<220>
<221> Variant
<222> (166)..(166)
<223> Xaa in position 166 is any or no amino acid

<220>
<221> Variant
<222> (168)..(173)
<223> Xaa in position 168 to 173 is any amino acid

<220>
<221> Variant
<222> (175)..(180)
<223> Xaa in position 175 to 180 is any amino acid

<220>
<221> Variant
<222> (182)..(184)
<223> Xaa in position 182 to 184 is any amino acid

<220>
<221> Variant
<222> (186)..(189)
<223> Xaa in position 186 to 189 is any amino acid

<220>
<221> Variant
<222> (190)..(191)
<223> Xaa in position 190 to 191 is any or no amino acid

<220>
<221> Variant
<222> (193)..(193)
<223> Xaa in position 193 is any amino acid

<220>
<221> Variant
<222> (197)..(198)
<223> Xaa in position 197 to 198 is any amino acid

<220>
<221> Variant
<222> (202)..(202)
<223> Xaa in position 202 is any amino acid

<220>
<221> Variant
<222> (204)..(204)
<223> Xaa in position 204 is any amino acid

<220>
<221> Variant
<222> (211)..(230)
<223> Xaa in position 211 to 230 is any amino acid

<220>
<221> Variant
<222> (231)..(237)
<223> Xaa in position 231 to 237 is any or no amino acid

```

```

<220>
<221> Variant
<222> (239)..(239)
<223> Xaa in position 239 is any amino acid

<220>
<221> Variant
<222> (242)..(242)
<223> Xaa in position 242 is any amino acid

<220>
<221> Variant
<222> (246)..(246)
<223> Xaa in position 246 is any amino acid

<220>
<221> Variant
<222> (248)..(270)
<223> Xaa in position 248 to 270 is any amino acid

<220>
<221> Variant
<222> (271)..(271)
<223> Xaa in position 271 is any or no amino acid

<220>
<221> Variant
<222> (273)..(276)
<223> Xaa in position 273 to 276 is any amino acid

<220>
<221> Variant
<222> (277)..(277)
<223> Xaa in position 277 is any or no amino acid

<220>
<221> Variant
<222> (279)..(285)
<223> Xaa in position 279 to 285 is any amino acid

<220>
<221> Variant
<222> (287)..(291)
<223> Xaa in position 287 to 291 is any amino acid

<220>
<221> Variant
<222> (293)..(295)
<223> Xaa in position 293 to 295 is any amino acid

<220>
<221> Variant
<222> (297)..(298)
<223> Xaa in position 297 to 298 is any amino acid

<220>
<221> Variant
<222> (300)..(300)
<223> Xaa in position 300 is any amino acid

<220>
<221> Variant
<222> (303)..(303)
<223> Xaa in position 303 is any amino acid

<220>
<221> Variant
<222> (306)..(306)
<223> Xaa in position 306 is any amino acid

```

```

<220>
<221> Variant
<222> (308)..(308)
<223> Xaa in position 308 is any amino acid

<220>
<221> Variant
<222> (310)..(310)
<223> Xaa in position 310 is any amino acid

<220>
<221> Variant
<222> (315)..(315)
<223> Xaa in position 315 is any amino acid

<220>
<221> Variant
<222> (317)..(318)
<223> Xaa in position 317 to 318 is any amino acid

<220>
<221> Variant
<222> (320)..(321)
<223> Xaa in position 320 to 321 is any amino acid

<220>
<221> Variant
<222> (324)..(327)
<223> Xaa in position 324 to 327 is any amino acid

<220>
<221> Variant
<222> (334)..(334)
<223> Xaa in position 334 is any amino acid

<220>
<221> Variant
<222> (339)..(341)
<223> Xaa in position 339 to 341 is any amino acid

<220>
<221> Variant
<222> (343)..(350)
<223> Xaa in position 343 to 350 is any amino acid

<220>
<221> Variant
<222> (352)..(352)
<223> Xaa in position 352 is any amino acid

<220>
<221> Variant
<222> (355)..(364)
<223> Xaa in position 355 to 364 is any amino acid

<220>
<221> Variant
<222> (366)..(368)
<223> Xaa in position 366 to 368 is any amino acid

<220>
<221> Variant
<222> (371)..(373)
<223> Xaa in position 371 to 373 is any amino acid

<220>
<221> Variant
<222> (375)..(382)

```

<223> Xaa in position 375 to 382 is any amino acid

<220>
 <221> Variant
 <222> (384)..(386)
 <223> Xaa in position 384 to 386 is any amino acid

<220>
 <221> Variant
 <222> (388)..(397)
 <223> Xaa in position 388 to 397 is any amino acid

<220>
 <221> Variant
 <222> (399)..(400)
 <223> Xaa in position 399 to 400 is any amino acid

<220>
 <221> Variant
 <222> (403)..(404)
 <223> Xaa in position 403 to 404 is any amino acid

<220>
 <221> Variant
 <222> (406)..(415)
 <223> Xaa in position 406 to 415 is any amino acid

<220>
 <221> Variant
 <222> (417)..(419)
 <223> Xaa in position 417 to 419 is any amino acid

<220>
 <221> Variant
 <222> (422)..(422)
 <223> Xaa in position 422 is any amino acid

<220>
 <221> Variant
 <222> (426)..(426)
 <223> Xaa in position 426 is any amino acid

<220>
 <221> Variant
 <222> (429)..(436)
 <223> Xaa in position 429 to 436 is any amino acid

<220>
 <221> Variant
 <222> (438)..(442)
 <223> Xaa in position 438 to 442 is any amino acid

<220>
 <221> Variant
 <222> (444)..(454)
 <223> Xaa in position 444 to 454 is any amino acid

<220>
 <221> Variant
 <222> (455)..(460)
 <223> Xaa in position 455 to 460 is any or no amino acid

<400> 9815
 Arg Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Gly Xaa Xaa
 1 5 10 15
 Xaa Val Pro Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Thr Xaa Arg Xaa Xaa
 20 25 30
 Xaa Asn Phe Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

PF59083SeqList PF59083.txt

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Ala	Ala	Ala	Xaa	Xaa	Asn	Xaa
	50					55					60				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	Xaa	Ala
65					70				75						80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa
				85					90					95	
Xaa	Xaa	Xaa	Xaa	Gln	Xaa	Gly	Xaa	Gly	Thr	Xaa	Xaa	Asn	Met	Asn	Xaa
				100				105					110		
Asn	Glu	Val	Xaa	Xaa	Asn	Xaa	Ala	Xaa	Glu	Xaa	Xaa	Gly	Xaa	Xaa	Xaa
	115						120					125			
Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Asn	Xaa	His	Val	Asn	Xaa	Xaa
	130					135					140				
Gln	Ser	Xaa	Asn	Asp	Xaa	Xaa	Pro	Thr	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Xaa
145					150					155					160
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa
				165						170				175	
Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys
				180				185					190		
Xaa	Gly	Arg	Thr	Xaa	Xaa	Gln	Asp	Ala	Xaa	Pro	Xaa	Thr	Leu	Gly	Gln
	195						200					205			
Glu	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	210					215					220				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Thr
225					230					235					240
Ala	Xaa	Gly	Thr	Gly	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				245				250						255	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala
				260				265						270	
Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Xaa	Xaa
				275				280					285		
Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Ala	Xaa	Xaa	Leu	Xaa	Lys	Ile	Xaa	Asn
	290					295					300				
Asp	Xaa	Arg	Xaa	Leu	Xaa	Ser	Gly	Pro	Arg	Xaa	Gly	Xaa	Xaa	Glu	Xaa
305					310					315					320
Xaa	Leu	Pro	Xaa	Xaa	Xaa	Xaa	Gly	Ser	Ser	Ile	Met	Pro	Xaa	Lys	Val
				325					330					335	
Asn	Pro	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Xaa
				340				345						350	
Gly	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa
	355					360						365			
Leu	Asn	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Xaa
	370					375						380			
Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa
385					390					395					400
Gly	Ile	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser
				405				410						415	
Xaa	Xaa	Xaa	Val	Thr	Xaa	Leu	Asn	Pro	Xaa	Ile	Gly	Xaa	Xaa	Xaa	Xaa
			420					425						430	
Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa
			435					440						445	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu			
	450					455						460			

<210> 9816

<211> 54

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (2)..(2)

<223> Xaa in position 2 is any amino acid

<220>

<221> Variant

<222> (3)..(3)
<223> Xaa in position 3 is Ala, Cys, Gly, Ser or Thr

<220>
<221> Variant
<222> (4)..(4)
<223> Xaa in position 4 is Asn or Gln

<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is Ile, Leu or Val

<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is any or no amino acid

<220>
<221> Variant
<222> (10)..(10)
<223> Xaa in position 10 is any amino acid

<220>
<221> Variant
<222> (12)..(12)
<223> Xaa in position 12 is any or no amino acid

<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is any amino acid

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is Ala, Cys, Asn, Ser or Thr

<220>
<221> Variant
<222> (18)..(19)
<223> Xaa in position 18 to 19 is any amino acid

<220>
<221> Variant
<222> (21)..(21)
<223> Xaa in position 21 is Phe, Ile, Leu or Val

<220>
<221> Variant
<222> (22)..(23)
<223> Xaa in position 22 to 23 is any amino acid

<220>
<221> Variant
<222> (25)..(26)
<223> Xaa in position 25 to 26 is any amino acid

<220>
<221> Variant
<222> (27)..(27)
<223> Xaa in position 27 is Ala, Glu or Gln

<220>
<221> Variant
<222> (28)..(28)
<223> Xaa in position 28 is any amino acid

<220>

<221> Variant
 <222> (35)..(35)
 <223> Xaa in position 35 is Ala or Gly

 <220>
 <221> Variant
 <222> (37)..(37)
 <223> Xaa in position 37 is Ile or Val

 <220>
 <221> Variant
 <222> (40)..(40)
 <223> Xaa in position 40 is Ser, Thr or Val

 <220>
 <221> Variant
 <222> (41)..(42)
 <223> Xaa in position 41 to 42 is any amino acid

 <220>
 <221> Variant
 <222> (44)..(44)
 <223> Xaa in position 44 is any amino acid

 <220>
 <221> Variant
 <222> (45)..(45)
 <223> Xaa in position 45 is Ile, Leu, Met or Val

 <220>
 <221> Variant
 <222> (46)..(46)
 <223> Xaa in position 46 is Asn, Ser or Thr

 <220>
 <221> Variant
 <222> (47)..(53)
 <223> Xaa in position 47 to 53 is any amino acid

 <220>
 <221> Variant
 <222> (54)..(54)
 <223> Xaa in position 54 is Ala, Gly or Ser

 <400> 9816
 Lys Xaa Xaa Xaa Asp Xaa Arg Xaa Leu Xaa Ser Xaa Gly Pro Xaa Xaa
 1 5 10 15
 Gly Xaa Xaa Glu Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Gly Ser Ser Ile
 20 25 30
 Met Pro Xaa Lys Xaa Asn Pro Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa
 50

 <210> 9817
 <211> 28
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> protein pattern

 <220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is any amino acid

 <220>

```

<221> Variant
<222> (3)..(4)
<223> Xaa in position 3 to 4 is any or no amino acid

<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is any amino acid

<220>
<221> Variant
<222> (7)..(8)
<223> Xaa in position 7 to 8 is any or no amino acid

<220>
<221> Variant
<222> (10)..(10)
<223> Xaa in position 10 is Gly or Thr

<220>
<221> Variant
<222> (12)..(12)
<223> Xaa in position 12 is Ala or Ser

<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is Gln or Ser

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is any amino acid

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is any amino acid

<220>
<221> Variant
<222> (24)..(24)
<223> Xaa in position 24 is Ile, Leu or Val

<220>
<221> Variant
<222> (25)..(25)
<223> Xaa in position 25 is Ala, Cys, Ser or Thr

<220>
<221> Variant
<222> (26)..(26)
<223> Xaa in position 26 is Gly, Asn, Ser or Thr

<220>
<221> Variant
<222> (27)..(27)
<223> Xaa in position 27 is any amino acid

<220>
<221> Variant
<222> (28)..(28)
<223> Xaa in position 28 is Ala, Gly or Leu

<400> 9817
Phe Xaa Xaa Xaa Val Xaa Xaa Xaa Gln Xaa Gly Xaa Gly Thr Xaa Xaa
1           5           10           15
Asn Met Asn Xaa Asn Glu Val Xaa Xaa Xaa Xaa Xaa
          20          25

```

```

<210> 9818
<211> 27
<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
<221> Variant
<222> (2)..(3)
<223> Xaa in position 2 to 3 is any amino acid

<220>
<221> Variant
<222> (4)..(4)
<223> Xaa in position 4 is Phe, Ile, Leu, Met or Val

<220>
<221> Variant
<222> (5)..(5)
<223> Xaa in position 5 is any amino acid

<220>
<221> Variant
<222> (7)..(7)
<223> Xaa in position 7 is any amino acid

<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is Ala or Gly

<220>
<221> Variant
<222> (11)..(13)
<223> Xaa in position 11 to 13 is any amino acid

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is any amino acid

<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is Ile, Leu, Met or Val

<220>
<221> Variant
<222> (19)..(19)
<223> Xaa in position 19 is any amino acid

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is Ala, Leu or Val

<220>
<221> Variant
<222> (22)..(22)
<223> Xaa in position 22 is any amino acid

<220>
<221> Variant
<222> (24)..(24)
<223> Xaa in position 24 is Phe or Ile

```

PF59083SeqList PF59083.txt

```

<220>
<221> Variant
<222> (25)..(25)
<223> Xaa in position 25 is any amino acid

<220>
<221> Variant
<222> (26)..(26)
<223> Xaa in position 26 is Ala, Gly, Ser or Thr

<220>
<221> Variant
<222> (27)..(27)
<223> Xaa in position 27 is Phe, Trp or Tyr

<400> 9818
Phe Xaa Xaa Xaa Xaa Lys Xaa Xaa Arg Thr Xaa Xaa Xaa Asp Ala Xaa
1      5      10      15
Pro Xaa Xaa Xaa Gly Xaa Glu Xaa Xaa Xaa Xaa
      20      25

<210> 9819
<211> 21
<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
<221> Variant
<222> (2)..(2)
<223> Xaa in position 2 is any amino acid

<220>
<221> Variant
<222> (3)..(3)
<223> Xaa in position 3 is Asp or His

<220>
<221> Variant
<222> (4)..(4)
<223> Xaa in position 4 is any amino acid

<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is any amino acid

<220>
<221> Variant
<222> (7)..(7)
<223> Xaa in position 7 is Ala, Cys, Gly or Ser

<220>
<221> Variant
<222> (10)..(10)
<223> Xaa in position 10 is Gln, Ser or Thr

<220>
<221> Variant
<222> (13)..(14)
<223> Xaa in position 13 to 14 is any amino acid

<220>
<221> Variant
<222> (16)..(16)

```

<223> Xaa in position 16 is Ala, Ser or Thr

<220>

<221> Variant

<222> (17)..(19)

<223> Xaa in position 17 to 19 is any amino acid

<220>

<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is Ile, Leu, Met or Val

<220>

<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is Ala, Gly, Ser or Thr

<400> 9819

Asn	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Gln	Ser	Xaa	Asn	Asp	Xaa	Xaa	Pro	Xaa
1				5				10						15	
Xaa	Xaa	Xaa	Xaa	Xaa											
				20											

<210> 9820

<211> 29

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (2)..(2)

<223> Xaa in position 2 is Ile or Leu

<220>

<221> Variant

<222> (3)..(3)

<223> Xaa in position 3 is any amino acid

<220>

<221> Variant

<222> (4)..(4)

<223> Xaa in position 4 is Ala, Pro or Val

<220>

<221> Variant

<222> (5)..(15)

<223> Xaa in position 5 to 15 is any amino acid

<220>

<221> Variant

<222> (16)..(16)

<223> Xaa in position 16 is Gly, Ser or Thr

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is Ala, Ile, Leu, Pro or Val

<220>

<221> Variant

<222> (18)..(18)

<223> Xaa in position 18 is any amino acid

<220>

<221> Variant

$\langle 220 \rangle$
$$\langle \bar{2}2\bar{2} \rangle \quad (20) \quad . \quad (20)$$
 $\langle 220 \rangle$ $\langle 222 \rangle \quad (22) \dots (22)$ $\langle 220 \rangle$

<222> (24) . . (27)

$\langle 220 \rangle$

<222> (29) . . (29)

<400> 9820

1 Xaa Xaa Xaa Xaa Thr Xaa Leu Xaa Xaa Xaa Xaa Gly Xaa
5 10
20 25

<211> 15

<212> PRT

 $\langle 220 \rangle$ $\langle 220 \rangle$

<222> (2) . . (2)

$\langle 220 \rangle$

<222> (4) . . (4)

 $\langle 220 \rangle$

<222> (5) . . (5)

 $\langle 220 \rangle$

$\langle 222 \rangle$ (6) . . (6)

$\langle 220 \rangle$

 $\langle 222 \rangle \quad (7) \dots (7)$

$\langle 220 \rangle$

<222> (9) . . (9)

 $\langle 220 \rangle$

```

<221> Variant
<222> (10)..(11)
<223> Xaa in position 10 to 11 is any amino acid

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is Phe or Tyr

<220>
<221> Variant
<222> (14)..(14)
<223> Xaa in position 14 is any amino acid

<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is Ile, Leu or Val

<400> 9821
Tyr Xaa Gly Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Asn Xaa Xaa Xaa
1      5      10      15

<210> 9822
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
<221> Variant
<222> (2)..(2)
<223> Xaa in position 2 is any amino acid

<220>
<221> Variant
<222> (3)..(3)
<223> Xaa in position 3 is Phe or Leu

<220>
<221> Variant
<222> (4)..(4)
<223> Xaa in position 4 is Glu or Gln

<220>
<221> Variant
<222> (7)..(7)
<223> Xaa in position 7 is Ala or Val

<220>
<221> Variant
<222> (8)..(9)
<223> Xaa in position 8 to 9 is any amino acid

<220>
<221> Variant
<222> (11)..(12)
<223> Xaa in position 11 to 12 is Ile, Leu, Met or Val

<220>
<221> Variant
<222> (13)..(15)
<223> Xaa in position 13 to 15 is any amino acid

<220>
<221> Variant

```

<222> (16)..(16)
 <223> Xaa in position 16 is Phe, Ile, Leu, Met or Val

 <220>
 <221> Variant
 <222> (17)..(18)
 <223> Xaa in position 17 to 18 is any amino acid

 <400> 9822
 Gly Xaa Xaa Xaa Leu Asn Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Ser

<210> 9823
 <211> 15
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is Ala or Gly

<220>
 <221> Variant
 <222> (3)..(3)
 <223> Xaa in position 3 is Ser or Thr

<220>
 <221> Variant
 <222> (5)..(5)
 <223> Xaa in position 5 is Ala, Ile or Val

<220>
 <221> Variant
 <222> (9)..(9)
 <223> Xaa in position 9 is Ile, Leu, Met or Val

<220>
 <221> Variant
 <222> (11)..(11)
 <223> Xaa in position 11 is Ala, Cys, Gly, Ser or Thr

<220>
 <221> Variant
 <222> (12)..(14)
 <223> Xaa in position 12 to 14 is any amino acid

<220>
 <221> Variant
 <222> (15)..(15)
 <223> Xaa in position 15 is Phe or Tyr

<400> 9823
 Gly Xaa Xaa Ala Xaa Gly Thr Gly Xaa Asn Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

<210> 9824
 <211> 1254
 <212> DNA
 <213> ESCHERICHIA COLI

<220>
 <221> CDS

PF59083SeqList PF59083.txt

<222> (1)..(1254)

<223> transl_table=11

<400> 9824

atg	aga	tat	acg	gag	gga	gat	atg	tcg	tca	ttt	gat	tac	ctg	aaa	act	48
Met	Arg	Tyr	Thr	Glu	Gly	Asp	Met	Ser	Ser	Phe	Asp	Tyr	Leu	Lys	Thr	
1				5				10					15			
gcc	atc	aag	caa	cag	ggc	tgc	acg	cta	cag	cag	gta	gct	gat	gcc	agc	96
Ala	Ile	Lys	Gln	Gln	Gly	Cys	Thr	Leu	Gln	Gln	Val	Ala	Asp	Ala	Ser	
			20					25					30			
ggt	atg	acc	aaa	ggg	tat	tta	agc	cag	tta	ctg	aat	gcc	aaa	atc	aaa	144
Gly	Met	Thr	Lys	Gly	Tyr	Leu	Ser	Gln	Leu	Leu	Asn	Ala	Lys	Ile	Lys	
			35				40					45				
agc	ccc	agc	gcg	caa	aag	ctg	gag	gcg	ttg	cac	cgt	ttt	ttg	ggg	ctt	192
Ser	Pro	Ser	Ala	Gln	Lys	Leu	Glu	Ala	Leu	His	Arg	Phe	Leu	Gly	Leu	
			50			55					60					
gag	ttt	ccc	cgg	cag	aag	aaa	acg	atc	ggt	gtc	gta	ttc	ggt	aag	ttc	240
Glu	Phe	Pro	Arg	Gln	Lys	Lys	Thr	Ile	Gly	Val	Val	Phe	Gly	Lys	Phe	
				70					75						80	
tac	cca	ctg	cat	acc	gga	cat	atc	tac	ctt	atc	cag	cgc	gcc	tgt	agc	288
Tyr	Pro	Leu	His	Thr	Gly	His	Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Cys	Ser	
				85					90					95		
cag	gtt	gac	gag	ctg	cat	atc	att	atg	ggt	ttt	gac	gat	acc	cgt	gac	336
Gln	Val	Asp	Glu	Leu	His	Ile	Ile	Met	Gly	Phe	Asp	Asp	Thr	Arg	Asp	
			100					105					110			
cgc	gcg	ttg	ttc	gaa	gac	agt	gcc	atg	tcg	cag	cag	ccg	acc	gtg	ccg	384
Arg	Ala	Leu	Phe	Glu	Asp	Ser	Ala	Met	Ser	Gln	Gln	Pro	Thr	Val	Pro	
			115				120					125				
gat	cgt	ctg	cgt	tgg	tta	ttg	caa	act	ttt	aaa	tat	cag	aaa	aat	att	432
Asp	Arg	Leu	Arg	Trp	Leu	Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile		
			130			135					140					
cgc	att	cat	gct	ttc	aac	gaa	gag	ggc	atg	gag	ccg	tat	ccg	cac	ggc	480
Arg	Ile	His	Ala	Phe	Asn	Glu	Glu	Gly	Met	Glu	Pro	Tyr	Pro	His	Gly	
				150					155						160	
tgg	gat	gtg	tgg	agc	aac	ggc	atc	aaa	aag	ttt	atg	gct	gaa	aaa	ggg	528
Trp	Asp	Val	Trp	Ser	Asn	Gly	Ile	Lys	Lys	Phe	Met	Ala	Glu	Lys	Gly	
				165					170					175		
atc	cag	ccg	gat	ctg	atc	tac	acc	tcg	gaa	gaa	gcc	gat	gcg	cca	cag	576
Ile	Gln	Pro	Asp	Leu	Ile	Tyr	Thr	Ser	Glu	Glu	Ala	Asp	Ala	Pro	Gln	
			180					185					190			
tat	atg	gaa	cat	ctg	ggg	atc	gag	acg	gtg	ctg	gtc	gat	ccg	aaa	cgt	624
Tyr	Met	Glu	His	Leu	Gly	Ile	Glu	Thr	Val	Leu	Val	Asp	Pro	Lys	Arg	
			195				200					205				
acc	ttt	atg	agt	atc	agc	ggt	gcg	cag	atc	cgc	gaa	aac	ccg	ttc	cgc	672
Thr	Phe	Met	Ser	Ile	Ser	Gly	Ala	Gln	Ile	Arg	Glu	Asn	Pro	Phe	Arg	
				210		215					220					
tac	tgg	gaa	tat	att	cct	acc	gaa	gtg	aag	ccg	ttt	ttt	gtg	cgt	acc	720
Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	
				225		230				235					240	
gtg	gcg	atc	ctt	ggc	ggc	gag	tcg	agc	ggt	aaa	tcc	acc	ctg	gta	aac	768
Val	Ala	Ile	Leu	Gly	Gly	Glu	Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	
				245					250					255		
aaa	ctt	gcc	aat	atc	ttc	aac	acc	acc	agt	gcg	tgg	gaa	tat	ggc	cgc	816
Lys	Leu	Ala	Asn	Ile	Phe	Asn	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Gly	Arg	
			260				265						270			
gat	tat	gtc	ttt	tca	cac	ctc	ggc	ggt	gat	gag	atc	gca	ttg	cag	tat	864
Asp	Tyr	Val	Phe	Ser	His	Leu	Gly	Gly	Asp	Glu	Ile	Ala	Leu	Gln	Tyr	
				275			280					285				
tct	gac	tac	gat	aaa	atc	gcg	ctg	ggc	cac	gct	caa	tac	att	gat	ttt	912
Ser	Asp	Tyr	Asp	Lys	Ile	Ala	Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe	
				290		295					300					
gcg	gtg	aaa	tat	gcc	aat	aaa	gtg	gca	ttt	atc	gat	acc	gat	ttt	gtc	960
Ala	Val	Lys	Tyr	Ala	Asn	Lys	Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	
				305		310				315					320	
acc	act	cag	gcg	ttc	tgc	aaa	aag	tac	gaa	ggg	cgg	gaa	cat	ccg	ttc	1008
Thr	Thr	Gln	Ala	Phe	Cys	Lys	Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	
				325					330					335		
gtg	cag	gcg	ctg	att	gat	gaa	tac	cgt	ttc	gat	ctg	gtg	atc	ctg	ctg	1056
Val	Gln	Ala	Leu	Ile	Asp	Glu	Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	

PF59083SeqList PF59083.txt

<div> <div>340</div> <div>345</div> <div>350</div> </div>																
gag Glu	aac Asn	aac Asn 355	acg Thr	ccg Pro	tgg Trp	gtg Val	gcg Ala 360	gat Asp	ggg Gly	tta Leu	cgc Arg	agc Ser 365	ctc Leu	ggc Gly	agt Ser	1104
tcg Ser	gtg Val 370	gat Asp	cgc Arg	aaa Lys	gag Glu	ttc Phe 375	cag Gln	aac Asn	ttg Leu	ctg Leu	gtg Val 380	gag Glu	atg Met	ctc Leu	gaa Glu	1152
gag Glu 385	aac Asn	aat Asn	atc Ile	gaa Glu 390	ttt Phe 390	gtg Val	cgg Arg	gtt Val	gaa Glu 395	gag Glu	gaa Glu	gat Asp	tac Tyr	gac Asp	agt Ser 400	1200
cgt Arg	ttc Phe	ctg Leu	cgc Arg	tgc Cys 405	gtg Val	gaa Glu	ctg Leu	gtg Val	cgg Arg 410	gag Glu	atg Met	atg Met	ggg Gly	gag Glu 415	cag Gln	1248
aga Arg	taa															1254

<210> 9825

<211> 417

<212> PRT

<213> ESCHERICHIA COLI

<400> 9825

Met	Arg	Tyr	Thr	Glu	Gly	Asp	Met	Ser	Ser	Phe	Asp	Tyr	Leu	Lys	Thr
1				5					10					15	
Ala	Ile	Lys	Gln	Gln	Gly	Cys	Thr	Leu	Gln	Gln	Val	Ala	Asp	Ala	Ser
			20					25					30		
Gly	Met	Thr	Lys	Gly	Tyr	Leu	Ser	Gln	Leu	Leu	Asn	Ala	Lys	Ile	Lys
		35					40					45			
Ser	Pro	Ser	Ala	Gln	Lys	Leu	Glu	Ala	Leu	His	Arg	Phe	Leu	Gly	Leu
	50					55					60				
Glu	Phe	Pro	Arg	Gln	Lys	Lys	Thr	Ile	Gly	Val	Val	Phe	Gly	Lys	Phe
65					70					75					80
Tyr	Pro	Leu	His	Thr	Gly	His	Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Cys	Ser
			85						90					95	
Gln	Val	Asp	Glu	Leu	His	Ile	Ile	Met	Gly	Phe	Asp	Asp	Thr	Arg	Asp
			100					105					110		
Arg	Ala	Leu	Phe	Glu	Asp	Ser	Ala	Met	Ser	Gln	Gln	Pro	Thr	Val	Pro
		115					120					125			
Asp	Arg	Leu	Arg	Trp	Leu	Leu	Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile
	130					135					140				
Arg	Ile	His	Ala	Phe	Asn	Glu	Glu	Gly	Met	Glu	Pro	Tyr	Pro	His	Gly
145					150					155					160
Trp	Asp	Val	Trp	Ser	Asn	Gly	Ile	Lys	Lys	Phe	Met	Ala	Glu	Lys	Gly
			165						170					175	
Ile	Gln	Pro	Asp	Leu	Ile	Tyr	Thr	Ser	Glu	Glu	Ala	Asp	Ala	Pro	Gln
			180					185					190		
Tyr	Met	Glu	His	Leu	Gly	Ile	Glu	Thr	Val	Leu	Val	Asp	Pro	Lys	Arg
		195					200					205			
Thr	Phe	Met	Ser	Ile	Ser	Gly	Ala	Gln	Ile	Arg	Glu	Asn	Pro	Phe	Arg
	210					215					220				
Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr
225					230					235				240	
Val	Ala	Ile	Leu	Gly	Gly	Glu	Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn
			245						250				255		
Lys	Leu	Ala	Asn	Ile	Phe	Asn	Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg
			260					265					270		
Asp	Tyr	Val	Phe	Ser	His	Leu	Gly	Gly	Asp	Glu	Ile	Ala	Leu	Gln	Tyr
		275					280					285			
Ser	Asp	Tyr	Asp	Lys	Ile	Ala	Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe
	290					295					300				
Ala	Val	Lys	Tyr	Ala	Asn	Lys	Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val
305					310					315				320	
Thr	Thr	Gln	Ala	Phe	Cys	Lys	Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe
			325						330				335		
Val	Gln	Ala	Leu	Ile	Asp	Glu	Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu
			340					345					350		
Glu	Asn	Asn	Thr	Pro	Trp	Val									

PF59083SeqList PF59083.txt

Ser Val Asp Arg Lys Glu Phe Gln Asn Leu Leu Val Glu Met Leu Glu
 370 375 380
 Glu Asn Asn Ile Glu Phe Val Arg Val Glu Glu Glu Asp Tyr Asp Ser
 385 390 395 400
 Arg Phe Leu Arg Cys Val Glu Leu Val Arg Glu Met Met Gly Glu Gln
 405 410 415
 Arg

<210> 9826
 <211> 1227
 <212> DNA
 <213> Xenorhabdus bovienii

<220>
 <221> CDS
 <222> (1)..(1227)
 <223> transl_table=11

<400> 9826
 atg ggg caa ttt gac tac ttg aaa gaa gct att aaa cag gcg agt tac 48
 Met Gly Gln Phe Asp Tyr Leu Lys Glu Ala Ile Lys Gln Ala Ser Tyr
 1 5 10 15
 aca ttg cag caa gtg gct gat gcc tgt gga atg aca aaa ggc tat ttg 96
 Thr Leu Gln Gln Val Ala Asp Ala Cys Gly Met Thr Lys Gly Tyr Leu
 20 25 30
 agc caa ctt att aac ggc aaa ata aag agt ccg agt gcg cag aaa ctg 144
 Ser Gln Leu Ile Asn Gly Lys Ile Lys Ser Pro Ser Ala Gln Lys Leu
 35 40 45
 gca tct att cat caa tat tta tta gcg tat ccc atg gaa aag aaa 192
 Ala Ser Ile His Gln Tyr Leu Gly Leu Ala Tyr Pro Met Glu Lys Lys
 50 55 60
 acc gtc ggt gtg gtg ttt ggt aaa ttt tac ccg ttg cat act ggg cat 240
 Thr Val Gly Val Val Phe Gly Lys Phe Tyr Pro Leu His Thr Gly His
 65 70 75 80
 att tat ttg atc cag cgg gca tcc agt cag gtc gat gaa ttg cac gtc 288
 Ile Tyr Leu Ile Gln Arg Ala Ser Ser Gln Val Asp Glu Leu His Val
 85 90 95
 gtc ctc tgt tat gac gaa ttg cgg gat cgt gaa ttg ttc atc aat agt 336
 Val Leu Cys Tyr Asp Glu Leu Arg Asp Arg Glu Leu Phe Ile Asn Ser
 100 105 110
 tct atg tct cag caa ccc aca gtc agt gac cgc ctg aga tgg ctt tta 384
 Ser Met Ser Gln Gln Pro Thr Val Ser Asp Arg Leu Arg Trp Leu Leu
 115 120 125
 caa aca ttc aaa tat caa aaa aat atc cac atc cac gtt ttt gat gaa 432
 Gln Thr Phe Lys Tyr Gln Lys Asn Ile His Ile His Val Phe Asp Glu
 130 135 140
 cat ggc atg gag cct tat ccg aat ggc tgg gaa gta tgg agc cgg gga 480
 His Gly Met Glu Pro Tyr Pro Asn Gly Trp Glu Val Trp Ser Arg Gly
 145 150 155 160
 gtg aag gca ttc atg gca gag aag agc atc aat cct gaa tat atc tat 528
 Val Lys Ala Phe Met Ala Glu Lys Ser Ile Asn Pro Glu Tyr Ile Tyr
 165 170 175
 tcc agt gaa gcg cag gat gta gca tgt tat aaa gaa tat ttc gat att 576
 Ser Ser Glu Ala Gln Asp Val Ala Cys Tyr Lys Glu Tyr Phe Asp Ile
 180 185 190
 gaa act atc ctt att gat cca caa cgt tca ttc atg aat atc agc ggc 624
 Glu Thr Ile Leu Ile Asp Pro Gln Arg Ser Phe Met Asn Ile Ser Gly
 195 200 205 210
 agc cag ata cgg cag gca cct ttt cgc tat tgg gaa tat att cca aca 672
 Ser Gln Ile Arg Gln Ala Pro Phe Arg Tyr Trp Glu Tyr Ile Pro Thr
 215 220 225
 gaa gtg aag cca ttt ttt gtg cgc acc gtg gca att ctg ggt ggt gag 720
 Glu Val Lys Pro Phe Val Arg Thr Val Ala Ile Leu Gly Gly Glu
 230 235 240
 tcg agt ggt aaa tcc aca ctg gta aac aag tta gcc aat atg ttt aac 768
 Ser Ser Gly Lys Ser Thr Leu Val Asn Lys Leu Ala Asn Met Phe Asn
 245 250 255
 aca acc agc gta tgg gaa tat ggg cga gag tac gtg ttc tcc cac ttg 816
 10339

PF59083SeqList PF59083.txt

Thr	Thr	Ser	Val	Trp	Glu	Tyr	Gly	Arg	Glu	Tyr	Val	Phe	Ser	His	Leu	
			260					265					270			
gga	ggg	gat	gaa	atg	gct	ctg	caa	tac	tca	gat	tac	gat	aaa	att	gca	864
Gly	Gly	Asp	Glu	Met	Ala	Leu	Gln	Tyr	Ser	Asp	Tyr	Asp	Lys	Ile	Ala	
		275					280					285				
ttg	gga	cat	gca	caa	tat	att	gat	ttt	tca	gtc	aaa	tat	gcc	aat	aaa	912
Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe	Ser	Val	Lys	Tyr	Ala	Asn	Lys	
	290					295					300					
gtt	gct	ttt	att	gac	act	gat	ttc	gtg	acg	aca	cag	gca	ttt	tgc	aag	960
Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	Thr	Thr	Gln	Ala	Phe	Cys	Lys	
305					310				315						320	
cgt	tat	gaa	gga	aaa	gag	cat	ccc	ttt	gta	cag	gcg	atg	att	gat	gaa	1008
Arg	Tyr	Glu	Gly	Lys	Glu	His	Pro	Phe	Val	Gln	Ala	Met	Ile	Asp	Glu	
			325					330						335		
tat	cga	ttt	gat	ctg	gtc	att	ctg	tta	gaa	aac	aac	acc	ccg	tgg	gtg	1056
Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	Glu	Asn	Asn	Thr	Pro	Trp	Val	
			340					345						350		
gct	gat	ggg	ctg	aga	agt	tta	ggg	agt	gaa	cgg	gaa	cgt	aaa	gag	ttt	1104
Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	Glu	Arg	Glu	Arg	Lys	Glu	Phe	
		355					360					365				
cag	cag	tta	ctt	gag	agt	ttg	ttg	aag	aaa	aat	aac	gtc	gat	tat	gtt	1152
Gln	Gln	Leu	Leu	Glu	Ser	Leu	Leu	Lys	Lys	Asn	Asn	Val	Asp	Tyr	Val	
	370					375						380				
tgt	gtc	aac	tca	gcg	gac	tat	gat	caa	cgt	ttt	ctg	cgc	tgt	att	gaa	1200
Cys	Val	Asn	Ser	Ala	Asp	Tyr	Asp	Gln	Arg	Phe	Leu	Arg	Cys	Ile	Glu	
385					390				395						400	
tta	gtt	caa	cac	atg	tta	atg	gcg	taa								1227
Leu	Val	Gln	His	Met	Leu	Met	Ala									
				405												

<210> 9827

<211> 408

<212> PRT

<213> Xenorhabdus bovienii

<400> 9827

Met	Gly	Gln	Phe	Asp	Tyr	Leu	Lys	Glu	Ala	Ile	Lys	Gln	Ala	Ser	Tyr	
1				5					10					15		
Thr	Leu	Gln	Gln	Val	Ala	Asp	Ala	Cys	Gly	Met	Thr	Lys	Gly	Tyr	Leu	
			20					25					30			
Ser	Gln	Leu	Ile	Asn	Gly	Lys	Ile	Lys	Ser	Pro	Ser	Ala	Gln	Lys	Leu	
		35					40					45				
Ala	Ser	Ile	His	Gln	Tyr	Leu	Gly	Leu	Ala	Tyr	Pro	Met	Glu	Lys	Lys	
	50					55					60					
Thr	Val	Gly	Val	Val	Phe	Gly	Lys	Phe	Tyr	Pro	Leu	His	Thr	Gly	His	
65					70				75						80	
Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Ser	Ser	Gln	Val	Asp	Glu	Leu	His	Val	
			85						90					95		
Val	Leu	Cys	Tyr	Asp	Glu	Leu	Arg	Asp	Arg	Glu	Leu	Phe	Ile	Asn	Ser	
		100						105					110			
Ser	Met	Ser	Gln	Gln	Pro	Thr	Val	Ser	Asp	Arg	Leu	Arg	Trp	Leu	Leu	
		115					120					125				
Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile	His	Ile	His	Val	Phe	Asp	Glu	
	130					135					140					
His	Gly	Met	Glu	Pro	Tyr	Pro	Asn	Gly	Trp	Glu	Val	Trp	Ser	Arg	Gly	
145				150				155							160	
Val	Lys	Ala	Phe	Met	Ala	Glu	Lys	Ser	Ile	Asn	Pro	Glu	Tyr	Ile	Tyr	
			165					170						175		
Ser	Ser	Glu	Ala	Gln	Asp	Val	Ala	Cys	Tyr	Lys	Glu	Tyr	Phe	Asp	Ile	
		180						185					190			
Glu	Thr	Ile	Leu	Ile	Asp	Pro	Gln	Arg	Ser	Phe	Met	Asn	Ile	Ser	Gly	
		195					200					205				
Ser	Gln	Ile	Arg	Gln	Ala	Pro	Phe	Arg	Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	
	210					215					220					
Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	Val	Ala	Ile	Leu	Gly	Gly	Glu	
225				230						235					240	
Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	Lys	Leu	Ala	Asn	Met	Phe	Asn	
			245					250						255		
Thr	Thr	Ser	Val	Trp	Glu	Tyr	Gly	Arg	Glu	Tyr	Val	Phe	Ser	His	Leu	

PF59083SeqList PF59083.txt

260 265 270
 Gly Gly Asp Glu Met Ala Leu Gln Tyr Ser Asp Tyr Asp Lys Ile Ala
 275 280 285
 Leu Gly His Ala Gln Tyr Ile Asp Phe Ser Val Lys Tyr Ala Asn Lys
 290 295 300
 Val Ala Phe Ile Asp Thr Phe Val Thr Thr Gln Ala Phe Cys Lys
 305 310 315 320
 Arg Tyr Glu Gly Lys Glu His Pro Phe Val Gln Ala Met Ile Asp Glu
 325 330 335
 Tyr Arg Phe Asp Leu Val Ile Leu Leu Glu Asn Asn Thr Pro Trp Val
 340 345 350
 Ala Asp Gly Leu Arg Ser Leu Gly Ser Glu Arg Glu Arg Lys Glu Phe
 355 360 365
 Gln Gln Leu Leu Glu Ser Leu Leu Lys Lys Asn Asn Val Asp Tyr Val
 370 375 380
 Cys Val Asn Ser Ala Asp Tyr Asp Gln Arg Phe Leu Arg Cys Ile Glu
 385 390 395 400
 Leu Val Gln His Met Leu Met Ala
 405

<210> 9828
 <211> 1272
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(1272)
 <223> transl_table=11

<400> 9828
 atg tca gca ttc caa tat tta caa gaa aaa cgt aaa aaa ttg aat ctc 48
 Met Ser Ala Phe Gln Tyr Leu Gln Glu Lys Arg Lys Lys Leu Asn Leu
 1 5 10 15
 aaa gta aat gat gtt tgc caa aga gcg aat att acc cgt gct tat ttc 96
 Lys Val Asn Asp Val Cys Gln Arg Ala Asn Ile Thr Arg Ala Tyr Phe
 20 25 30
 aat caa tta gtc agc gga aaa att aaa agc ccg agt gcg aca aaa ctg 144
 Asn Gln Leu Val Ser Gly Lys Ile Lys Ser Pro Ser Ala Thr Lys Leu
 35 40 45
 act gcg cta cat cgt gtg cta caa att gat gcg ccg aat aat aaa aaa 192
 Thr Ala Leu His Arg Val Leu Gln Ile Asp Ala Pro Asn Asn Lys Lys
 50 55 60
 gtc ggt gtg att ttc ggt aaa ttt tat ccg gtt cac acc ggg cat att 240
 Val Gly Val Ile Phe Gly Lys Phe Tyr Pro Val His Thr Gly His Ile
 65 70 75 80
 aat atg atc tat gaa gcc ttc agt aaa gtg gat gaa gtg cat gtg att 288
 Asn Met Ile Tyr Glu Ala Phe Ser Lys Val Asp Glu Val His Val Ile
 85 90 95
 gtt tgt agc gat acg gaa cgg gat tta aaa ctg ttt tac gac agt aaa 336
 Val Cys Ser Asp Thr Glu Arg Asp Leu Lys Leu Phe Tyr Asp Ser Lys
 100 105 110
 atg aag cgt atg ccc acc gta caa gat cgt ttg cgt tgg atg caa cag 384
 Met Lys Arg Met Pro Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln
 115 120 125
 atc ttt aaa tat cag aaa aat caa att ttt atc cac cac tta atc gag 432
 Ile Phe Lys Tyr Gln Lys Asn Gln Ile Phe Ile His His Leu Ile Glu
 130 135 140
 gac ggc tta cca aat tac ccg aac ggc tgg caa gcg tgg gct gaa cgg 480
 Asp Gly Leu Pro Asn Tyr Pro Asn Gly Trp Gln Ala Trp Ala Glu Arg
 145 150 155 160
 gtt aaa gac tta ttt aaa gaa aaa gga ttt acg cca agt atc gtc ttc 528
 Val Lys Asp Leu Phe Lys Glu Lys Gly Phe Thr Pro Ser Ile Val Phe
 165 170 175
 agt agc gaa att caa gac aaa gct cct tat gaa aaa tat ctc aat ttg 576
 Ser Ser Glu Ile Gln Asp Lys Ala Pro Tyr Glu Lys Tyr Leu Asn Leu
 180 185 190
 gac gta tct tta gtc gat ccc gaa cgc gta ttt ttt aat gtg tcc gct 624
 Asp Val Ser Leu Val Asp Pro Glu Arg Val Phe Asn Val Ser Ala

PF59083SeqList PF59083.txt

195	200	205	
aca aaa att cgt aac gaa cca ttc cat tat tgg aag ttt atc cca aaa	210	215	220
Thr Lys Ile Arg Asn Glu Pro Phe His Tyr Trp Lys Phe Ile Pro Lys	225	230	235
gaa gta cgt ccg ttt ttc gca aaa acc att gcc atc tta ggt ggt gag	240	245	250
Glu Val Arg Pro Phe Phe Ala Lys Thr Ile Ala Ile Leu Gly Gly Glu	255	260	265
agc agc ggt aaa acc gta ttg gtg aac aaa ttg gca acg gtc ttc aac	270	275	280
Ser Ser Gly Lys Thr Val Leu Val Asn Lys Leu Ala Thr Val Phe Asn	285	290	295
acc act tcc gct tgg gaa tac ggg cgc gaa ttc gta ttt gaa aaa ctg	300	305	310
Thr Thr Ser Ala Trp Glu Tyr Gly Arg Glu Phe Val Phe Glu Lys Leu	315	320	325
ggc ggt gac gaa cag gcc atg caa tat tcc gat tat cct caa atg gcg	330	335	340
Gly Gly Asp Glu Gln Ala Met Gln Tyr Ser Asp Tyr Pro Gln Met Ala	345	350	355
tta gga cat caa cgt tac atc gat tat gct gtg cga cac gcc cac aaa	360	365	370
Leu Gly His Gln Arg Tyr Ile Asp Tyr Ala Val Arg His Ala His Lys	375	380	385
gtc gcc att att gat acg gat ttc atc acc aca cag gca ttt tgt att	390	395	400
Val Ala Ile Ile Asp Thr Asp Phe Ile Thr Thr Gln Ala Phe Cys Ile	405	410	415
caa tac gaa ggc aaa gca cac ccg ttt ttg gat tcc atg att aaa gaa	420		
Gln Tyr Glu Gly Lys Ala His Pro Phe Leu Asp Ser Met Ile Lys Glu			
tat cct ttt gat gtc acc att ttg tta aac aat aac acg caa tgg gtt			
Tyr Pro Phe Asp Val Thr Ile Leu Leu Asn Asn Asn Thr Gln Trp Val			
gat gac ggt ttg cgt agc ctg ggc aat caa aaa cag cga caa cgt ttc			
Asp Asp Gly Leu Arg Ser Leu Gly Asn Gln Lys Gln Arg Gln Arg Phe			
caa cag tta ctc aaa aaa ttg tta gat aaa tac aat gtc cca tac att			
Gln Gln Leu Leu Lys Lys Leu Leu Asp Lys Tyr Asn Val Pro Tyr Ile			
gaa att gaa tcg cca agt tat ttg gag cgc tat aat cgg gta aaa gaa			
Glu Ile Glu Ser Pro Ser Tyr Leu Glu Arg Tyr Asn Arg Val Lys Glu			
att gtg gaa aaa atc ctc aat gaa gaa gaa ctg cct gaa tta agc agc			
Ile Val Glu Lys Ile Leu Asn Glu Glu Glu Leu Pro Glu Leu Ser Ser			
gat cac ggc aat tct att ttt taa			
Asp His Gly Asn Ser Ile Phe			

<210> 9829

<211> 423

<212> PRT

<213> Actinobacillus actinomycetemcomitans

<400> 9829

Met Ser Ala Phe Gln Tyr Leu Gln Glu Lys Arg Lys Lys Leu Asn Leu	1	5	10	15
Lys Val Asn Asp Val Cys Gln Arg Ala Asn Ile Thr Arg Ala Tyr Phe	20	25	30	35
Asn Gln Leu Val Ser Gly Lys Ile Lys Ser Pro Ser Ala Thr Lys Leu	40	45	50	55
Thr Ala Leu His Arg Val Leu Gln Ile Asp Ala Pro Asn Asn Lys Lys	60	65	70	75
Val Gly Val Ile Phe Gly Lys Phe Tyr Pro Val His Thr Gly His Ile	80	85	90	95
Asn Met Ile Tyr Glu Ala Phe Ser Lys Val Asp Glu Val His Val Ile	100	105	110	115
Val Cys Ser Asp Thr Glu Arg Asp Leu Lys Leu Phe Tyr Asp Ser Lys	120	125	130	135
Met Lys Arg Met Pro Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln	140	145	150	155
Ile Phe Lys Tyr Gln Lys Asn Gln Ile Phe Ile His His Leu Ile Glu	160	165	170	175
Asp Gly Leu Pro Asn Tyr Pro Asn Gly Trp Gln Ala Trp Ala Glu Arg	180	185	190	195

PF59083SeqList PF59083.txt

```

145          150          155          160
Val Lys Asp Leu Phe Lys Glu Lys Gly Phe Thr Pro Ser Ile Val Phe
Ser Ser Glu Ile Gln Asp Lys Ala Pro Tyr Glu Lys Tyr Leu Asn Leu
Asp Val Ser 180 Val Asp Pro Glu 185 Val Phe Phe Asn 190 Val Ser Ala
Thr Lys 195 Ile Arg Asn Glu 200 Phe His Tyr Trp Lys Phe Ile Pro Lys
Glu 210 Val Arg Pro Phe Phe 215 Lys Thr Ile Ala Ile Leu Gly Gly Glu
225 Ser Ser Gly Lys Thr Val Leu Val Asn Lys Leu Ala Thr Val Phe Asn
Thr Thr Ser Ala Trp Glu Tyr Gly Arg Glu Phe Val Phe Glu Lys Leu
Gly Gly Asp 260 Gln Ala Met Gln Tyr Ser Asp Tyr Pro Gln Met Ala
Leu Gly His Gln Arg Tyr Ile Asp Tyr Ala Val Arg His Ala His Lys
Val 290 Ala Ile Ile Asp Thr Asp Phe Ile Thr Thr Gln Ala Phe Cys Ile
305 Gln Tyr Glu Gly Lys Ala His Pro Phe Leu Asp Ser Met Ile Lys Glu
Tyr Pro Phe Asp Val Thr Ile Leu Leu Asn Asn Asn Thr Gln Trp Val
Asp Asp Gly 340 Leu Arg Ser Leu Gly Asn Gln Lys Gln Arg Gln Arg Phe
Gln Gln Leu Leu Lys Lys Leu Leu Asp Lys Tyr Asn Val Pro Tyr Ile
Glu 370 Ile Glu Ser Pro Ser Tyr Leu Glu Arg Tyr Asn Arg Val Lys Glu
385 Ile Val Glu Lys Ile Leu Asn Glu Glu Glu Leu Pro Glu Leu Ser Ser
Asp His Gly Asn 405 Ser Ile Phe
420

```

<210> 9830

<211> 1287

<212> DNA

<213> Pasteurella multocida subsp. multocida str. Pm70

<220>

<221> CDS

<222> (1)..(1287)

<223> transl_table=11

<400> 9830

```

atg tcc acg ttt gcc tac tta caa caa aag cgt aaa caa ctg aat tta      48
Met Ser Thr Phe Ala Tyr Leu Gln Gln Lys Arg Lys Gln Leu Asn Leu
1          5          10          15
aaa gtt aat gag atc tgt gca caa gcc aat att aca cgt gcg tat ttt      96
Lys Val Asn Glu Ile Cys Ala Gln Ala Asn Ile Thr Arg Ala Tyr Phe
20          25          30
aat caa ctc gtg agt gga aaa atc aaa aat cca agc gca aca aag ctc      144
Asn Gln Leu Val Ser Gly Lys Ile Lys Asn Pro Ser Ala Thr Lys Leu
35          40          45
agt gca tta cat aaa gtg ttg cag atc acc gaa ccg aat aat aag aaa      192
Ser Ala Leu His Lys Val Leu Gln Ile Thr Glu Pro Asn Asn Lys Lys
50          55          60
gtc ggt gtg att ttt ggc aaa ttt tat cct gtc cat acc ggt cat att      240
Val Gly Val Ile Phe Gly Lys Phe Tyr Pro Val His Thr Gly His Ile
65          70          75
aat atg atc tat gaa gcc ttt agt aaa gtg gat gaa ata cac gtc att      288
Asn Met Ile Tyr Glu Ala Phe Ser Lys Val Asp Glu Ile His Val Ile
80          85          90          95
gtc tgt agt gat aca gaa cgt gac tta aaa ctc ttt tat gac agc aaa      336
Val Cys Ser Asp Thr Glu Arg Asp Leu Lys Leu Phe Tyr Asp Ser Lys
100          105          110
atg aaa cgt atg ccg aca gtg caa gat cgc tta cgt tgg atg caa cag      384

```

PF59083SeqList PF59083.txt

Met	Lys	Arg	Met	Pro	Thr	Val	Gln	Asp	Arg	Leu	Arg	Trp	Met	Gln	Gln	
		115					120					125				
att	ttt	aaa	tac	caa	aaa	aac	cag	att	ttt	att	cat	cat	ctt	gtt	gaa	432
Ile	Phe	Lys	Tyr	Gln	Lys	Asn	Gln	Ile	Phe	Ile	His	His	Leu	Val	Glu	
	130					135					140					
gac	gga	att	cca	agc	tac	cca	aat	ggt	tgg	gaa	gcg	tgg	gcg	ttg	caa	480
Asp	Gly	Ile	Pro	Ser	Tyr	Pro	Asn	Gly	Trp	Glu	Ala	Trp	Ala	Leu	Gln	
	145				150					155					160	
gtc	aag	aac	ctc	ttt	aaa	gaa	aaa	cat	ttc	aat	cca	acc	gta	gtt	ttc	528
Val	Lys	Asn	Leu	Phe	Lys	Glu	Lys	His	Phe	Asn	Pro	Thr	Val	Val	Phe	
				165					170					175		
agt	agc	gaa	gtg	caa	gat	aaa	gca	cct	tat	gaa	aaa	tac	ctt	ggt	tta	576
Ser	Ser	Glu	Val	Gln	Asp	Lys	Ala	Pro	Tyr	Glu	Lys	Tyr	Leu	Gly	Leu	
			180					185					190			
gaa	gtt	tcc	tta	gtc	gat	cct	gag	cga	caa	ttt	ttt	aat	gtc	tct	gcg	624
Glu	Val	Ser	Leu	Val	Asp	Pro	Glu	Arg	Gln	Phe	Phe	Asn	Val	Ser	Ala	
		195				200						205				
aca	aaa	atc	cgc	aat	aac	cca	ttt	cac	tat	tgg	aaa	ttt	atc	cca	aaa	672
Thr	Lys	Ile	Arg	Asn	Asn	Pro	Phe	His	Tyr	Trp	Lys	Phe	Ile	Pro	Lys	
	210					215					220					
gaa	gta	cgc	ccg	ttc	ttt	gcc	aaa	act	atc	gct	att	tta	gga	ggg	gaa	720
Glu	Val	Arg	Pro	Phe	Phe	Ala	Lys	Thr	Ile	Ala	Ile	Leu	Gly	Gly	Glu	
	225				230					235					240	
agc	agt	ggt	aaa	act	gta	ctg	gtc	aat	aaa	tta	gcc	aca	gta	ttc	aat	768
Ser	Ser	Gly	Lys	Thr	Val	Leu	Val	Asn	Lys	Leu	Ala	Thr	Val	Phe	Asn	
				245					250					255		
acc	acg	tct	gcc	tgg	gaa	tat	gga	cgc	gag	ttt	gtt	ttc	gag	aaa	tta	816
Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	Glu	Phe	Val	Phe	Glu	Lys	Leu	
			260					265					270			
ggg	gga	gat	gaa	gcn	gcn	atg	caa	tat	tct	gat	tac	cca	caa	atg	gca	864
Gly	Gly	Asp	Glu	Gln	Ala	Met	Gln	Tyr	Ser	Asp	Tyr	Pro	Gln	Met	Ala	
		275				280						285				
ctg	ggg	cac	caa	cgc	tat	att	gat	tat	gcg	gta	cgt	cat	gca	cat	aaa	912
Leu	Gly	His	Gln	Arg	Tyr	Ile	Asp	Tyr	Ala	Val	Arg	His	Ala	His	Lys	
	290					295					300					
gtg	gcg	att	att	gat	aca	gat	ttc	atc	acc	aca	gct	ttt	tgt	att		960
Val	Ala	Ile	Ile	Asp	Thr	Asp	Phe	Ile	Thr	Thr	Gln	Ala	Phe	Cys	Ile	
	305				310					315				320		
caa	tac	gaa	gga	aaa	gcn	cat	cct	ttc	tta	gat	tcc	atg	atc	aaa	gaa	1008
Gln	Tyr	Glu	Gly	Lys	Ala	His	Pro	Phe	Leu	Asp	Ser	Met	Ile	Lys	Glu	
				325					330					335		
tat	cca	ttc	gat	gtc	aca	att	tta	tta	aat	aac	aac	act	aaa	tgg	gtg	1056
Tyr	Pro	Phe	Asp	Val	Thr	Ile	Leu	Leu	Asn	Asn	Asn	Thr	Lys	Trp	Val	
			340					345					350			
gat	gat	ggc	tta	cgt	agt	tta	ggt	aat	cat	aaa	caa	cgc	caa	cgt	ttt	1104
Asp	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Asn	His	Lys	Gln	Arg	Gln	Arg	Phe	
		355					360					365				
caa	ctc	tta	cta	aaa	aaa	tta	ctc	gat	aaa	tac	aat	gta	cct	tat	att	1152
Gln	Leu	Leu	Leu	Lys	Lys	Leu	Leu	Asp	Lys	Tyr	Asn	Val	Pro	Tyr	Ile	
	370					375					380					
gaa	att	gaa	tcg	cca	agt	tat	tta	gaa	cgt	tat	aat	cag	gtc	aaa	cag	1200
Glu	Ile	Glu	Ser	Pro	Ser	Tyr	Leu	Glu	Arg	Tyr	Asn	Gln	Val	Lys	Gln	
	385				390				395					400		
att	gtc	gag	aaa	atc	cta	aat	gaa	gaa	gaa	att	cct	aat	tta	atg	cat	1248
Ile	Val	Glu	Lys	Ile	Leu	Asn	Glu	Glu	Glu	Ile	Pro	Asn	Leu	Met	His	
				405				410						415		
gat	cat	ggg	aca	aca	tcc	att	ttt	gag	gaa	gaa	gaa	tga				1287
Asp	His	Gly	Thr	Thr	Ser	Ile	Phe	Glu	Glu	Glu	Glu					
			420					425								

<210> 9831

<211> 428

<212> PRT

<213> Pasteurella multocida subsp. multocida str. Pm70

<400> 9831

Met	Ser	Thr	Phe	Ala	Tyr	Leu	Gln	Gln	Lys	Arg	Lys	Gln	Leu	Asn	Leu
1				5					10					15	
Lys	Val	Asn	Glu	Ile	Cys	Ala	Gln	Ala	Asn	Ile	Thr	Arg	Ala	Tyr	Phe

Seite 10344

PF59083SeqList PF59083.txt

```

      20      25      30
Asn Gln Leu Val Ser Gly Lys Ile Lys Asn Pro Ser Ala Thr Lys Leu
      35      40      45
Ser Ala Leu His Lys Val Leu Gln Ile Thr Glu Pro Asn Asn Lys Lys
      50      55      60
Val Gly Val Ile Phe Gly Lys Phe Tyr Pro Val His Thr Gly His Ile
      65      70      75      80
Asn Met Ile Tyr Glu Ala Phe Ser Lys Val Asp Glu Ile His Val Ile
      85      90      95
Val Cys Ser Asp Thr Glu Arg Asp Leu Lys Leu Phe Tyr Asp Ser Lys
      100      105      110
Met Lys Arg Met Pro Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln
      115      120      125
Ile Phe Lys Tyr Gln Lys Asn Gln Ile Phe Ile His His Leu Val Glu
      130      135      140
Asp Gly Ile Pro Ser Tyr Pro Asn Gly Trp Glu Ala Trp Ala Leu Gln
      145      150      155      160
Val Lys Asn Leu Phe Lys Glu Lys His Phe Asn Pro Thr Val Val Phe
      165      170      175
Ser Ser Glu Val Gln Asp Lys Ala Pro Tyr Glu Lys Tyr Leu Gly Leu
      180      185      190
Glu Val Ser Leu Val Asp Pro Glu Arg Gln Phe Phe Asn Val Ser Ala
      195      200      205
Thr Lys Ile Arg Asn Asn Pro Phe His Tyr Trp Lys Phe Ile Pro Lys
      210      215      220
Glu Val Arg Pro Phe Phe Ala Lys Thr Ile Ala Ile Leu Gly Gly Glu
      225      230      235      240
Ser Ser Gly Lys Thr Val Leu Val Asn Lys Leu Ala Thr Val Phe Asn
      245      250      255
Thr Thr Ser Ala Trp Glu Tyr Gly Arg Glu Phe Val Phe Glu Lys Leu
      260      265      270
Gly Gly Asp Glu Gln Ala Met Gln Tyr Ser Asp Tyr Pro Gln Met Ala
      275      280      285
Leu Gly His Gln Arg Tyr Ile Asp Tyr Ala Val Arg His Ala His Lys
      290      295      300
Val Ala Ile Ile Asp Thr Asp Phe Ile Thr Thr Gln Ala Phe Cys Ile
      305      310      315      320
Gln Tyr Glu Gly Lys Ala His Pro Phe Leu Asp Ser Met Ile Lys Glu
      325      330      335
Tyr Pro Phe Asp Val Thr Ile Leu Leu Asn Asn Asn Thr Lys Trp Val
      340      345      350
Asp Asp Gly Leu Arg Ser Leu Gly Asn His Lys Gln Arg Gln Arg Phe
      355      360      365
Gln Leu Leu Lys Lys Leu Leu Asp Lys Tyr Asn Val Pro Tyr Ile
      370      375      380
Glu Ile Glu Ser Pro Ser Tyr Leu Glu Arg Tyr Asn Gln Val Lys Gln
      385      390      395      400
Ile Val Glu Lys Ile Leu Asn Glu Glu Glu Ile Pro Asn Leu Met His
      405      410      415
Asp His Gly Thr Ser Ile Phe Glu Glu Glu
      420      425

```

<210> 9832

<211> 1233

<212> DNA

<213> Escherichia coli CFT073

<220>

<221> CDS

<222> (1)..(1233)

<223> transl_table=11

<400> 9832

```

atg tcg tca ttt gat tac ctg aaa act gcc att aag caa cag ggc tgc      48
Met Ser Ser Phe Asp Tyr Leu Lys Thr Ala Ile Lys Gln Gln Gly Cys
      1      5      10      15
acg cta cag cag gta gct gat gcc agc ggt atg acc aaa ggg tat tta      96
Thr Leu Gln Gln Val Ala Asp Ala Ser Gly Met Thr Lys Gly Tyr Leu
      20      25      30

```

PF59083SeqList PF59083.txt																
agc	cag	tta	ctg	aat	gcc	aaa	att	aaa	agc	ccc	agc	gcg	caa	aaa	ctg	144
Ser	Gln	Leu	Leu	Asn	Ala	Lys	Ile	Lys	Ser	Pro	Ser	Ala	Gln	Lys	Leu	
		35					40					45				
gag	gca	ttg	cac	cgt	ttt	ttg	ggg	ctt	gag	ttt	ccc	cgg	cag	aag	aaa	192
Glu	Ala	Leu	His	Arg	Phe	Leu	Gly	Leu	Glu	Phe	Pro	Arg	Gln	Lys	Lys	
		50				55					60					
acg	atc	ggt	gtc	gta	ttc	ggt	aag	ttt	tac	ccg	ctg	cat	act	gga	cat	240
Thr	Ile	Gly	Val	Val	Phe	Gly	Lys	Phe	Tyr	Pro	Leu	His	Thr	Gly	His	
		65			70				75					80		
atc	tac	ctt	atc	cag	cgc	gcc	tgt	agc	cag	ggt	gac	gag	ctg	cat	atc	288
Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Cys	Ser	Gln	Val	Asp	Glu	Leu	His	Ile	
				85					90					95		
att	atg	ggt	ttt	gac	gat	acc	cgc	gac	cgc	gca	ttg	ttc	gaa	gac	agc	336
Ile	Met	Gly	Phe	Asp	Asp	Thr	Arg	Asp	Arg	Ala	Leu	Phe	Glu	Asp	Ser	
		100						105					110			
gcc	atg	tcg	cag	cag	cca	acc	gtg	ccg	gat	cgt	ctg	cgc	tgg	tta	ttg	384
Ala	Met	Ser	Gln	Gln	Pro	Thr	Val	Pro	Asp	Arg	Leu	Arg	Trp	Leu	Leu	
		115					120					125				
cag	acc	ttt	aag	tat	caa	aaa	aat	atc	cgc	att	cat	gct	ttt	aac	gaa	432
Gln	Thr	Phe	Lys	Tyr	Gln	Asn	Ile	Arg	Ile	His	Ala	Phe	Asn	Glu		
		130				135					140					
gag	ggc	atg	gaa	ccg	tat	cca	cat	ggc	tgg	gat	gtg	tgg	agc	aac	ggc	480
Glu	Gly	Met	Glu	Pro	Tyr	Pro	His	Gly	Trp	Asp	Val	Trp	Ser	Asn	Gly	
		145			150				155					160		
atc	aaa	aag	ttt	atg	gcc	gaa	aaa	ggc	att	cag	ccg	gac	ctg	atc	tac	528
Ile	Lys	Lys	Phe	Met	Ala	Glu	Lys	Gly	Ile	Gln	Pro	Asp	Leu	Ile	Tyr	
				165					170					175		
acc	tcg	gaa	gaa	gcc	gat	gcg	ccg	cag	tat	atg	gaa	cat	ctg	ggg	atc	576
Thr	Ser	Glu	Glu	Ala	Asp	Ala	Pro	Gln	Tyr	Met	Glu	His	Leu	Gly	Ile	
		180					185						190			
gag	acg	gtg	ctg	gtc	gat	ccg	aag	cgt	acc	ttt	atg	agt	atc	agc	ggt	624
Glu	Thr	Val	Leu	Val	Asp	Pro	Lys	Arg	Thr	Phe	Met	Ser	Ile	Ser	Gly	
		195					200					205				
gcg	cag	atc	cgc	gaa	aac	ccg	ttc	cgc	tac	tgg	gaa	tat	att	cct	acg	672
Ala	Gln	Ile	Arg	Glu	Asn	Pro	Phe	Arg	Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	
		210				215					220					
gaa	gtt	aag	ccg	ttc	ttt	gtg	cgt	acc	gtg	gcg	atc	ctt	ggc	ggc	gag	720
Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	Val	Ala	Ile	Leu	Gly	Gly	Glu	
		225			230				235						240	
tcg	agc	ggt	aaa	tcc	acc	ctg	gta	aac	aaa	ctt	gcc	aat	atc	ttc	aac	768
Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	Lys	Leu	Ala	Asn	Ile	Phe	Asn	
				245					250					255		
act	acc	agt	gca	tgg	gaa	tat	ggt	cgc	gat	tat	gtc	ttt	tca	cac	ctt	816
Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	Asp	Tyr	Val	Phe	Ser	His	Leu	
		260						265					270			
ggc	ggt	gat	gag	att	gcg	ttg	cag	tat	tcc	gac	tac	gat	aaa	atc	gcg	864
Gly	Gly	Asp	Glu	Ile	Ala	Leu	Gln	Tyr	Ser	Asp	Tyr	Asp	Lys	Ile	Ala	
		275					280					285				
ctg	gga	cac	gcg	caa	tat	att	gat	ttt	gca	gtg	aaa	tat	gcc	aat	aaa	912
Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe	Ala	Val	Lys	Tyr	Ala	Asn	Lys	
		290				295					300					
gtg	gcg	ttt	atc	gac	acc	gat	ttt	gtc	act	acc	cag	gcg	ttc	tgc	aaa	960
Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	Thr	Thr	Gln	Ala	Phe	Cys	Lys	
		305			310				315					320		
aag	tac	gaa	ggg	cgt	gag	cat	ccg	ttc	gtg	cag	gcg	ttg	att	gat	gaa	1008
Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	Val	Gln	Ala	Leu	Ile	Asp	Glu	
				325				330						335		
tac	cgt	ttc	gat	ctg	gtg	atc	ctg	ctg	gag	aac	aac	acg	ccg	tgg	gtg	1056
Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	Glu	Asn	Asn	Thr	Pro	Trp	Val	
			340					345					350			
gcg	gat	ggt	tta	cgc	agc	ctc	ggc	agt	tcg	gtg	gat	cgc	aaa	gag	ttc	1104
Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	Ser	Val	Asp	Arg	Lys	Glu	Phe	
		355					360					365				
cag	aac	ttg	ctg	gtg	gag	atg	ctg	gaa	gag	aac	aat	atc	gaa	ttc	gtg	1152
Gln	Asn	Leu	Leu	Val	Glu	Met	Leu	Glu	Glu	Asn	Asn	Ile	Glu	Phe	Val	
		370				375					380					
cgg	gtt	gaa	gag	gac	gat	tac	gac	agc	cgt	ttc	ctg	cgc	tgc	gtg	gag	1200
Arg	Val	Glu	Glu	Asp	Asp	Tyr	Asp	Ser	Arg	Phe	Leu	Arg	Cys	Val	Glu	
		385			390					395					400	

ctg gtg cgg gag atg atg ggg gag caa aga taa
 Leu Val Arg Glu Met Met Gly Glu Gln Arg
 405 410

<210> 9833
 <211> 410
 <212> PRT
 <213> Escherichia coli CFT073

<400> 9833
 Met Ser Ser Phe Asp Tyr Leu Lys Thr Ala Ile Lys Gln Gln Gly Cys
 1 5 10 15
 Thr Leu Gln Gln Val Ala Asp Ala Ser Gly Met Thr Lys Gly Tyr Leu
 20 25 30
 Ser Gln Leu Leu Asn Ala Lys Ile Lys Ser Pro Ser Ala Gln Lys Leu
 35 40 45
 Glu Ala Leu His Arg Phe Leu Gly Leu Glu Phe Pro Arg Gln Lys Lys
 50 55 60
 Thr Ile Gly Val Val Phe Gly Lys Phe Tyr Pro Leu His Thr Gly His
 65 70 75 80
 Ile Tyr Leu Ile Gln Arg Ala Cys Ser Gln Val Asp Glu Leu His Ile
 85 90 95
 Ile Met Gly Phe Asp Asp Thr Arg Asp Arg Ala Leu Phe Glu Asp Ser
 100 105 110
 Ala Met Ser Gln Gln Pro Thr Val Pro Asp Arg Leu Arg Trp Leu Leu
 115 120 125
 Gln Thr Phe Lys Tyr Gln Lys Asn Ile Arg Ile His Ala Phe Asn Glu
 130 135 140
 Glu Gly Met Glu Pro Tyr Pro His Gly Trp Asp Val Trp Ser Asn Gly
 145 150 155 160
 Ile Lys Lys Phe Met Ala Glu Lys Gly Ile Gln Pro Asp Leu Ile Tyr
 165 170 175
 Thr Ser Glu Glu Ala Asp Ala Pro Gln Tyr Met Glu His Leu Gly Ile
 180 185 190
 Glu Thr Val Leu Val Asp Pro Lys Arg Thr Phe Met Ser Ile Ser Gly
 195 200 205
 Ala Gln Ile Arg Glu Asn Pro Phe Arg Tyr Trp Glu Tyr Ile Pro Thr
 210 215 220
 Glu Val Lys Pro Phe Phe Val Arg Thr Val Ala Ile Leu Gly Gly Glu
 225 230 235 240
 Ser Ser Gly Lys Ser Thr Leu Val Asn Lys Leu Ala Asn Ile Phe Asn
 245 250 255
 Thr Thr Ser Ala Trp Glu Tyr Gly Arg Asp Tyr Val Phe Ser His Leu
 260 265 270
 Gly Gly Asp Glu Ile Ala Leu Gln Tyr Ser Asp Tyr Asp Lys Ile Ala
 275 280 285
 Leu Gly His Ala Gln Tyr Ile Asp Phe Ala Val Lys Tyr Ala Asn Lys
 290 295 300
 Val Ala Phe Ile Asp Thr Asp Phe Val Thr Thr Gln Ala Phe Cys Lys
 305 310 315 320
 Lys Tyr Glu Gly Arg Glu His Pro Phe Val Gln Ala Leu Ile Asp Glu
 325 330 335
 Tyr Arg Phe Asp Leu Val Ile Leu Leu Glu Asn Asn Thr Pro Trp Val
 340 345 350
 Ala Asp Gly Leu Arg Ser Leu Gly Ser Ser Val Asp Arg Lys Glu Phe
 355 360 365
 Gln Asn Leu Leu Val Glu Met Leu Glu Glu Asn Asn Ile Glu Phe Val
 370 375 380
 Arg Val Glu Glu Asp Asp Tyr Asp Ser Arg Phe Leu Arg Cys Val Glu
 385 390 395 400
 Leu Val Arg Glu Met Met Gly Glu Gln Arg
 405 410

<210> 9834
 <211> 1236
 <212> DNA
 <213> Photorhabdus luminescens subsp. laumondii TT01

<220>

PF59083SeqList PF59083.txt

<221> CDS

<222> (1)..(1236)

<223> transl_table=11

<400> 9834

atg ggg caa ttt gac tac ctt aaa gaa gcg att aaa cag aca ggt tat	48
Met Gly Gln Phe Asp Tyr Leu Lys Glu Ala Ile Lys Gln Thr Gly Tyr	
1 5 10 15	
acg ttg caa cag gtt gcc gat gca agt ggt atg acc aaa ggt tat ctt	96
Thr Leu Gln Gln Val Ala Asp Ala Ser Gly Met Thr Lys Gly Tyr Leu	
20 25 30	
agc caa tta att aat gac aaa att aaa agt cct agt gcc caa aaa ctg	144
Ser Gln Leu Ile Asn Asp Lys Ile Lys Ser Pro Ser Ala Gln Lys Leu	
35 40 45	
gcg gcg ctc cat cac tat ctg agg ttg caa tat cct gtg caa aat aaa	192
Ala Ala Leu His His Tyr Leu Arg Leu Gln Tyr Pro Val Gln Asn Lys	
50 55 60	
act gtt gga gtg gta ttc ggc aaa ttc tat cca ttg cat act ggg cat	240
Thr Val Gly Val Val Phe Gly Lys Phe Tyr Pro Leu His Thr Gly His	
65 70 75 80	
atc tat ctg att caa cgg gcc tgt agt cag gtg gat gag ttg cat att	288
Ile Tyr Leu Ile Gln Arg Ala Cys Ser Gln Val Asp Glu Leu His Ile	
85 90 95	
atc ctt tgc cat gat gag cct aga gat cgg gag cta ttt atg agt agt	336
Ile Leu Cys His Asp Glu Pro Arg Asp Arg Glu Leu Phe Met Ser Ser	
100 105 110	
tcc atg tct cag caa ccc acg gtg agt gat cgc ttg cgc tgg ttg ctt	384
Ser Met Ser Gln Gln Pro Thr Val Ser Asp Arg Leu Arg Trp Leu Leu	
115 120 125	
caa aca ttt aag tat cag aaa aat att cat att cac tct ttt gat gaa	432
Gln Thr Phe Lys Tyr Gln Lys Asn Ile His Ile His Ser Phe Asp Glu	
130 135 140	
cag gga att gaa ccc tat cca cat ggt tgg gat gtg tgg agt gat ggc	480
Gln Gly Ile Glu Pro Tyr Pro His Gly Trp Asp Val Trp Ser Asp Gly	
145 150 155 160	
atg aaa gcc ttt atg tca aag aaa ggc att cat ccc act tat ata tat	528
Met Lys Ala Phe Met Ser Lys Lys Gly Ile His Pro Thr Tyr Ile Tyr	
165 170 175	
tcc agc gaa act cag gat tct ccc cga tat aaa gag cat tta gga att	576
Ser Ser Glu Thr Gln Asp Ser Pro Arg Tyr Lys Glu His Leu Gly Ile	
180 185 190	
gag aca att ctt atc gat cca caa cgt tcg ttt atg aaa atc agt ggt	624
Glu Thr Ile Leu Ile Asp Pro Gln Arg Ser Phe Met Lys Ile Ser Gly	
195 200 205	
cgg cat att cgc caa gat cca ttc cgt cat tgg gaa tat att cct acc	672
Arg His Ile Arg Gln Asp Pro Phe Arg His Trp Glu Tyr Ile Pro Thr	
210 215 220	
gaa gtg aaa cct ttc ttt gtt cgt acc gta gcg att ctt ggt gga gaa	720
Glu Val Lys Pro Phe Phe Val Arg Thr Val Ala Ile Leu Gly Gly Glu	
225 230 235 240	
tct agt ggt aaa tct aca tta gtt aac aaa ttg gca aat att ttt aat	768
Ser Ser Gly Lys Ser Thr Leu Val Asn Lys Leu Ala Asn Ile Phe Asn	
245 250 255	
acg aca agt gct tgg gaa tat ggt cgt gat tat gtt ttt tct cat ctg	816
Thr Thr Ser Ala Trp Glu Tyr Gly Arg Asp Tyr Val Phe Ser His Leu	
260 265 270	
ggg gga gat gag atg gcg cta caa tat tcg gac tat gac aag att gca	864
Gly Gly Asp Glu Met Ala Leu Gln Tyr Ser Asp Tyr Asp Lys Ile Ala	
275 280 285	
ttg gga caa gcc caa tat att gat ttt gcc gta aaa tat gcg aat aag	912
Leu Gly Gln Ala Gln Tyr Ile Asp Phe Ala Val Lys Tyr Ala Asn Lys	
290 295 300	
gtt aca ttt atc gat acc gat ttt gtc act acc caa gca ttc tgt aag	960
Val Thr Phe Ile Asp Thr Asp Phe Val Thr Thr Gln Ala Phe Cys Lys	
305 310 315 320	
cga tat gaa gga cgt gaa cac ccg ttt gtt cag gca tta att gat gaa	1008
Arg Tyr Glu Gly Arg Glu His Pro Phe Val Gln Ala Leu Ile Asp Glu	
325 330 335	
tac cga ttt gat ttg gtc att cta ctg gaa aac aac act cct tgg gtt	1056

PF59083SeqList PF59083.txt

Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Glu	Asn	Asn	Thr	Pro	Trp	Val		
			340				345					350				
gct	gac	ggt	ttg	cgt	agc	ctt	ggc	agc	gag	cag	gat	cgt	aaa	gcg	ttt	1104
Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	Glu	Gln	Asp	Arg	Lys	Ala	Phe	
		355					360					365				
cag	caa	ctg	ctg	gag	gat	atg	ctg	aaa	agt	aat	aat	att	gaa	tat	gtc	1152
Gln	Gln	Leu	Leu	Glu	Asp	Met	Leu	Lys	Ser	Asn	Asn	Ile	Glu	Tyr	Val	
		370				375					380					
aat	gtg	gat	tca	ccc	gat	tat	gat	cag	cgt	ttc	cta	cgt	tgt	att	gag	1200
Asn	Val	Asp	Ser	Pro	Asp	Tyr	Asp	Gln	Arg	Phe	Leu	Arg	Cys	Ile	Glu	
		385			390					395					400	
ctc	att	cag	caa	ctt	tta	gcg	gct	aat	cct	aaa	tga					1236
Leu	Ile	Gln	Gln	Leu	Leu	Ala	Ala	Asn	Pro	Lys						
				405					410							

<210> 9835

<211> 411

<212> PRT

<213> Photorhabdus luminescens subsp. laumondii TT01

<400> 9835

Met	Gly	Gln	Phe	Asp	Tyr	Leu	Lys	Glu	Ala	Ile	Lys	Gln	Thr	Gly	Tyr	
1				5				10						15		
Thr	Leu	Gln	Gln	Val	Ala	Asp	Ala	Ser	Gly	Met	Thr	Lys	Gly	Tyr	Leu	
			20					25					30			
Ser	Gln	Leu	Ile	Asn	Asp	Lys	Ile	Lys	Ser	Pro	Ser	Ala	Gln	Lys	Leu	
		35				40						45				
Ala	Ala	Leu	His	His	Tyr	Leu	Arg	Leu	Gln	Tyr	Pro	Val	Gln	Asn	Lys	
	50				55					60						
Thr	Val	Gly	Val	Val	Phe	Gly	Lys	Phe	Tyr	Pro	Leu	His	Thr	Gly	His	
65					70				75						80	
Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Cys	Ser	Gln	Val	Asp	Glu	Leu	His	Ile	
			85					90						95		
Ile	Leu	Cys	His	Asp	Glu	Pro	Arg	Asp	Arg	Glu	Leu	Phe	Met	Ser	Ser	
		100						105					110			
Ser	Met	Ser	Gln	Gln	Pro	Thr	Val	Ser	Asp	Arg	Leu	Arg	Trp	Leu	Leu	
		115					120					125				
Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile	His	Ile	His	Ser	Phe	Asp	Glu	
	130					135					140					
Gln	Gly	Ile	Glu	Pro	Tyr	Pro	His	Gly	Trp	Asp	Val	Trp	Ser	Asp	Gly	
145					150				155						160	
Met	Lys	Ala	Phe	Met	Ser	Lys	Lys	Gly	Ile	His	Pro	Thr	Tyr	Ile	Tyr	
			165					170						175		
Ser	Ser	Glu	Thr	Gln	Asp	Ser	Pro	Arg	Tyr	Lys	Glu	His	Leu	Gly	Ile	
		180						185					190			
Glu	Thr	Ile	Leu	Ile	Asp	Pro	Gln	Arg	Ser	Phe	Met	Lys	Ile	Ser	Gly	
		195					200					205				
Arg	His	Ile	Arg	Gln	Asp	Pro	Phe	Arg	His	Trp	Glu	Tyr	Ile	Pro	Thr	
	210					215					220					
Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	Val	Ala	Ile	Leu	Gly	Gly	Glu	
225					230					235					240	
Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	Lys	Leu	Ala	Asn	Ile	Phe	Asn	
			245						250					255		
Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	Asp	Tyr	Val	Phe	Ser	His	Leu	
		260						265					270			
Gly	Gly	Asp	Glu	Met	Ala	Leu	Gln	Tyr	Ser	Asp	Tyr	Asp	Lys	Ile	Ala	
		275					280					285				
Leu	Gly	Gln	Ala	Gln	Tyr	Ile	Asp	Phe	Ala	Val	Lys	Tyr	Ala	Asn	Lys	
	290					295					300					
Val	Thr	Phe	Ile	Asp	Thr	Asp	Phe	Val	Thr	Thr	Gln	Ala	Phe	Cys	Lys	
305					310					315					320	
Arg	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	Val	Gln	Ala	Leu	Ile	Asp	Glu	
			325						330					335		
Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	Glu	Asn	Asn	Thr	Pro	Trp	Val	
			340					345					350			
Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	Glu	Gln	Asp	Arg	Lys	Ala	Phe	
		355					360					365				
Gln	Gln	Leu	Leu	Glu	Asp	Met	Leu	Lys	Ser	Asn	Asn	Ile	Glu	Tyr	Val	
		370				375					380					

PF59083SeqList PF59083.txt

Asn Val Asp Ser Pro Asp Tyr Asp Gln Arg Phe Leu Arg Cys Ile Glu
 385 390 395 400
 Leu Ile Gln Gln Leu Leu Ala Ala Asn Pro Lys
 405 410

<210> 9836
 <211> 1233
 <212> DNA
 <213> Klebsiella pneumoniae subsp. pneumoniae MGH 78578

<220>
 <221> CDS
 <222> (1)..(1233)
 <223> transl_table=11

<400> 9836
 atg tcg tca ttt gac tat tta aaa agc gcc att aag cag aaa ggc tgt 48
 Met Ser Ser Phe Asp Tyr Leu Lys Ser Ala Ile Lys Gln Lys Gly Cys
 1 5 10 15
 acc ctg cag cag gtg gcg gaa gcc agc gga atg acc aag ggg tat ctt 96
 Thr Leu Gln Gln Val Ala Glu Ala Ser Gly Met Thr Lys Gly Tyr Leu
 20 25 30
 agc cag ctg ctg aat gcc aaa atc aaa agc ccg agc gcg cag aag ctt 144
 Ser Gln Leu Leu Asn Ala Lys Ile Lys Ser Pro Ser Ala Gln Lys Leu
 35 40 45
 gaa gcg ctg cat cgt ttc ctc ggg ctg gag ttt ccc cgc cga cag aaa 192
 Glu Ala Leu His Arg Phe Leu Gly Leu Glu Phe Pro Arg Arg Gln Lys
 50 55 60
 agc gtc ggg gtg gtg ttt ggt aag ttt tac cca ctg cat acc ggg cat 240
 Ser Val Gly Val Val Phe Gly Lys Phe Tyr Pro Leu His Thr Gly His
 65 70 75 80
 atc tac ctg ata cag cgc gcc tgt agc cag gtc gat gag ctg cat atc 288
 Ile Tyr Leu Ile Gln Arg Ala Cys Ser Gln Val Asp Glu Leu His Ile
 85 90 95
 att atg ggc tat gac gat acc cgc gac cgc gag ctg ttt gaa gag agc 336
 Ile Met Gly Tyr Asp Asp Thr Arg Asp Arg Glu Leu Phe Glu Glu Ser
 100 105 110
 gcc atg tcg caa cag ccg acg gtg cct gac cgc ctg cgc tgg ctg ctg 384
 Ala Met Ser Gln Gln Pro Thr Val Pro Asp Arg Leu Arg Trp Leu Leu
 115 120 125
 caa acc ttt aaa tat cag aag aat att cgc atc cac gcc ttc aat gaa 432
 Gln Thr Phe Lys Tyr Gln Lys Asn Ile Arg Ile His Ala Phe Asn Glu
 130 135 140
 gag ggg atg gag ccc tat ccg cac ggc tgg gac gtc tgg agc cat ggg 480
 Glu Gly Met Glu Pro Tyr Pro His Gly Trp Asp Val Trp Ser His Gly
 145 150 155 160
 atc cgc gct ttt atg agc gaa aaa ggg atc gag ccg aac cgg atc tat 528
 Ile Arg Ala Phe Met Ser Glu Lys Gly Ile Glu Pro Asn Arg Ile Tyr
 165 170 175
 acc tcg gaa gag gcc gat gcg ccg cag tac ctt gag cat ctg ggg atc 576
 Thr Ser Glu Glu Ala Asp Ala Pro Gln Tyr Leu Glu His Leu Gly Ile
 180 185 190
 gag acg gtg ctt atc gat cct aag cgg acc ttt atg aat att agc ggc 624
 Glu Thr Val Leu Ile Asp Pro Lys Arg Thr Phe Met Asn Ile Ser Gly
 195 200 205
 ggg cag atc cgc gag aac ccg ttc cgc tac tgg gaa tat att ccg acg 672
 Gly Gln Ile Arg Glu Asn Pro Phe Arg Tyr Trp Glu Tyr Ile Pro Thr
 210 215 220
 gaa gtg aaa ccg ttc ttt gtg cgg acg gtg gcg atc ctc ggc ggc gag 720
 Glu Val Lys Pro Phe Val Arg Thr Val Ala Ile Leu Gly Gly Glu
 225 230 235 240
 tcg agc ggt aaa tcg acg ctg gtc aat aaa ctc gcc aat atc ttc aat 768
 Ser Ser Gly Lys Ser Thr Leu Val Asn Lys Leu Ala Asn Ile Phe Asn
 245 250 255
 acc acc agc gcc tgg gaa tat ggc cgg gat tat gtt ttt tcg cat ctc 816
 Thr Thr Ser Ala Trp Glu Tyr Gly Arg Asp Tyr Val Phe Ser His Leu
 260 265 270
 ggc ggc gat gag atg gcg ctc cag tat tcg gat tac gat aaa att gcc 864
 Gly Gly Asp Glu Met Ala Leu Gln Tyr Ser Asp Tyr Asp Lys Ile Ala

PF59083SeqList PF59083.txt

275	280	285	
ctt ggg cat gcg cag tat att gat ttt gcg gtg aaa tat gcc aac aag	280	285	912
Leu Gly His Ala Gln Tyr Ile Asp Phe Ala Val Lys Tyr Ala Asn Lys	290	300	
gtg gcg ttc atc gat acc gac ttc gtc agc act cag gcc ttc tgt ctg	295	310	960
Val Ala Phe Ile Asp Thr Asp Phe Val Ser Thr Gln Ala Phe Cys Leu	310	315	
305 aag tac gag gga cgt gag cac ccg ttt gtg cag gcg ctg att gat gaa	325	335	1008
Lys Tyr Glu Gly Arg Glu His Pro Phe Val Gln Ala Leu Ile Asp Glu	330	340	
tac cgc ttc gac ctg gtg atc ctg ctg gag aac aat acc ccg tgg gtg	340	350	1056
Tyr Arg Phe Asp Leu Val Ile Leu Leu Glu Asn Asn Thr Pro Trp Val	345	355	
gcc gat gga ctg cgc agt ctt ggg agc tcg gtg gat cgt aaa gag ttt	355	365	1104
Ala Asp Gly Leu Arg Ser Leu Gly Ser Ser Val Asp Arg Lys Glu Phe	360	370	
cag tcg ttg ctg gta tcg ctg ctg aaa gag aac gag atc gaa ttc gtc	375	380	1152
Gln Ser Leu Leu Val Ser Leu Leu Lys Glu Asn Glu Ile Glu Phe Val	380	390	
cat gtg aag gag tcg gac tac gat gcc cgg ttc ctg cgc tgc gtc gag	385	395	1200
His Val Lys Glu Ser Asp Tyr Asp Ala Arg Phe Leu Arg Cys Val Glu	390	400	
ctg gtg aaa cag ctg atg ggc gag cag ggg tag	405	410	1233
Leu Val Lys Gln Leu Met Gly Glu Gln Gly			

<210> 9837

<211> 410

<212> PRT

<213> Klebsiella pneumoniae subsp. pneumoniae MGH 78578

<400> 9837

Met Ser Ser Phe Asp Tyr Leu Lys Ser Ala Ile Lys Gln Lys Gly Cys	5	10	15
1 Thr Leu Gln Gln Val Ala Glu Ala Ser Gly Met Thr Lys Gly Tyr Leu	20	25	30
Ser Gln Leu Leu Asn Ala Lys Ile Lys Ser Pro Ser Ala Gln Lys Leu	35	40	45
Glu Ala Leu His Arg Phe Leu Gly Leu Glu Phe Pro Arg Arg Gln Lys	50	55	60
Ser Val Gly Val Val Phe Gly Lys Phe Tyr Pro Leu His Thr Gly His	65	70	75
Ile Tyr Leu Ile Gln Arg Ala Cys Ser Gln Val Asp Glu Leu His Ile	80	85	90
Ile Met Gly Tyr Asp Asp Thr Arg Asp Arg Glu Leu Phe Glu Glu Ser	95	100	105
Ala Met Ser Gln Gln Pro Thr Val Pro Asp Arg Leu Arg Trp Leu Leu	110	115	120
Gln Thr Phe Lys Tyr Gln Lys Asn Ile Arg Ile His Ala Phe Asn Glu	125	130	135
Glu Gly Met Glu Pro Tyr Pro His Gly Trp Asp Val Trp Ser His Gly	140	145	150
Ile Arg Ala Phe Met Ser Glu Lys Gly Ile Glu Pro Asn Arg Ile Tyr	155	160	165
Thr Ser Glu Glu Ala Asp Ala Pro Gln Tyr Leu Glu His Leu Gly Ile	170	175	180
Glu Thr Val Leu Ile Asp Pro Lys Arg Thr Phe Met Asn Ile Ser Gly	185	190	195
Gly Gln Ile Arg Glu Asn Pro Phe Arg Tyr Trp Glu Tyr Ile Pro Thr	200	205	210
Glu Val Lys Pro Phe Phe Val Arg Thr Val Ala Ile Leu Gly Gly Glu	215	220	225
Ser Ser Gly Lys Ser Thr Leu Val Asn Lys Leu Ala Asn Ile Phe Asn	230	235	240
Thr Thr Ser Ala Trp Glu Tyr Gly Arg Asp Tyr Val Phe Ser His Leu	245	250	255
Gly Gly Asp Glu Met Ala Leu Gln Tyr Ser Asp Tyr Asp Lys Ile Ala	260	265	270
Leu Gly His Ala Gln Tyr Ile Asp Phe Ala Val Lys Tyr Ala Asn Lys	275	280	285

PF59083SeqList PF59083.txt

```

290          295          300
Val Ala Phe Ile Asp Thr Asp Phe Val Ser Thr Gln Ala Phe Cys Leu
305 Lys Tyr Glu Gly Arg 310 Glu His Pro Phe Val 315 Gln Ala Leu Ile Asp 320
Tyr Arg Phe Asp 325 Val Ile Leu Leu 330 Glu Asn Asn Thr Pro Trp Val 335
Ala Asp Gly Leu Arg Ser Leu Gly Ser Ser Val Asp Arg Lys Glu Phe 340
Gln Ser Leu Leu Val Ser Leu 350 Lys Glu Asn Glu Ile Glu Phe Val 355
His Val Lys Glu Ser Asp Tyr Asp Ala Arg Phe Leu Arg Cys Val Glu 365
385 Leu Val Lys Gln Leu Met Gly Glu Gln Gly 380 390 395 400
405          410

```

<210> 9838

<211> 1233

<212> DNA

<213> Salmonella enterica subsp. arizonae serovar 62:z4,z23:--

<220>

<221> CDS

<222> (1)..(1233)

<223> transl_table=11

<400> 9838

```

gtg tca tcg ttc gac tat ctc aaa acc gcg att aag cag caa ggt tgc      48
Met Ser Ser Phe Asp Tyr Leu Lys Thr Ala Ile Lys Gln Gln Gly Cys
1          5          10          15
act ctg caa cag gtg gct gac gcc agc ggt atg acc aag ggg tat ctg      96
Thr Leu Gln Gln Val Ala Asp Ala Ser Gly Met Thr Lys Gly Tyr Leu
20          25          30
agt cag tta ctt aac gcc aaa att aaa agc ccc agc gcg caa aaa ctg      144
Ser Gln Leu Leu Asn Ala Lys Ile Lys Ser Pro Ser Ala Gln Lys Leu
35          40          45
gaa gcg ctg cac cgt ttt ctt gga ctg gaa ttt ccc cgc cag caa aaa      192
Glu Ala Leu His Arg Phe Leu Gly Leu Glu Phe Pro Arg Gln Gln Lys
50          55          60
aac att ggc gtg gtg ttc ggt aaa ttt tat ccg ttg cat acc gga cac      240
Asn Ile Gly Val Val Phe Gly Lys Phe Tyr Pro Leu His Thr Gly His
65          70          75          80
atc tat ttg atc cag cgc gcc tgt agc cag gtg gat gag ttg cat atc      288
Ile Tyr Leu Ile Gln Arg Ala Cys Ser Gln Val Asp Glu Leu His Ile
85          90          95
gtt atg gga tat gac gat acg cgc gat cgc ggg ctg ttt gag gat agc      336
Val Met Gly Tyr Asp Asp Thr Arg Asp Arg Gly Leu Phe Glu Asp Ser
100          105          110
gct atg tcg cag cag cct acc gtg tcg gat cga ctg cgc tgg ttg ctg      384
Ala Met Ser Gln Gln Pro Thr Val Ser Asp Arg Leu Arg Trp Leu Leu
115          120          125
caa acc ttc aaa tac caa aaa aat att cgt atc cac gcc ttt aat gaa      432
Gln Thr Phe Lys Tyr Gln Lys Asn Ile Arg Ile His Ala Phe Asn Glu
130          135          140
gag ggg atg gag cct tat ccg cat ggc tgg gac gtc tgg agc aac ggc      480
Glu Gly Met Glu Pro Tyr Pro His Gly Trp Asp Val Trp Ser Asn Gly
145          150          155          160
att aaa gcg ttt atg gca gag aag gga ata cag ccg agc tgg atc tac      528
Ile Lys Ala Phe Met Ala Glu Lys Gly Ile Gln Pro Ser Trp Ile Tyr
165          170          175
act tcc gaa gag gct gat gcg ccg cag tac ctt gaa cat tta ggg att      576
Thr Ser Glu Glu Ala Asp Ala Pro Gln Tyr Leu Glu His Leu Gly Ile
180          185          190
gag acg gtg ctg gtc gat cct gaa cgc acg ttt atg aat atc agc ggg      624
Glu Thr Val Leu Val Asp Pro Glu Arg Thr Phe Met Asn Ile Ser Gly
195          200          205          210
gcg caa atc cgc gag aat ccg ttt cgc tac tgg gaa tat atc cct acc      672
Ala Gln Ile Arg Glu Asn Pro Phe Arg Tyr Trp Glu Tyr Ile Pro Thr
210          215          220

```


PF59083SeqList PF59083.txt

gaa	gtg	aag	ccg	ttt	ttc	gtg	cgc	acc	gtc	gcg	att	ctg	ggc	ggg	gaa	720
Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	Val	Ala	Ile	Leu	Gly	Gly	Glu	
225				230					235						240	
tca	agc	ggc	aag	tct	acg	ctg	gtc	aat	aag	ctc	gcc	aat	att	ttt	aat	768
Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	Lys	Leu	Ala	Asn	Ile	Phe	Asn	
				245					250					255		
act	acc	agc	gcc	tgg	gaa	tat	ggc	cgc	gac	tat	gtc	ttt	tcg	cat	ctg	816
Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	Asp	Tyr	Val	Phe	Ser	His	Leu	
			260				265					270				
ggc	ggc	gat	gag	atg	gcg	tta	cag	tat	tcc	gac	tac	gat	aaa	atc	gcg	864
Gly	Gly	Asp	Glu	Met	Ala	Leu	Gln	Tyr	Ser	Asp	Tyr	Asp	Lys	Ile	Ala	
		275					280					285				
ctg	ggc	cat	gcg	caa	tat	att	gat	ttt	gca	gta	aaa	tac	gcg	aat	aaa	912
Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe	Ala	Val	Lys	Tyr	Ala	Asn	Lys	
	290					295					300					
gtg	gca	ttt	atc	gat	act	gat	ttc	gtc	acc	acc	cag	gca	ttt	tgc	aaa	960
Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	Thr	Thr	Gln	Ala	Phe	Cys	Lys	
305				310					315						320	
aaa	tac	gaa	ggg	cgc	gag	cat	cca	ttt	gtc	cag	gcg	ctg	att	gat	gag	1008
Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	Val	Gln	Ala	Leu	Ile	Asp	Glu	
				325					330					335		
tat	cgc	ttc	gac	ctg	gtg	att	ttg	ctg	gag	aac	aat	acg	ccg	tgg	gta	1056
Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	Glu	Asn	Asn	Thr	Pro	Trp	Val	
			340				345						350			
gct	gac	ggg	ctg	cga	agt	ctg	ggc	agc	gca	gtg	gat	cgc	aaa	gcg	ttc	1104
Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	Ala	Val	Asp	Arg	Lys	Ala	Phe	
		355					360					365				
caa	agc	ctg	ttg	gtc	gag	atg	ctg	aaa	gag	aac	aac	atc	gag	ttt	gtt	1152
Gln	Ser	Leu	Leu	Val	Glu	Met	Leu	Lys	Glu	Asn	Asn	Ile	Glu	Phe	Val	
	370					375					380					
cac	gtt	aaa	gag	gct	gat	tac	gat	ggc	cgc	ttt	ttg	cgc	tgc	gtg	gag	1200
His	Val	Lys	Glu	Ala	Asp	Tyr	Asp	Gly	Arg	Phe	Leu	Arg	Cys	Val	Glu	
385				390						395					400	
ctg	gtg	aaa	gag	atg	atg	ggc	gag	cag	gga	taa						1233
Leu	Val	Lys	Glu	Met	Met	Gly	Glu	Gln	Gly							
				405					410							

<210> 9839

<211> 410

<212> PRT

<213> Salmonella enterica subsp. arizonae serovar 62:z4,z23:--

<400> 9839

Met	Ser	Ser	Phe	Asp	Tyr	Leu	Lys	Thr	Ala	Ile	Lys	Gln	Gln	Gly	Cys	
1				5					10					15		
Thr	Leu	Gln	Gln	Val	Ala	Asp	Ala	Ser	Gly	Met	Thr	Lys	Gly	Tyr	Leu	
			20					25					30			
Ser	Gln	Leu	Leu	Asn	Ala	Lys	Ile	Lys	Ser	Pro	Ser	Ala	Gln	Lys	Leu	
		35					40					45				
Glu	Ala	Leu	His	Arg	Phe	Leu	Gly	Leu	Glu	Phe	Pro	Arg	Gln	Gln	Lys	
	50					55				60						
Asn	Ile	Gly	Val	Val	Phe	Gly	Lys	Phe	Tyr	Pro	Leu	His	Thr	Gly	His	
65					70				75					80		
Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Cys	Ser	Gln	Val	Asp	Glu	Leu	His	Ile	
			85						90					95		
Val	Met	Gly	Tyr	Asp	Asp	Thr	Arg	Asp	Arg	Gly	Leu	Phe	Glu	Asp	Ser	
			100					105					110			
Ala	Met	Ser	Gln	Gln	Pro	Thr	Val	Ser	Asp	Arg	Leu	Arg	Trp	Leu	Leu	
		115					120					125				
Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile	Arg	Ile	His	Ala	Phe	Asn	Glu	
	130					135					140					
Glu	Gly	Met	Glu	Pro	Tyr	Pro	His	Gly	Trp	Asp	Val	Trp	Ser	Asn	Gly	
145					150					155					160	
Ile	Lys	Ala	Phe	Met	Ala	Glu	Lys	Gly	Ile	Gln	Pro	Ser	Trp	Ile	Tyr	
			165						170					175		
Thr	Ser	Glu	Glu	Ala	Asp	Ala	Pro	Gln	Tyr	Leu	Glu	His	Leu	Gly	Ile	
			180					185					190			
Glu	Thr	Val	Leu	Val	Asp	Pro	Glu	Arg	Thr	Phe	Met	Asn	Ile	Ser	Gly	
		195					200					205				

PF59083SeqList PF59083.txt

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

<210> 9840

<211> 1254

<212> DNA

<213> Pectobacterium atrosepticum SCRI1043

<220>

<221> CDS

<222> (1)..(1254)

<223> transl_table=11

<400> 9840

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

PF59083SeqList PF59083.txt

Ile	Gln	Ala	Phe	Met	Gln	Glu	Lys	Ser	Ile	Thr	Pro	Asn	Phe	Val	Tyr	
acc	agc	gaa	gaa	cag	gat	gct	ctg	caa	tat	cgt	gag	cat	ctg	ggc	att	576
Thr	Ser	Glu	Glu	Gln	Asp	Ala	Leu	Gln	Tyr	Arg	Glu	His	Leu	Gly	Ile	
		180						185					190			
gag	gcc	atc	ttg	atc	gac	ccg	caa	cga	tcc	ttt	atg	aac	atc	agc	ggc	624
Glu	Ala	Ile	Leu	Ile	Asp	Pro	Gln	Arg	Ser	Phe	Met	Asn	Ile	Ser	Gly	
		195					200					205				
tcc	cag	atc	cgc	cac	gat	ccc	ttc	cgt	tat	tgg	gac	tat	atc	cca	acc	672
Ser	Gln	Ile	Arg	His	Asp	Pro	Phe	Arg	Tyr	Trp	Asp	Tyr	Ile	Pro	Thr	
		210				215					220					
gaa	gtg	aag	ccg	ttc	ttt	gtg	cgt	acc	gtt	gct	att	ctt	ggc	ggg	gaa	720
Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	Val	Ala	Ile	Leu	Gly	Gly	Glu	
225					230				235						240	
tcc	agt	ggt	aaa	tcc	acg	ctg	gta	aac	aag	ctg	gct	aat	atc	ttc	aac	768
Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	Lys	Leu	Ala	Asn	Ile	Phe	Asn	
				245				250						255		
acc	acc	agc	gcc	ttg	gaa	tat	ggt	cgc	gat	tat	gta	ttc	tct	cat	ctg	816
Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	Asp	Tyr	Val	Phe	Ser	His	Leu	
			260					265					270			
ggt	ggc	gac	gag	atg	gcg	ttg	cag	tat	tcc	gac	tat	gac	aag	att	gca	864
Gly	Gly	Asp	Glu	Met	Ala	Leu	Gln	Tyr	Ser	Asp	Tyr	Asp	Lys	Ile	Ala	
		275				280						285				
ctg	ggt	cag	gca	cag	tac	att	gat	ttt	gcg	gta	aaa	tat	gcc	aat	aaa	912
Leu	Gly	Gln	Ala	Gln	Tyr	Ile	Asp	Phe	Ala	Val	Lys	Tyr	Ala	Asn	Lys	
		290				295					300					
gtg	gcc	ttt	atc	gac	acc	gat	ttt	gtc	acc	act	cag	gcg	ttc	tgc	aaa	960
Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	Thr	Thr	Gln	Ala	Phe	Cys	Lys	
305					310				315						320	
aaa	tat	gaa	ggc	cgt	gaa	cac	ccg	ttc	gtt	cag	gca	cta	gtc	gac	gaa	1008
Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	Val	Gln	Ala	Leu	Val	Asp	Glu	
				325				330						335		
tac	cgc	ttc	gat	ctg	gtg	att	ttg	ctg	gaa	aac	aac	acg	ccg	ttg	gta	1056
Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	Glu	Asn	Asn	Thr	Pro	Trp	Val	
			340					345					350			
gcc	gac	ggg	ctg	cgc	agt	tta	ggc	agt	acc	acc	gct	cgt	tcg	gaa	ttc	1104
Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	Thr	Thr	Ala	Arg	Ser	Glu	Phe	
		355					360					365				
cag	gac	ctg	ctg	aaa	acg	atg	ctg	gct	aaa	aat	aat	atc	ccg	tac	gtg	1152
Gln	Asp	Leu	Leu	Lys	Thr	Met	Leu	Ala	Lys	Asn	Asn	Ile	Pro	Tyr	Val	
		370				375						380				
tac	atc	aaa	gaa	ccg	gat	tac	gat	tcg	cgt	ttc	ctg	cac	tgt	gtg	gaa	1200
Tyr	Ile	Lys	Glu	Pro	Asp	Tyr	Asp	Ser	Arg	Phe	Leu	His	Cys	Val	Glu	
385					390				395						400	
ttg	gta	cag	cag	atg	ttg	ggc	cac	gat	cgg	tcg	ccc	gaa	cag	ata	aaa	1248
Leu	Val	Gln	Gln	Met	Leu	Gly	His	Asp	Arg	Ser	Pro	Glu	Gln	Ile	Lys	
				405				410						415		
aac	tag															1254
Asn																

<210> 9841

<211> 417

<212> PRT

<213> Pectobacterium atrosepticum SCRI1043

<400> 9841

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

PF59083SeqList PF59083.txt

Ile Leu Gly Tyr Asp Glu Pro Arg Asp Arg Leu Leu Phe Glu Asn Ser
 100 105 110
 Ser Met Ser Gln Gln Pro Thr Val Ser Asp Arg Leu Arg Trp Leu Leu
 115 120 125
 Gln Thr Phe Lys Tyr Gln Lys Asn Ile His Ile His Ala Phe Asn Glu
 130 135 140
 Gln Gly Met Glu Pro Tyr Pro His Gly Trp Asp Val Trp Ser Lys Gly
 145 150 155 160
 Ile Gln Ala Phe Met Gln Glu Lys Ser Ile Thr Pro Asn Phe Val Tyr
 165 170 175
 Thr Ser Glu Glu Gln Asp Ala Leu Gln Tyr Arg Glu His Leu Gly Ile
 180 185 190
 Glu Ala Ile Leu Ile Asp Pro Gln Arg Ser Phe Met Asn Ile Ser Gly
 195 200 205
 Ser Gln Ile Arg His Asp Pro Phe Arg Tyr Trp Asp Tyr Ile Pro Thr
 210 215 220
 Glu Val Lys Pro Phe Phe Val Arg Thr Val Ala Ile Leu Gly Gly Glu
 225 230 235 240
 Ser Ser Gly Lys Ser Thr Leu Val Asn Lys Leu Ala Asn Ile Phe Asn
 245 250 255
 Thr Thr Ser Ala Trp Glu Tyr Gly Arg Asp Tyr Val Phe Ser His Leu
 260 265 270
 Gly Gly Asp Glu Met Ala Leu Gln Tyr Ser Asp Tyr Asp Lys Ile Ala
 275 280 285
 Leu Gly Gln Ala Gln Tyr Ile Asp Phe Ala Val Lys Tyr Ala Asn Lys
 290 295 300
 Val Ala Phe Ile Asp Thr Asp Phe Val Thr Thr Gln Ala Phe Cys Lys
 305 310 315 320
 Lys Tyr Glu Gly Arg Glu His Pro Phe Val Gln Ala Leu Val Asp Glu
 325 330 335
 Tyr Arg Phe Asp Leu Val Ile Leu Leu Glu Asn Asn Thr Pro Trp Val
 340 345 350
 Ala Asp Gly Leu Arg Ser Leu Gly Ser Thr Thr Ala Arg Ser Glu Phe
 355 360 365
 Gln Asp Leu Leu Lys Thr Met Leu Ala Lys Asn Asn Ile Pro Tyr Val
 370 375 380
 Tyr Ile Lys Glu Pro Asp Tyr Asp Ser Arg Phe Leu His Cys Val Glu
 385 390 395 400
 Leu Val Gln Gln Met Leu Gly His Asp Arg Ser Pro Glu Gln Ile Lys
 405 410 415
 Asn

<210> 9842

<211> 1260

<212> DNA

<213> Mannheimia succiniciproducens MBEL55E

<220>

<221> CDS

<222> (1)..(1260)

<223> transl_table=11

<400> 9842

atg tct aat ttt tct tat tta caa caa aaa cgt aaa caa cta aat ctc	48
Met Ser Asn Phe Ser Tyr Leu Gln Gln Lys Arg Lys Gln Leu Asn Leu	
1 5 10 15	
aag gta aac gat atc tgt gag caa gct aat gtt acg cgg gct tac ttt	96
Lys Val Asn Asp Ile Cys Glu Gln Ala Asn Val Thr Arg Ala Tyr Phe	
20 25 30	
aat caa ctt gta agt gga aaa att aaa aac ccc agt gcg gca aaa tta	144
Asn Gln Leu Val Ser Gly Lys Ile Lys Asn Pro Ser Ala Ala Lys Leu	
35 40 45	
acg gca tta cat aaa gca tta caa att acg gaa caa gac aac aaa aaa	192
Thr Ala Leu His Lys Ala Leu Gln Ile Thr Glu Gln Asp Asn Lys Lys	
50 55 60	
gtc ggc gtg att ttt ggc aaa ttt tat ccc gtg cat acc ggc cat atc	240
Val Gly Val Ile Phe Gly Lys Phe Tyr Pro Val His Thr Gly His Ile	
65 70 75 80	

PF59083SeqList PF59083.txt

aat atg atc tat gag gcc ttc agt aaa gtg gat gag cta cat gta att	288
Asn Met Ile Tyr Glu Ala Phe Ser Lys Val Asp Glu Leu His Val Ile	
85 90 95	
gtg tgc agc gat acc gaa cgt gat ttg cag ctt ttc tat gac agc aaa	336
Val Cys Ser Asp Thr Glu Arg Asp Leu Gln Leu Phe Tyr Asp Ser Lys	
100 105 110	
atg aag cgt atg cca aca gtg caa gat cgt ttg cgc tgg atg caa caa	384
Met Lys Arg Met Pro Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln	
115 120 125	
att ttc aaa tat caa aag aat cag att ttt att cac aat ctg gtg gaa	432
Ile Phe Lys Tyr Gln Lys Asn Gln Ile Phe Ile His Asn Leu Val Glu	
130 135 140	
gac ggt att ccg agt tat ccg aac ggc tgg cga gcc tgg tcc aat gcg	480
Asp Gly Ile Pro Ser Tyr Pro Asn Gly Trp Arg Ala Trp Ser Asn Ala	
145 150 155 160	
gca aaa gca tta ttt aaa gaa aaa gaa att aat ccg acg gta gta ttc	528
Ala Lys Ala Leu Phe Lys Glu Lys Glu Ile Asn Pro Thr Val Val Phe	
165 170 175	
agc agc gaa ccg cag gat aaa gcg cct tat gaa aaa tac ctt aat tta	576
Ser Ser Glu Pro Gln Asp Lys Ala Pro Tyr Glu Lys Tyr Leu Asn Leu	
180 185 190	
gaa gta cat ttg gtt gat ccg gcg cgc gaa tct ttt aat gta tcc gcc	624
Glu Val His Leu Val Asp Pro Ala Arg Glu Ser Phe Asn Val Ser Ala	
195 200 205	
aca aaa atc cgc act cag ccg ttt aaa tat tgg aaa tat att cca aaa	672
Thr Lys Ile Arg Thr Gln Pro Phe Lys Tyr Trp Lys Tyr Ile Pro Lys	
210 215 220	
gaa gtg cgc ccg ttc ttt gcc aaa acc ata gct att tta gga gga gaa	720
Glu Val Arg Pro Phe Phe Ala Lys Thr Ile Ala Ile Leu Gly Gly Glu	
225 230 235 240	
agt agc ggt aaa tcc gtg ctt gtc aac aaa ttg gcg acg gtt ttt aat	768
Ser Ser Gly Lys Ser Val Leu Val Asn Lys Leu Ala Thr Val Phe Asn	
245 250 255	
acg act tcc gct tgg gaa tac gga cgt gat ttc gta ttt gat aaa ctt	816
Thr Thr Ser Ala Trp Glu Tyr Gly Arg Asp Phe Val Phe Asp Lys Leu	
260 265 270	
ggc ggc gac gaa caa gcc atg caa tat tct gat tat ccg caa atg gcg	864
Gly Gly Asp Glu Gln Ala Met Gln Tyr Ser Asp Tyr Pro Gln Met Ala	
275 280 285	
ctc ggc cat cag cat tat att gat tat gcc gtg cgt cat gct cat aaa	912
Leu Gly His Gln His Tyr Ile Asp Tyr Ala Val Arg His Ala His Lys	
290 295 300	
gta gca ttt att gat acg gat ttc att acc acg caa gca ttt tgt att	960
Val Ala Phe Ile Asp Thr Asp Phe Ile Thr Thr Gln Ala Phe Cys Ile	
305 310 315 320	
caa tat gaa gga aaa ccg cac ccg ttt ttg gat tct atg att aaa gaa	1008
Gln Tyr Glu Gly Lys Pro His Pro Phe Leu Asp Ser Met Ile Lys Glu	
325 330 335	
tat cct ttt gat gtg act ata ttg cta aat aat aat aca aaa tgg gta	1056
Tyr Pro Phe Asp Val Thr Ile Leu Leu Asn Asn Asn Thr Lys Trp Val	
340 345 350	
gat gac gga cta cgt agc ctg ggc gat tat aaa caa cgc caa cgt ttt	1104
Asp Asp Gly Leu Arg Ser Leu Gly Asp Tyr Lys Gln Arg Gln Arg Phe	
355 360 365	
caa cag tta ctg aaa aaa ttg tta gat aaa tat aaa gtt cct tat att	1152
Gln Gln Leu Leu Lys Lys Leu Leu Asp Lys Tyr Lys Val Pro Tyr Ile	
370 375 380	
gaa att gag tca cca agt tat tta gaa cgc tat gat caa gca aaa gcg	1200
Glu Ile Glu Ser Pro Ser Tyr Leu Glu Arg Tyr Asp Gln Ala Lys Ala	
385 390 395 400	
att gtt gaa aaa gta ctg aat gat gaa gaa gtc tcg gaa ctg act cat	1248
Ile Val Glu Lys Val Leu Asn Asp Glu Glu Val Ser Glu Leu Thr His	
405 410 415	
gaa aac gat taa	1260
Glu Asn Asp	

<210> 9843

<211> 419

PF59083SeqList PF59083.txt

<212> PRT

<213> Mannheimia succiniciproducens MBEL55E

<400> 9843

```

Met Ser Asn Phe Ser Tyr Leu Gln Gln Lys Arg Lys Gln Leu Asn Leu
1      5      10      15
Lys Val Asn Asp Ile Cys Glu Gln Ala Asn Val Thr Arg Ala Tyr Phe
      20      25      30
Asn Gln Leu Val Ser Gly Lys Ile Lys Asn Pro Ser Ala Ala Lys Leu
      35      40      45
Thr Ala Leu His Lys Ala Leu Gln Ile Thr Glu Gln Asp Asn Lys Lys
      50      55      60
Val Gly Val Ile Phe Gly Lys Phe Tyr Pro Val His Thr Gly His Ile
65      70      75
Asn Met Ile Tyr Glu Ala Phe Ser Lys Val Asp Glu Leu His Val Ile
      85      90      95
Val Cys Ser Asp Thr Glu Arg Asp Leu Gln Leu Phe Tyr Asp Ser Lys
      100      105      110
Met Lys Arg Met Pro Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln
      115      120      125
Ile Phe Lys Tyr Gln Lys Asn Gln Ile Phe Ile His Asn Leu Val Glu
130      135      140
Asp Gly Ile Pro Ser Tyr Pro Asn Gly Trp Arg Ala Trp Ser Asn Ala
145      150      155
Ala Lys Ala Leu Phe Lys Glu Lys Glu Ile Asn Pro Thr Val Val Phe
      165      170      175
Ser Ser Glu Pro Gln Asp Lys Ala Pro Tyr Glu Lys Tyr Leu Asn Leu
      180      185      190
Glu Val His Leu Val Asp Pro Ala Arg Glu Ser Phe Asn Val Ser Ala
      195      200      205
Thr Lys Ile Arg Thr Gln Pro Phe Lys Tyr Trp Lys Tyr Ile Pro Lys
210      215      220
Glu Val Arg Pro Phe Phe Ala Lys Thr Ile Ala Ile Leu Gly Gly Glu
225      230      235
Ser Ser Gly Lys Ser Val Leu Val Asn Lys Leu Ala Thr Val Phe Asn
      245      250      255
Thr Thr Ser Ala Trp Glu Tyr Gly Arg Asp Phe Val Phe Asp Lys Leu
      260      265      270
Gly Gly Asp Glu Gln Ala Met Gln Tyr Ser Asp Tyr Pro Gln Met Ala
      275      280      285
Leu Gly His Gln His Tyr Ile Asp Tyr Ala Val Arg His Ala His Lys
      290      295      300
Val Ala Phe Ile Asp Thr Asp Phe Ile Thr Thr Gln Ala Phe Cys Ile
305      310      315
Gln Tyr Glu Gly Lys Pro His Pro Phe Leu Asp Ser Met Ile Lys Glu
      325      330      335
Tyr Pro Phe Asp Val Thr Ile Leu Leu Asn Asn Asn Thr Lys Trp Val
      340      345      350
Asp Asp Gly Leu Arg Ser Leu Gly Asp Tyr Lys Gln Arg Gln Arg Phe
      355      360      365
Gln Gln Leu Leu Lys Lys Leu Leu Asp Lys Tyr Lys Val Pro Tyr Ile
      370      375      380
Glu Ile Glu Ser Pro Ser Tyr Leu Glu Arg Tyr Asp Gln Ala Lys Ala
385      390      395
Ile Val Glu Lys Val Leu Asn Asp Glu Glu Val Ser Glu Leu Thr His
      405      410      415
Glu Asn Asp

```

<210> 9844

<211> 1266

<212> DNA

<213> Haemophilus influenzae 86-028NP

<220>

<221> CDS

<222> (1)..(1266)

<223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 9844
gtg ggc ttt acc acc ggt agg gaa ttt cac cct gcc ctg aga atg cga      48
Met Gly Phe Thr Thr 5 Gly Arg Glu Phe His Pro Ala Leu Arg Met Arg
1 5 10 15
gct aag tat aac gca aaa tac cta ggc act aaa tca gaa cgt gaa aaa      96
Ala Lys Tyr Asn Ala Lys Tyr Leu Gly Thr Lys Ser Glu Arg Glu Lys
20 25 30
tat ttt cat tta gcc tac aat aaa cac act caa ttc tta cgc tat caa      144
Tyr Phe His Leu Ala Tyr Asn Lys His Thr Gln Phe Leu Arg Tyr Gln
35 40 45
gag cag att atg tca aaa aca aaa gag aaa aaa gtc ggt gtc att ttc      192
Glu Gln Ile Met Ser Lys Thr Lys Glu Lys Lys Val Gly Val Ile Phe
50 55 60
ggg aaa ttt tat cct gta cac aca ggt cat ata aat atg att tat gaa      240
Gly Lys Phe Tyr Pro Val His Thr Gly His Ile Asn Met Ile Tyr Glu
65 70 75 80
gcg ttc agt aaa gtc gat gaa cta cac gtt atc gtg tgt agt gac acg      288
Ala Phe Ser Lys Val Asp Glu Leu His Val Ile Val Cys Ser Asp Thr
85 90 95
gtg cgc gat ttg aaa tta ttt tac gat agt aaa atg aaa cgc atg cca      336
Val Arg Asp Leu Lys Leu Phe Tyr Asp Ser Lys Met Lys Arg Met Pro
100 105 110
acc gtg caa gat cgt ttg cgt tgg atg cag caa att ttc aaa tat caa      384
Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln Ile Phe Lys Tyr Gln
115 120 125
aaa aat cag att ttt att cat cat ttg att gaa gac ggt att cca agt      432
Lys Asn Gln Ile Phe Ile His His Leu Ile Glu Asp Gly Ile Pro Ser
130 135 140
tat cca aac ggc tgg caa tct tgg agt gaa gca gtt aaa acc cta ttt      480
Tyr Pro Asn Gly Trp Ser Trp Ser Glu Ala Val Lys Thr Leu Phe
145 150 155 160
cat gaa aaa cat ttt gaa cct tca atc gta ttt agt agc gag cct caa      528
His Glu Lys His Phe Glu Pro Ser Ile Val Phe Ser Ser Glu Pro Gln
165 170 175
gat aaa gcg cct tac gag aaa tac tta ggt tta gaa gta tcg tta gtc      576
Asp Lys Ala Pro Tyr Glu Lys Tyr Leu Gly Leu Glu Val Ser Leu Val
180 185 190
gat cct gac gcg act ttc ttt aat gtg tcc gca acc aaa att cgc acc      624
Asp Pro Asp Arg Thr Phe Phe Asn Val Ser Ala Thr Lys Ile Arg Thr
195 200 205
act cca ttc caa tat tgg aag ttt att ccg aaa gaa gct cgt cct ttc      672
Thr Pro Phe Gln Tyr Trp Lys Phe Ile Pro Lys Glu Ala Arg Pro Phe
210 215 220
ttt gcc aaa acg gtg gcg att tta ggg gga gaa agc agt ggt aaa agc      720
Phe Ala Lys Thr Val Ala Ile Leu Gly Gly Glu Ser Ser Gly Lys Ser
225 230 235 240
gtg cta gtt aat aag tta gcc gcc gta ttt aat acc act tct gcg tgg      768
Val Leu Val Asn Lys Leu Ala Ala Val Phe Asn Thr Thr Ser Ala Trp
245 250 255
gaa tac ggg cgt gaa ttt gta ttt gaa aag ctc ggt ggc gac gag caa      816
Glu Tyr Gly Arg Glu Phe Val Phe Glu Lys Leu Gly Gly Asp Glu Gln
260 265 270
gcg atg caa tat tct gac tat ccg caa atg gcg ctt ggt cat caa cga      864
Ala Met Gln Tyr Ser Asp Tyr Pro Gln Met Ala Leu Gly His Gln Arg
275 280 285
tac att gat tat gcc gtg cgc cat tct cat aaa att gca ttt att gat      912
Tyr Ile Asp Tyr Ala Val Arg His Ser His Lys Ile Ala Phe Ile Asp
290 295 300
acg gat ttc att acc acg caa gcg ttc tgc att caa tat gaa gga aaa      960
Thr Asp Phe Ile Thr Gln Ala Phe Cys Ile Gln Tyr Glu Gly Lys
305 310 315 320
gct cat cca ttt tta gac tca atg att aaa gaa tat ccc ttc gat gtc      1008
Ala His Pro Phe Leu Asp Ser Met Ile Lys Glu Tyr Pro Phe Asp Val
325 330 335
act att tta ctt aaa aat aat act gaa tgg gtg gat gat ggc ttg cgc      1056
Thr Ile Leu Leu Lys Asn Asn Thr Glu Trp Val Asp Asp Gly Leu Arg
340 345 350
agc tta ggc tca caa aaa caa cgc caa caa ttt caa caa cta ctc aaa      1104
Ser Leu Gly Ser Gln Lys Gln Arg Gln Gln Phe Gln Leu Leu Lys

```

PF59083SeqList PF59083.txt

355	360	365	
aaa ctg tta gat aaa tat aaa gtt cct tat ata gag att gaa tct cca			1152
Lys Leu Leu Asp Lys Tyr Lys Val Pro Tyr Ile Glu Ile Glu Ser Pro			
370	375	380	
agt tat ctt gat cgc tat aac caa gtt aaa gca gtc att gag aaa gtg			1200
Ser Tyr Leu Asp Arg Tyr Asn Gln Val Lys Ala Val Ile Glu Lys Val			
385	390	395	400
tta aat gaa gag gaa atc agt gaa tta caa aac aca acc ttt cct ata			1248
Leu Asn Glu Glu Glu Ile Ser Glu Leu Gln Asn Thr Thr Phe Pro Ile			
405	410	415	
aaa ggg aca tct caa tga			1266
Lys Gly Thr Ser Gln			
420			

<210> 9845

<211> 421

<212> PRT

<213> Haemophilus influenzae 86-028NP

<400> 9845

Met Gly Phe Thr Thr Gly Arg Glu Phe His Pro Ala Leu Arg Met Arg	
1 5 10 15	
Ala Lys Tyr Asn Ala Lys Tyr Leu Gly Thr Lys Ser Glu Arg Glu Lys	
20 25 30	
Tyr Phe His Leu Ala Tyr Asn Lys His Thr Gln Phe Leu Arg Tyr Gln	
35 40 45	
Glu Gln Ile Met Ser Lys Thr Lys Glu Lys Lys Val Gly Val Ile Phe	
50 55 60	
Gly Lys Phe Tyr Pro Val His Thr Gly His Ile Asn Met Ile Tyr Glu	
65 70 75 80	
Ala Phe Ser Lys Val Asp Glu Leu His Val Ile Val Cys Ser Asp Thr	
85 90 95	
Val Arg Asp Leu Lys Leu Phe Tyr Asp Ser Lys Met Lys Arg Met Pro	
100 105 110	
Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln Ile Phe Lys Tyr Gln	
115 120 125	
Lys Asn Gln Ile Phe Ile His His Leu Ile Glu Asp Gly Ile Pro Ser	
130 135 140	
Tyr Pro Asn Gly Trp Gln Ser Trp Ser Glu Ala Val Lys Thr Leu Phe	
145 150 155 160	
His Glu Lys His Phe Glu Pro Ser Ile Val Phe Ser Ser Glu Pro Gln	
165 170 175	
Asp Lys Ala Pro Tyr Glu Lys Tyr Leu Gly Leu Glu Val Ser Leu Val	
180 185 190	
Asp Pro Asp Arg Thr Phe Phe Asn Val Ser Ala Thr Lys Ile Arg Thr	
195 200 205	
Thr Pro Phe Gln Tyr Trp Lys Phe Ile Pro Lys Glu Ala Arg Pro Phe	
210 215 220	
Phe Ala Lys Thr Val Ala Ile Leu Gly Gly Glu Ser Ser Gly Lys Ser	
225 230 235 240	
Val Leu Val Asn Lys Leu Ala Ala Val Phe Asn Thr Thr Ser Ala Trp	
245 250 255	
Glu Tyr Gly Arg Glu Phe Val Phe Glu Lys Leu Gly Gly Asp Glu Gln	
260 265 270	
Ala Met Gln Tyr Ser Asp Tyr Pro Gln Met Ala Leu Gly His Gln Arg	
275 280 285	
Tyr Ile Asp Tyr Ala Val Arg His Ser His Lys Ile Ala Phe Ile Asp	
290 295 300	
Thr Asp Phe Ile Thr Thr Gln Ala Phe Cys Ile Gln Tyr Glu Gly Lys	
305 310 315 320	
Ala His Pro Phe Leu Asp Ser Met Ile Lys Glu Tyr Pro Phe Asp Val	
325 330 335	
Thr Ile Leu Leu Lys Asn Asn Thr Glu Trp Val Asp Asp Gly Leu Arg	
340 345 350	
Ser Leu Gly Ser Gln Lys Gln Arg Gln Gln Phe Gln Gln Leu Lys	
355 360 365	
Lys Leu Leu Asp Lys Tyr Lys Val Pro Tyr Ile Glu Ile Glu Ser Pro	
370 375 380	
Ser Tyr Leu Asp Arg Tyr Asn Gln Val Lys Ala Val Ile Glu Lys Val	

PF59083SeqList PF59083.txt

385 Leu Asn Glu Glu Glu 390 Ile Ser Glu Leu Gln 395 Asn Thr Thr Phe 400 Pro Ile
Lys Gly Thr Ser 405 Gln 410 415

```
<210> 9846
<211> 1278
<212> DNA
<213> Haemophilus somnus 129PT
```

```
<220>
<221> CDS
<222> (1)..(1278)
<223> transl_table=11
```

<400>	9846																
atg	tcg	aat	ttc	agc	tat	ctg	caa	caa	aaa	cgt	aag	caa	tta	aat	ttg		48
Met	Ser	Asn	Phe	Ser	Tyr	Leu	Gln	Gln	Lys	Arg	Lys	Gln	Leu	Asn	Leu		
1				5					10					15			
aaa	gtt	aat	gat	ctt	tgt	acg	caa	gcc	aat	att	act	cgt	gct	tat	ttt		96
Lys	Val	Asn	Asp	Leu	Cys	Thr	Gln	Ala	Asn	Ile	Thr	Arg	Ala	Tyr	Phe		
			20					25					30				
aat	caa	tta	gta	agt	gga	aaa	att	aaa	aat	cca	agt	gcg	aca	aaa	ctt		144
Asn	Gln	Leu	Val	Ser	Gly	Lys	Ile	Lys	Asn	Pro	Ser	Ala	Thr	Lys	Leu		
			35				40					45					
tca	gca	ttg	cat	aaa	gtg	tta	cag	atc	act	gaa	caa	gat	aac	aaa	aaa		192
Ser	Ala	Leu	His	Lys	Val	Leu	Gln	Ile	Thr	Glu	Gln	Asp	Asn	Lys	Lys		
	50					55					60						
gta	ggc	gtt	att	ttt	ggt	aaa	ttt	tat	ccc	gtt	cat	acc	ggc	cac	att		240
Val	Gly	Val	Ile	Phe	Gly	Lys	Phe	Tyr	Pro	Val	His	Thr	Gly	His	Ile		
65					70					75					80		
aat	atg	att	tac	gaa	gca	ttt	agc	aaa	gta	gat	gaa	ctt	cat	gtc	gtt		288
Asn	Met	Ile	Tyr	Glu	Ala	Phe	Ser	Lys	Val	Asp	Glu	Leu	His	Val	Val		
				85					90					95			
gta	tgt	agt	gat	act	gag	cga	gat	tta	aaa	cta	ttc	tat	gac	agt	aaa		336
Val	Cys	Ser	Asp	Thr	Glu	Arg	Asp	Leu	Lys	Leu	Phe	Tyr	Asp	Ser	Lys		
			100				105						110				
atg	aaa	cga	atg	cca	act	gtg	caa	gat	cgc	tta	cgt	tgg	atg	caa	caa		384
Met	Lys	Arg	Met	Pro	Thr	Val	Gln	Asp	Arg	Leu	Arg	Trp	Met	Gln	Gln		
		115				120						125					
att	ttt	aaa	tat	cag	aaa	aat	caa	att	gtt	att	cat	cat	ctt	att	gaa		432
Ile	Phe	Lys	Tyr	Gln	Lys	Asn	Gln	Ile	Val	Ile	His	His	Leu	Ile	Glu		
	130					135					140						
gat	ggt	cta	cca	agt	tat	ccc	aat	ggc	tgg	gcg	gca	tgg	gct	gaa	cag		480
Asp	Gly	Leu	Pro	Ser	Tyr	Pro	Asn	Gly	Trp	Ala	Ala	Trp	Ala	Glu	Gln		
145					150				155					160			
gta	aaa	tat	cta	ttt	aag	gaa	aaa	aac	gtt	aat	cct	agc	gtg	gtt	ttt		528
Val	Lys	Tyr	Leu	Phe	Lys	Glu	Lys	Asn	Val	Asn	Pro	Ser	Val	Val	Phe		
				165					170					175			
agc	agt	gaa	atc	caa	gat	aaa	gta	cct	tat	gaa	aaa	tat	tta	aat	tta		576
Ser	Ser	Glu	Ile	Gln	Asp	Lys	Val	Pro	Tyr	Glu	Lys	Tyr	Leu	Asn	Leu		
			180				185						190				
caa	gtc	gaa	tta	gtt	gat	cca	aaa	cgc	tta	ttc	ctt	aat	att	tct	gca		624
Gln	Val	Glu	Leu	Val	Asp	Pro	Lys	Arg	Arg	Phe	Leu	Asn	I				

PF59083SeqList PF59083.txt

Gly	Gly	Asn	Glu	Gln	Ala	Met	Gln	Tyr	Ser	Asp	Tyr	Pro	Gln	Ile	Ala	
		275					280					285				
tta	ggt	cat	cag	cgt	tat	att	gat	tat	gcc	gtc	agg	cat	gca	cac	aaa	912
Leu	Gly	His	Gln	Arg	Tyr	Ile	Asp	Tyr	Ala	Val	Arg	His	Ala	His	Lys	
	290					295					300					
gtt	gca	att	gta	gat	aca	gac	ttt	att	aca	act	cag	gca	ttt	tgt	att	960
Val	Ala	Ile	Val	Asp	Thr	Asp	Phe	Ile	Thr	Thr	Gln	Ala	Phe	Cys	Ile	
305					310					315					320	
cag	tat	gaa	gga	aaa	gca	cac	cct	ttc	tta	gac	tcc	atg	atc	aaa	gaa	1008
Gln	Tyr	Glu	Gly	Lys	Ala	His	Pro	Phe	Leu	Asp	Ser	Met	Ile	Lys	Glu	
				325					330					335		
tat	ccc	ttt	gat	gtg	acc	att	tta	tta	aat	aat	aat	acc	caa	tgg	gta	1056
Tyr	Pro	Phe	Asp	Val	Thr	Ile	Leu	Leu	Asn	Asn	Asn	Thr	Gln	Trp	Val	
			340				345						350			
gat	gat	ggc	ttg	cgt	agc	tta	gga	aat	gct	aaa	caa	cgt	caa	cgc	ttc	1104
Asp	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Asn	Ala	Lys	Gln	Arg	Gln	Arg	Phe	
		355					360					365				
caa	caa	ctc	tta	aaa	aaa	tta	tta	gat	aag	cat	agt	gta	cct	tat	att	1152
Gln	Gln	Leu	Leu	Lys	Lys	Leu	Leu	Asp	Lys	His	Ser	Val	Pro	Tyr	Ile	
		370				375					380					
gaa	att	gac	tca	ccc	agt	tac	ttg	gaa	cgt	tat	aat	caa	gtg	aaa	aat	1200
Glu	Ile	Asp	Ser	Pro	Ser	Tyr	Leu	Glu	Arg	Tyr	Asn	Gln	Val	Lys	Asn	
385					390					395					400	
att	gtt	gag	aaa	gta	ctc	aac	gaa	gaa	ctt	ttg	gac	tta	gcc	gtg	gaa	1248
Ile	Val	Glu	Lys	Val	Leu	Asn	Glu	Glu	Leu	Leu	Asp	Leu	Ala	Val	Glu	
				405					410					415		
aca	atc	aca	cct	tca	att	ttt	aag	gaa	taa							1278
Thr	Ile	Thr	Pro	Ser	Ile	Phe	Lys	Glu								
			420					425								

<210> 9847

<211> 425

<212> PRT

<213> Haemophilus somnus 129PT

<400> 9847

Met	Ser	Asn	Phe	Ser	Tyr	Leu	Gln	Gln	Lys	Arg	Lys	Gln	Leu	Asn	Leu	
1				5					10					15		
Lys	Val	Asn	Asp	Leu	Cys	Thr	Gln	Ala	Asn	Ile	Thr	Arg	Ala	Tyr	Phe	
			20					25					30			
Asn	Gln	Leu	Val	Ser	Gly	Lys	Ile	Lys	Asn	Pro	Ser	Ala	Thr	Lys	Leu	
		35				40						45				
Ser	Ala	Leu	His	Lys	Val	Leu	Gln	Ile	Thr	Glu	Gln	Asp	Asn	Lys	Lys	
	50					55				60						
Val	Gly	Val	Ile	Phe	Gly	Lys	Phe	Tyr	Pro	Val	His	Thr	Gly	His	Ile	
65					70				75						80	
Asn	Met	Ile	Tyr	Glu	Ala	Phe	Ser	Lys	Val	Asp	Glu	Leu	His	Val	Val	
				85					90					95		
Val	Cys	Ser	Asp	Thr	Glu	Arg	Asp	Leu	Lys	Leu	Phe	Tyr	Asp	Ser	Lys	
			100					105					110			
Met	Lys	Arg	Met	Pro	Thr	Val	Gln	Asp	Arg	Leu	Arg	Trp	Met	Gln	Gln	
		115					120					125				
Ile	Phe	Lys	Tyr	Gln	Lys	Asn	Gln	Ile	Val	Ile	His	His	Leu	Ile	Glu	
	130					135					140					
Asp	Gly	Leu	Pro	Ser	Tyr	Pro	Asn	Gly	Trp	Ala	Ala	Trp	Ala	Glu	Gln	
145					150				155					160		
Val	Lys	Tyr	Leu	Phe	Lys	Glu	Lys	Asn	Val	Asn	Pro	Ser	Val	Val	Phe	
				165					170					175		
Ser	Ser	Glu	Ile	Gln	Asp	Lys	Val	Pro	Tyr	Glu	Lys	Tyr	Leu	Asn	Leu	
			180					185					190			
Gln	Val	Glu	Leu	Val	Asp	Pro	Lys	Arg	Arg	Phe	Leu	Asn	Ile	Ser	Ala	
		195				200						205				
Thr	Lys	Ile	Arg	Asn	Asn	Pro	Phe	His	Tyr	Trp	Lys	Phe	Ile	Pro	Lys	
	210					215					220					
Glu	Val	Arg	Pro	Phe	Phe	Ala	Lys	Thr	Ile	Ala	Ile	Leu	Gly	Gly	Glu	
225					230					235					240	
Ser	Ser	Gly	Lys	Thr	Thr	Leu	Val	Asn	Lys	Leu	Ala	Thr	Val	Phe	Asn	
				245					250					255		
Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	Glu	Phe	Val	Phe	Glu	Lys	Leu	

PF59083SeqList PF59083.txt

```

      260      265      270
Gly Gly Asn Glu Gln Ala Met Gln Tyr Ser Asp Tyr Pro Gln Ile Ala
      275      280      285
Leu Gly His Gln Arg Tyr Ile Asp Tyr Ala Val Arg His Ala His Lys
      290      295      300
Val Ala Ile Val Asp Thr Phe Ile Thr Thr Gln Ala Phe Cys Ile
      305      310      315
Gln Tyr Glu Gly Lys Ala His Pro Phe Leu Asp Ser Met Ile Lys Glu
      320      325      330
Tyr Pro Phe Asp Val Thr Ile Leu Leu Asn Asn Asn Thr Gln Trp Val
      335      340      345
Asp Asp Gly Leu Arg Ser Leu Gly Asn Ala Lys Gln Arg Gln Arg Phe
      350      355      360
Gln Gln Leu Leu Lys Lys Leu Leu Asp Lys His Ser Val Pro Tyr Ile
      365      370      375
Glu Ile Asp Ser Pro Ser Tyr Leu Glu Arg Tyr Asn Gln Val Lys Asn
      380      385      390
Ile Val Glu Lys Val Leu Asn Glu Glu Leu Leu Asp Leu Ala Val Glu
      400      405      410
Thr Ile Thr Pro Ser Ile Phe Lys Glu
      415      420      425

```

<210> 9848

<211> 1278

<212> DNA

<213> Haemophilus somnus 2336

<220>

<221> CDS

<222> (1)..(1278)

<223> transl_table=11

<400> 9848

```

atg tcg agt ttc agc tat ctg caa caa aaa cgt aag caa tta aat ctg      48
Met Ser Ser Phe Ser Tyr Leu Gln Gln Lys Arg Lys Gln Leu Asn Leu
      1      5      10
aag gtt aat gag ctt tgt aca caa gcc aat atc act cgt gct tat ttt      96
Lys Val Asn Glu Leu Cys Thr Gln Ala Asn Ile Thr Arg Ala Tyr Phe
      20      25      30
aac caa tta gtg agt gga aaa att aaa aat cca agt gcc aca aaa ctt      144
Asn Gln Leu Val Ser Gly Lys Ile Lys Asn Pro Ser Ala Thr Lys Leu
      35      40      45
tca gca ttg cat aaa gca cta cag att act gaa caa gat aac aaa aaa      192
Ser Ala Leu His Lys Ala Leu Gln Ile Thr Glu Gln Asp Asn Lys Lys
      50      55      60
ata ggc gtt att ttc ggc aaa ttt tat ccc gtt cat acc ggt cat att      240
Ile Gly Val Ile Phe Gly Lys Phe Tyr Pro Val His Thr Gly His Ile
      65      70      75
aat atg att tat gaa gca ttt agc aaa gta gat gag ctt cat gtg gtt      288
Asn Met Ile Tyr Glu Ala Phe Ser Lys Val Asp Glu Leu His Val Val
      80      85      90
gta tgt agc gat aca gaa cga gat tta aaa cta ttt tat gac agt aaa      336
Val Cys Ser Asp Thr Glu Arg Asp Leu Lys Leu Phe Tyr Asp Ser Lys
      100      105      110
atg aaa cga atg cca act gta cag gat cgc tta cgt tgg atg caa caa      384
Met Lys Arg Met Pro Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln
      115      120      125
att ttt aaa tat cag aaa aat aaa att gtt att cat cat ctt att gaa      432
Ile Phe Lys Tyr Gln Lys Asn Lys Ile Val Ile His His Leu Ile Glu
      130      135      140
gat ggt cta cca agt tat ccc aat ggc tgg tct gca tgg gct gaa caa      480
Asp Gly Leu Pro Ser Tyr Pro Asn Gly Trp Ser Ala Trp Ala Glu Gln
      145      150      155
gta aaa cgt cta ttc aag gaa aaa aac gtt aat cct agc gtg gtt ttt      528
Val Lys Arg Leu Phe Lys Glu Lys Asn Val Asn Pro Ser Val Val Phe
      160      165      170
agc agt gaa atc caa gat aaa gta cct tat gaa aaa tat tta aat tta      576
Ser Ser Glu Ile Gln Asp Lys Val Pro Tyr Glu Lys Tyr Leu Asn Leu
      175      180      185

```

PF59083SeqList PF59083.txt

caa gtc gaa tta gtt gat cca	aaa cgc cga ttc ctt aat att tct gca	624
Gln Val Glu Leu Val Asp Pro	Lys Arg Arg Phe Leu Asn Ile Ser Ala	
	195 200 205	
aca aaa att cgt aac aat cca	ttt cac tat tgg aaa ttc att cct aaa	672
Thr Lys Ile Arg Asn Asn Pro	Phe His Tyr Trp Lys Phe Ile Pro Lys	
	210 215 220	
gaa gtt cgc cca ttt ttt gca	aaa aca att gct att tta ggt gga gaa	720
Glu Val Arg Pro Phe Phe Ala	Lys Thr Ile Ala Ile Leu Gly Gly Glu	
	225 230 235 240	
agt agc ggt aaa aca act ctt	ggt aat aag cta gct aca gta ttt aat	768
Ser Ser Gly Lys Thr Leu Val	Asn Lys Leu Ala Thr Val Phe Asn	
	245 250 255	
act aca tca gct tgg gaa tat	gga cgt gaa ttt gtt ttt gaa aaa ctg	816
Thr Thr Ser Ala Trp Glu Tyr	Gly Arg Glu Phe Val Phe Glu Lys Leu	
	260 265 270	
gga ggt aat gaa caa gct atg	caa tat tct gat tat cca caa ata gca	864
Gly Gly Asn Glu Gln Ala Met	Gln Tyr Ser Asp Tyr Pro Gln Ile Ala	
	275 280 285	
tta ggt cat cag cgt tat att	gat tat gcc gtc agg cat gca cac aaa	912
Leu Gly His Gln Arg Tyr Ile	Asp Tyr Ala Val Arg His Ala His Lys	
	290 295 300	
gtt gca att gta gat aca gac	ttt att aca act cag gca ttt tgt att	960
Val Ala Ile Val Asp Thr Asp	Phe Ile Thr Thr Gln Ala Phe Cys Ile	
	305 310 315 320	
cag tat gaa gga aaa gca cac	cct ttc tta gac tcc atg atc aaa gaa	1008
Gln Tyr Glu Gly Lys Ala His	Pro Phe Leu Asp Ser Met Ile Lys Glu	
	325 330 335	
tat cct ttt gat gtg acc att	tta tta aat aat aat acc caa tgg gta	1056
Tyr Pro Phe Asp Val Thr Ile	Leu Leu Asn Asn Asn Thr Gln Trp Val	
	340 345 350	
gat gat ggc ttg cgt agc tta	gga aat gct aaa caa cgt caa cgc ttc	1104
Asp Asp Gly Leu Arg Ser Leu	Gly Asn Ala Lys Gln Arg Gln Arg Phe	
	355 360 365	
caa caa ctc tta aaa aaa tta	tta gat aag cat agt gta cct tat att	1152
Gln Gln Leu Leu Lys Lys Leu	Leu Asp Lys His Ser Val Pro Tyr Ile	
	370 375 380	
gaa att gac tca ccc agt tac	ttg gaa cgt tat aat caa gtg aaa aat	1200
Glu Ile Asp Ser Pro Ser Tyr	Leu Glu Arg Tyr Asn Gln Val Lys Asn	
	385 390 400	
att gtt gag aaa gta ctc aac	gaa gaa att ttg gac tta gcc gtg gaa	1248
Ile Val Glu Lys Val Leu Asn	Glu Glu Ile Leu Asp Leu Ala Val Glu	
	405 410 415	
aca atc aca cct tca att ttt	aag gaa taa	1278
Thr Ile Thr Pro Ser Ile Phe	Lys Glu	
	420 425	

<210> 9849

<211> 425

<212> PRT

<213> Haemophilus somnus 2336

<400> 9849

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

PF59083SeqList PF59083.txt

```

130      135      140
Asp Gly Leu Pro Ser Tyr Pro Asn Gly Trp Ser Ala Trp Ala Glu Gln
145 Val Lys Arg Leu Phe Lys Glu Lys Asn Val Asn Pro Ser Val Val Phe
165
Ser Ser Glu Ile Gln Asp Lys Val Pro Tyr Glu Lys Tyr Leu Asn Leu
180
Gln Val Glu Leu Val Asp Pro Lys Arg Arg Phe Leu Asn Ile Ser Ala
195
Thr Lys Ile Arg Asn Asn Pro Phe His Tyr Trp Lys Phe Ile Pro Lys
210
Glu Val Arg Pro Phe Phe Ala Lys Thr Ile Ala Ile Leu Gly Gly Glu
225 Ser Ser Gly Lys Thr Thr Leu Val Asn Lys Leu Ala Thr Val Phe Asn
245
Thr Thr Ser Ala Trp Glu Tyr Gly Arg Glu Phe Val Phe Glu Lys Leu
260
Gly Gly Asn Glu Gln Ala Met Gln Tyr Ser Asp Tyr Pro Gln Ile Ala
275
Leu Gly His Gln Arg Tyr Ile Asp Tyr Ala Val Arg His Ala His Lys
290
Val Ala Ile Val Asp Thr Asp Phe Ile Thr Thr Gln Ala Phe Cys Ile
305 Gln Tyr Glu Gly Lys Ala His Pro Phe Leu Asp Ser Met Ile Lys Glu
325
Tyr Pro Phe Asp Val Thr Ile Leu Leu Asn Asn Thr Gln Trp Val
340
Asp Asp Gly Leu Arg Ser Leu Gly Asn Ala Lys Gln Arg Gln Arg Phe
355
Gln Gln Leu Leu Lys Lys Leu Leu Asp Lys His Ser Val Pro Tyr Ile
370
Glu Ile Asp Ser Pro Ser Tyr Leu Glu Arg Tyr Asn Gln Val Lys Asn
385 Ile Val Glu Lys Val Leu Asn Glu Glu Ile Leu Asp Leu Ala Val Glu
405
Thr Ile Thr Pro Ser Ile Phe Lys Glu
420      425

```

<210> 9850

<211> 1224

<212> DNA

<213> Haemophilus influenzae R2846

<220>

<221> CDS

<222> (1)..(1224)

<223> transl_table=11

<400> 9850

```

atg cga gct aag tat aac gca aaa tac cta ggc act aaa tca gaa cgt      48
Met Arg Ala Lys Tyr Asn Ala Lys Tyr Leu Gly Thr Lys Ser Glu Arg
1      5      10      15
gaa aaa tat ttt cat tta gcc tac aat aaa cac act caa ttc tta cgc      96
Glu Lys Tyr Phe His Leu Ala Tyr Asn Lys His Thr Gln Phe Leu Arg
20      25      30
tat caa gag cag att atg tca aaa aca aaa gag aaa aaa gtc ggt gtc      144
Tyr Gln Glu Gln Ile Met Ser Lys Thr Lys Glu Lys Lys Val Gly Val
35      40      45
att ttc ggg aaa ttt tat cct gta cac aca ggt cat ata aat atg att      192
Ile Phe Gly Lys Phe Tyr Pro Val His Thr Gly His Ile Asn Met Ile
50      55      60
tat gaa gcg ttc agt aaa gtc gat gaa cta cac gtt atc gtg tgt agt      240
Tyr Glu Ala Phe Ser Lys Val Asp Glu Leu His Val Ile Val Cys Ser
65      70      75
gac act gtg cgc gat ttg aaa tta ttt tac gat agt aaa atg aaa cgc      288
Asp Thr Val Arg Asp Leu Lys Leu Phe Tyr Asp Ser Lys Met Lys Arg
85      90      95
atg cca acc gtg caa gat cgt ttg cgt tgg atg cag caa att ttc aaa      336
Met Pro Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln Ile Phe Lys

```

PF59083SeqList PF59083.txt

			100				105			110							
tat	caa	aaa	aat	cag	att	ttt	att	cat	cat	ttg	att	gaa	gac	ggt	att		384
Tyr	Gln	Lys	Asn	Gln	Ile	Phe	Ile	His	His	Leu	Ile	Glu	Asp	Gly	Ile		
		115					120					125					
cca	agt	tat	cca	aac	ggc	tgg	caa	tct	tgg	agt	gaa	gca	ggt	aaa	acc		432
Pro	Ser	Tyr	Pro	Asn	Gly	Trp	Gln	Ser	Trp	Ser	Glu	Ala	Val	Lys	Thr		
	130					135					140						
cta	ttt	cat	gaa	aaa	cat	ttt	gaa	cct	tca	atc	gta	ttt	agt	agc	gag		480
Leu	Phe	His	Glu	Lys	His	Phe	Glu	Pro	Ser	Ile	Val	Phe	Ser	Ser	Glu		
	145				150					155					160		
cct	caa	gat	aaa	gcg	cct	tac	gag	aaa	tac	tta	ggt	tta	gaa	gta	tcg		528
Pro	Gln	Asp	Lys	Ala	Pro	Tyr	Glu	Lys	Tyr	Leu	Gly	Leu	Glu	Val	Ser		
				165					170						175		
tta	gtc	gat	cct	gac	cgc	act	ttc	ttt	aat	gtg	tcc	gca	acc	aaa	att		576
Leu	Val	Asp	Pro	Asp	Arg	Thr	Phe	Asn	Val	Ser	Ala	Thr	Lys	Ile			
			180					185						190			
cgc	acc	act	cca	ttc	caa	tat	tgg	aag	ttt	att	ccg	aaa	gaa	gct	cgt		624
Arg	Thr	Thr	Pro	Phe	Gln	Tyr	Trp	Lys	Phe	Ile	Pro	Lys	Glu	Ala	Arg		
		195					200					205					
cct	ttc	ttt	gcc	aaa	acg	gtg	gcg	att	tta	ggg	gga	gaa	agc	agt	ggt		672
Pro	Phe	Phe	Ala	Lys	Thr	Val	Ala	Ile	Leu	Gly	Gly	Glu	Ser	Ser	Gly		
	210					215					220						
aaa	agc	gtg	cta	ggt	aat	aag	tta	gcc	gcc	gta	ttt	aat	acc	act	tct		720
Lys	Ser	Val	Leu	Val	Asn	Lys	Leu	Ala	Ala	Val	Phe	Asn	Thr	Thr	Ser		
	225				230					235					240		
gcg	tgg	gaa	tac	ggg	cg	gaa	ttt	gta	ttt	gaa	aag	ctc	ggt	ggc	gac		768
Ala	Trp	Glu	Tyr	Gly	Arg	Glu	Phe	Val	Phe	Glu	Lys	Leu	Gly	Gly	Asp		
			245					250						255			
gag	caa	gcg	atg	caa	tat	tct	gac	tat	ccg	caa	atg	gcg	ctt	ggt	cat		816
Glu	Gln	Ala	Met	Gln	Tyr	Ser	Asp	Tyr	Pro	Gln	Met	Ala	Leu	Gly	His		
			260					265						270			
caa	cga	tac	att	gat	tat	gcc	gtg	cg	cat	tct	cat	aaa	att	gca	ttt		864
Gln	Arg	Tyr	Ile	Asp	Tyr	Ala	Val	Arg	His	Ser	His	Lys	Ile	Ala	Phe		
		275					280					285					
att	gat	aca	gat	ttc	att	acc	acg	caa	gca	ttc	tgc	att	caa	tat	gaa		912
Ile	Asp	Thr	Asp	Phe	Ile	Thr	Thr	Gln	Ala	Phe	Cys	Ile	Gln	Tyr	Glu		
	290					295					300						
gga	aaa	gcc	cat	cct	ttt	tta	gac	tca	atg	att	aaa	gaa	tat	ccc	ttc		960
Gly	Lys	Ala	His	Pro	Phe	Leu	Asp	Ser	Met	Ile	Lys	Glu	Tyr	Pro	Phe		
					310					315					320		
gat	gtc	act	att	tta	ctt	aaa	aac	aat	act	gaa	tgg	gtg	gat	gat	ggc		1008
Asp	Val	Thr	Ile	Leu	Leu	Lys	Asn	Asn	Thr	Glu	Trp	Val	Asp	Asp	Gly		
				325					330					335			
ttg	cg	agc	tta	ggc	tca	caa	aaa	caa	cg	caa	caa	ttt	caa	caa	cta		1056
Leu	Arg	Ser	Leu	Gly	Ser	Gln	Lys	Gln	Arg	Gln	Gln	Phe	Gln	Gln	Leu		
			340					345						350			
ctc	aaa	aaa	ctg	tta	gat	aaa	tat	aaa	gtt	cct	tat	ata	gag	att	gaa		1104
Leu	Lys	Lys	Leu	Leu	Asp	Lys	Tyr	Lys	Val	Pro	Tyr	Ile	Glu	Ile	Glu		
		355					360					365					
tca	cca	agt	tat	ctt	gat	cg	tat	aac	caa	gtt	aaa	gca	gtc	att	gag		1152
Ser	Pro	Ser	Tyr	Leu	Asp	Arg	Tyr	Asn	Gln	Val	Lys	Ala	Val	Ile	Glu		
					375						380						
aaa	gtg	tta	aat	gaa	gag	gaa	atc	agt	gaa	tta	caa	aac	aca	acc	ttt		1200
Lys	Val	Leu	Asn	Glu	Glu	Glu	Ile	Ser	Glu	Leu	Gln	Asn	Thr	Thr	Phe		
	385				390					395					400		
cct	ata	aaa	ggg	aca	tct	caa	tga										1224
Pro	Ile	Lys	Gly	Thr	Ser	Gln											
				405													

<210> 9851

<211> 407

<212> PRT

<213> Haemophilus influenzae R2846

<400> 9851

Met Arg Ala Lys Tyr Asn Ala Lys Tyr Leu Gly Thr Lys Ser Glu Arg

1 5 10 15

Glu Lys Tyr Phe His Leu Ala Tyr Asn Lys His Thr Gln Phe Leu Arg

20 25 30

PF59083SeqList PF59083.txt

Tyr Gln Glu Gln Ile Met Ser Lys Thr Lys Glu Lys Val Gly Val
 35 40 45
 Ile Phe Gly Lys Phe Tyr Pro Val His Thr Gly His Ile Asn Met Ile
 50 55 60
 Tyr Glu Ala Phe Ser Lys Val Asp Glu Leu His Val Ile Val Cys Ser
 65 70 75 80
 Asp Thr Val Arg Asp Leu Lys Leu Phe Tyr Asp Ser Lys Met Lys Arg
 85 90 95
 Met Pro Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln Ile Phe Lys
 100 105 110
 Tyr Gln Lys Asn Gln Ile Phe Ile His His Leu Ile Glu Asp Gly Ile
 115 120 125
 Pro Ser Tyr Pro Asn Gly Trp Gln Ser Trp Ser Glu Ala Val Lys Thr
 130 135 140
 Leu Phe His Glu Lys His Phe Glu Pro Ser Ile Val Phe Ser Ser Glu
 145 150 155 160
 Pro Gln Asp Lys Ala Pro Tyr Glu Lys Tyr Leu Gly Leu Glu Val Ser
 165 170 175
 Leu Val Asp Pro Asp Arg Thr Phe Phe Asn Val Ser Ala Thr Lys Ile
 180 185 190
 Arg Thr Thr Pro Phe Gln Tyr Trp Lys Phe Ile Pro Lys Glu Ala Arg
 195 200 205
 Pro Phe Phe Ala Lys Thr Val Ala Ile Leu Gly Gly Glu Ser Ser Gly
 210 215 220
 Lys Ser Val Leu Val Asn Lys Leu Ala Ala Val Phe Asn Thr Thr Ser
 225 230 235 240
 Ala Trp Glu Tyr Gly Arg Glu Phe Val Phe Glu Lys Leu Gly Gly Asp
 245 250 255
 Glu Gln Ala Met Gln Tyr Ser Asp Tyr Pro Gln Met Ala Leu Gly His
 260 265 270
 Gln Arg Tyr Ile Asp Tyr Ala Val Arg His Ser His Lys Ile Ala Phe
 275 280 285
 Ile Asp Thr Asp Phe Ile Thr Thr Gln Ala Phe Cys Ile Gln Tyr Glu
 290 295 300
 Gly Lys Ala His Pro Phe Leu Asp Ser Met Ile Lys Glu Tyr Pro Phe
 305 310 315 320
 Asp Val Thr Ile Leu Leu Lys Asn Asn Thr Glu Trp Val Asp Asp Gly
 325 330 335
 Leu Arg Ser Leu Gly Ser Gln Lys Gln Arg Gln Gln Phe Gln Gln Leu
 340 345 350
 Leu Lys Lys Leu Leu Asp Lys Tyr Lys Val Pro Tyr Ile Glu Ile Glu
 355 360 365
 Ser Pro Ser Tyr Leu Asp Arg Tyr Asn Gln Val Lys Ala Val Ile Glu
 370 375 380
 Lys Val Leu Asn Glu Glu Ile Ser Glu Leu Gln Asn Thr Thr Phe
 385 390 395 400
 Pro Ile Lys Gly Thr Ser Gln
 405

<210> 9852
 <211> 1254
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1254)
 <223> transl_table=11

<400> 9852
 atg agg aat acg gag gga gat atg tcg tca ttt gat tac ctg aaa act 48
 Met Arg Asn Thr Glu Gly Asp Met Ser Ser Phe Asp Tyr Leu Lys Thr
 1 5 10 15
 gcc atc aag caa cag ggc tgc acg cta cag cag gtg gct gat gcc agc 96
 Ala Ile Lys Gln Gln Gly Cys Thr Leu Gln Gln Val Ala Asp Ala Ser
 20 25 30
 ggt atg acc aaa ggg tat tta agc cag tta ctg aat gcc aaa atc aaa 144
 Gly Met Thr Lys Gly Tyr Leu Ser Gln Leu Leu Asn Ala Lys Ile Lys
 35 40 45

PF59083SeqList PF59083.txt

agc	ccc	agc	gcg	caa	aag	ctg	gag	gcg	ttg	cac	cgt	ttt	ttg	ggg	ctt	192
Ser	Pro	Ser	Ala	Gln	Lys	Leu	Glu	Ala	Leu	His	Arg	Phe	Leu	Gly	Leu	
	50					55					60					
gag	ttt	ccc	cgg	cag	aag	aaa	acc	att	ggt	gtg	gta	ttc	ggt	aag	ttc	240
Glu	Phe	Pro	Arg	Gln	Lys	Lys	Thr	Ile	Gly	Val	Val	Phe	Gly	Lys	Phe	
65					70					75					80	
tac	ccg	ctg	cat	acc	gga	cat	atc	tac	ctt	atc	cag	cgc	gcc	tgt	agc	288
Tyr	Pro	Leu	His	Thr	Gly	His	Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Cys	Ser	
				85					90					95		
cag	gtt	gac	gaa	ctg	cat	atc	att	atg	ggt	ttt	gac	gat	acc	cgc	gat	336
Gln	Val	Asp	Glu	Leu	His	Ile	Ile	Met	Gly	Phe	Asp	Asp	Thr	Arg	Asp	
			100					105					110			
cgc	gcg	ttg	ttt	gaa	gac	agc	gct	atg	tcg	cag	cag	ccc	acc	gtg	ccg	384
Arg	Ala	Leu	Phe	Glu	Asp	Ser	Ala	Met	Ser	Gln	Gln	Pro	Thr	Val	Pro	
		115					120					125				
gat	cgt	ctg	cgc	tgg	tta	tta	caa	act	ttt	aaa	tat	cag	aaa	aat	att	432
Asp	Arg	Leu	Arg	Trp	Leu	Leu	Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile	
	130				135						140					
cgc	att	cat	gct	ttc	aac	gaa	gag	ggc	atg	gag	ccg	tat	ccg	cac	ggc	480
Arg	Ile	His	Ala	Phe	Asn	Glu	Glu	Gly	Met	Glu	Pro	Tyr	Pro	His	Gly	
145					150					155					160	
tgg	gat	gtg	tgg	agc	aac	ggc	atc	aaa	aag	ttt	atg	gct	gaa	aag	ggg	528
Trp	Asp	Val	Trp	Ser	Asn	Gly	Ile	Lys	Lys	Phe	Met	Ala	Glu	Lys	Gly	
				165					170					175		
att	cag	ccg	gac	ctg	atc	tac	acc	tcg	gaa	gaa	gcc	gat	gcg	cca	cag	576
Ile	Gln	Pro	Asp	Leu	Ile	Tyr	Thr	Ser	Glu	Glu	Ala	Asp	Ala	Pro	Gln	
			180					185					190			
tat	atg	gaa	cat	ctg	ggg	atc	gat	acg	gtg	ctg	gtc	gat	ccg	aaa	cgt	624
Tyr	Met	Glu	His	Leu	Gly	Ile	Asp	Thr	Val	Leu	Val	Asp	Pro	Lys	Arg	
		195					200					205				
acc	ttt	atg	agt	atc	agc	ggt	gcg	cag	atc	cgc	gaa	aac	ccg	ttc	cgc	672
Thr	Phe	Met	Ser	Ile	Ser	Gly	Ala	Gln	Ile	Arg	Glu	Asn	Pro	Phe	Arg	
	210					215					220					
tac	tgg	gaa	tat	att	cct	acg	gaa	gtg	aag	ccg	ttc	ttt	gta	cgt	acc	720
Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	
225					230					235					240	
gtg	gcg	atc	ctt	ggt	ggc	gag	tcg	aac	ggt	aaa	tcc	acc	ctg	gta	aac	768
Val	Ala	Ile	Leu	Gly	Gly	Glu	Ser	Asn	Gly	Lys	Ser	Thr	Leu	Val	Asn	
				245					250					255		
aaa	ctt	gcc	aat	atc	ttc	aat	acc	acc	agt	gcg	tgg	gaa	tat	ggt	cgc	816
Lys	Leu	Ala	Asn	Ile	Phe	Asn	Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	
			260					265					270			
gat	tat	gtc	ttt	tca	cac	ctc	ggc	ggt	gat	gag	atc	gca	ttg	cag	tat	864
Asp	Tyr	Val	Phe	Ser	His	Leu	Gly	Gly	Asp	Glu	Ile	Ala	Leu	Gln	Tyr	
		275					280					285				
tcc	gat	tac	gat	aaa	atc	gcg	ctg	ggc	cac	gca	caa	tac	att	gat	ttt	912
Ser	Asp	Tyr	Asp	Lys	Ile	Ala	Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe	
	290					295				300						
gca	gtg	aaa	tat	gcc	aat	aaa	gtg	gcg	ttt	att	gac	act	gat	ttt	gtc	960
Ala	Val	Lys	Tyr	Ala	Asn	Lys	Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	
305					310					315					320	
act	acc	cag	gcg	ttc	tgc	aaa	aag	tac	gaa	ggg	cgt	gag	cat	ccg	ttc	1008
Thr	Thr	Gln	Ala	Phe	Cys	Lys	Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	
				325					330					335		
gta	cag	gcg	ttg	att	gat	gaa	tac	cgt	ttc	gat	ctg	gtg	atc	ctg	ctg	1056
Val	Gln	Ala	Leu	Ile	Asp	Glu	Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	
			340					345					350			
gag	aac	aac	acg	ccg	tgg	gtg	gcg	gat	ggt	tta	cgc	agc	ctc	ggc	agt	1104
Glu	Asn	Asn	Thr	Pro	Trp	Val	Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	
		355					360					365				
tcg	gtg	gat	cgc	aaa	gag	ttc	cag	aac	ttg	ctg	gtg	gag	atg	ctg	gaa	1152
Ser	Val	Asp	Arg	Lys	Glu	Phe	Gln	Asn	Leu	Leu	Val	Glu	Met	Leu	Glu	
		370				375					380					
gag	aac	aat	atc	gaa	ttc	gtg	cgg	gtt	gaa	gag	gac	gat	tat	gac	agc	1200
Glu	Asn	Asn	Ile	Glu	Phe	Val	Arg	Val	Glu	Glu	Asp	Asp	Tyr	Asp	Ser	
					390					395					400	
cgt	ttc	ctg	cgc	tgc	gtg	gag	ctg	gtg	cgg	gag	atg	atg	ggg	gag	cag	1248
Arg	Phe	Leu	Arg	Cys	Val	Glu	Leu	Val	Arg	Glu	Met	Met	Gly	Glu	Gln	
				405					410					415		

aga taa
Arg

<210> 9853
<211> 417
<212> PRT
<213> Escherichia coli

<400> 9853
Met Arg Asn Thr Glu Gly Asp Met Ser Ser Phe Asp Tyr Leu Lys Thr
1 5 10 15
Ala Ile Lys Gln Gln Gly Cys Thr Leu Gln Gln Val Ala Asp Ala Ser
20 25 30
Gly Met Thr Lys Gly Tyr Leu Ser Gln Leu Leu Asn Ala Lys Ile Lys
35 40 45
Ser Pro Ser Ala Gln Lys Leu Glu Ala Leu His Arg Phe Leu Gly Leu
50 55 60
Glu Phe Pro Arg Gln Lys Lys Thr Ile Gly Val Val Phe Gly Lys Phe
65 70 75 80
Tyr Pro Leu His Thr Gly His Ile Tyr Leu Ile Gln Arg Ala Cys Ser
85 90 95
Gln Val Asp Glu Leu His Ile Ile Met Gly Phe Asp Asp Thr Arg Asp
100 105 110
Arg Ala Leu Phe Glu Asp Ser Ala Met Ser Gln Gln Pro Thr Val Pro
115 120 125
Asp Arg Leu Arg Trp Leu Leu Gln Thr Phe Lys Tyr Gln Lys Asn Ile
130 135 140
Arg Ile His Ala Phe Asn Glu Glu Gly Met Glu Pro Tyr Pro His Gly
145 150 155 160
Trp Asp Val Trp Ser Asn Gly Ile Lys Lys Phe Met Ala Glu Lys Gly
165 170 175
Ile Gln Pro Asp Leu Ile Tyr Thr Ser Glu Glu Ala Asp Ala Pro Gln
180 185 190
Tyr Met Glu His Leu Gly Ile Asp Thr Val Leu Val Asp Pro Lys Arg
195 200 205
Thr Phe Met Ser Ile Ser Gly Ala Gln Ile Arg Glu Asn Pro Phe Arg
210 215 220
Tyr Trp Glu Tyr Ile Pro Thr Glu Val Lys Pro Phe Phe Val Arg Thr
225 230 235 240
Val Ala Ile Leu Gly Gly Glu Ser Asn Gly Lys Ser Thr Leu Val Asn
245 250 255
Lys Leu Ala Asn Ile Phe Asn Thr Thr Ser Ala Trp Glu Tyr Gly Arg
260 265 270
Asp Tyr Val Phe Ser His Leu Gly Gly Asp Glu Ile Ala Leu Gln Tyr
275 280 285
Ser Asp Tyr Asp Lys Ile Ala Leu Gly His Ala Gln Tyr Ile Asp Phe
290 295 300
Ala Val Lys Tyr Ala Asn Lys Val Ala Phe Ile Asp Thr Asp Phe Val
305 310 315 320
Thr Thr Gln Ala Phe Cys Lys Lys Tyr Glu Gly Arg Glu His Pro Phe
325 330 335
Val Gln Ala Leu Ile Asp Glu Tyr Arg Phe Asp Leu Val Ile Leu Leu
340 345 350
Glu Asn Asn Thr Pro Trp Val Ala Asp Gly Leu Arg Ser Leu Gly Ser
355 360 365
Ser Val Asp Arg Lys Glu Phe Gln Asn Leu Leu Val Glu Met Leu Glu
370 375 380
Glu Asn Asn Ile Glu Phe Val Arg Val Glu Glu Asp Asp Tyr Asp Ser
385 390 395 400
Arg Phe Leu Arg Cys Val Glu Leu Val Arg Glu Met Met Gly Glu Gln
405 410 415
Arg

<210> 9854
<211> 1260
<212> DNA
<213> Salmonella paratyphi A

PF59083SeqList PF59083.txt

<220>
 <221> CDS
 <222> (1)..(1260)
 <223> transl_table=11

<400> 9854

atg cga ttt ttc cag cag gag gct ctt gtg tca tcg ttc gac tat ctc	48
Met Arg Phe Phe Gln Gln Glu Ala Leu Val Ser Ser Phe Asp Tyr Leu	
1 5 10 15	
aaa acc gcg att aag cag caa ggt tgc act ctg caa cag gtg gct gac	96
Lys Thr Ala Ile Lys Gln Gln Gly Cys Thr Leu Gln Gln Val Ala Asp	
20 25 30	
gcc agc ggt atg acc aag ggg tat ctg agt cag tta ctt aac gcc aaa	144
Ala Ser Gly Met Thr Lys Gly Tyr Leu Ser Gln Leu Asn Ala Lys	
35 40 45	
atc aaa agc ccc agc gcg caa aaa ctg gag gcg cta cac cgt ttt ctc	192
Ile Lys Ser Pro Ser Ala Gln Lys Leu Glu Ala Leu His Arg Phe Leu	
50 55 60	
ggg ctg gag ttt ccc cgc cga cag aaa aac att ggc gtg gtg ttc ggt	240
Gly Leu Glu Phe Pro Arg Gln Lys Asn Ile Gly Val Val Phe Gly	
65 70 75 80	
aaa ttt tat cca ttg cat acc ggg cac atc tac ttg atc cag cgc gcc	288
Lys Phe Tyr Pro Leu His Thr Gly His Ile Tyr Leu Ile Gln Arg Ala	
85 90 95	
tgt agc cag gtg gat gag ttg cac atc att atg gga tat gac gat acg	336
Cys Ser Gln Val Asp Glu Leu His Ile Ile Met Gly Tyr Asp Asp Thr	
100 105 110	
cgc gac cgc ggg ctg ttt gaa gat agc gcc atg tcg cag cag ccc acc	384
Arg Asp Arg Gly Leu Phe Glu Asp Ser Ala Met Ser Gln Gln Pro Thr	
115 120 125	
gtg tcg gat cgc ctg cgc tgg tta ttg caa acc ttc aaa tac caa aaa	432
Val Ser Asp Arg Leu Arg Trp Leu Leu Gln Thr Phe Lys Tyr Gln Lys	
130 135 140	
aat att cgc atc cac gcc ttt aat gaa gag ggg atg gag cct tat ccg	480
Asn Ile Arg Ile His Ala Phe Asn Glu Glu Gly Met Glu Pro Tyr Pro	
145 150 155 160	
cat ggc tgg gac gtc tgg agc aac ggc att aaa gcg ttt atg gca gag	528
His Gly Trp Asp Val Trp Ser Asn Gly Ile Lys Ala Phe Met Ala Glu	
165 170 175	
aag gga ata cag ccg agc tgg atc tac act tcc gaa gag gct gat gcg	576
Lys Gly Ile Gln Pro Ser Trp Ile Tyr Thr Ser Glu Glu Ala Asp Ala	
180 185 190	
ccg cag tat ctt gag cat tta ggg att gag acg gtg ctg gtc gat cct	624
Pro Gln Tyr Leu Glu His Leu Gly Ile Glu Thr Val Leu Val Asp Pro	
195 200 205	
gaa cgc acg ttt atg aat atc agc ggg gcg caa atc cgc gaa aat ccg	672
Glu Arg Thr Phe Met Asn Ile Ser Gly Ala Gln Ile Arg Glu Asn Pro	
210 215 220	
ttt cgt tac tgg gaa tat att cct acc gaa gtg ccg ttt ttt gtg	720
Phe Arg Tyr Trp Glu Tyr Ile Pro Thr Glu Val Lys Pro Phe Phe Val	
225 230 235 240	
cgt acc gtc gcg att ctg ggc ggg gaa tca agc ggc aag tct acg ctg	768
Arg Thr Val Ala Ile Leu Gly Gly Glu Ser Ser Gly Lys Ser Thr Leu	
245 250 255	
gtc aat aag ctc gcc aat att ttt aat acc acc agc gcc tgg gaa tat	816
Val Asn Lys Leu Ala Asn Ile Phe Asn Thr Thr Ser Ala Trp Glu Tyr	
260 265 270	
ggc cgc gac tat gtc ttt tcg cat ctg ggc ggc gat gag ata gcg tta	864
Gly Arg Asp Tyr Val Phe Ser His Leu Gly Gly Asp Glu Ile Ala Leu	
275 280 285	
cag tat tcc gac tac gat aaa att gcg ctg ggc cat gcg caa tat att	912
Gln Tyr Ser Asp Tyr Asp Lys Ile Ala Leu Gly His Ala Gln Tyr Ile	
290 295 300	
gat ttc gca gtg aaa tat gcg aat aaa gtg gcg ttt atc gat acc gat	960
Asp Phe Ala Val Lys Tyr Ala Asn Lys Val Ala Phe Ile Asp Thr Asp	
305 310 315 320	
ttc gtc acc acc cag gca ttt tgc aaa aaa tac gaa ggg cgc gag cat	1008
Phe Val Thr Thr Gln Ala Phe Cys Lys Lys Tyr Glu Gly Arg Glu His	

PF59083SeqList PF59083.txt

ccg	ttt	gtc	cag	gcg	ctg	atc	gac	gag	tat	cgc	ttc	gac	ctg	gtg	att	1056
Pro	Phe	Val	Gln	Ala	Leu	Ile	Asp	Glu	Tyr	Arg	Phe	Asp	Leu	Val	Ile	
			340					345					350			
ttg	ctg	gag	aat	aat	acg	ccg	tgg	gta	gct	gac	gga	ctg	cga	agc	ctg	1104
Leu	Leu	Glu	Asn	Asn	Thr	Pro	Trp	Val	Ala	Asp	Gly	Leu	Arg	Ser	Leu	
		355					360					365				
ggc	agt	tca	gtg	gat	cgc	aaa	gcg	ttc	cag	agc	ctg	ttg	gtc	gag	atg	1152
Gly	Ser	Ser	Val	Asp	Arg	Lys	Ala	Phe	Gln	Ser	Leu	Leu	Val	Glu	Met	
	370					375					380					
ctg	aaa	gag	aac	aac	att	gag	ttc	gtt	cac	gtt	aaa	gag	gct	gat	tac	1200
Leu	Lys	Glu	Asn	Asn	Ile	Glu	Phe	Val	His	Val	Lys	Glu	Ala	Asp	Tyr	
	385				390					395					400	
gat	ggc	cgt	ttt	ttg	cgt	tgt	gtg	gaa	ctg	gtg	aaa	gag	atg	atg	ggc	1248
Asp	Gly	Arg	Phe	Leu	Arg	Cys	Val	Glu	Leu	Val	Lys	Glu	Met	Met	Gly	
			405					410						415		
gag	cag	gga	taa													1260
Glu	Gln	Gly														

<210> 9855

<211> 419

<212> PRT

<213> Salmonella paratyphi A

<400> 9855

Met	Arg	Phe	Phe	Gln	Gln	Glu	Ala	Leu	Val	Ser	Ser	Phe	Asp	Tyr	Leu	
1				5					10					15		
Lys	Thr	Ala	Ile	Lys	Gln	Gln	Gly	Cys	Thr	Leu	Gln	Gln	Val	Ala	Asp	
			20					25					30			
Ala	Ser	Gly	Met	Thr	Lys	Gly	Tyr	Leu	Ser	Gln	Leu	Leu	Asn	Ala	Lys	
		35					40					45				
Ile	Lys	Ser	Pro	Ser	Ala	Gln	Lys	Leu	Glu	Ala	Leu	His	Arg	Phe	Leu	
	50				55					60						
Gly	Leu	Glu	Phe	Pro	Arg	Arg	Gln	Lys	Asn	Ile	Gly	Val	Val	Phe	Gly	
65					70				75						80	
Lys	Phe	Tyr	Pro	Leu	His	Thr	Gly	His	Ile	Tyr	Leu	Ile	Gln	Arg	Ala	
			85					90					95			
Cys	Ser	Gln	Val	Asp	Glu	Leu	His	Ile	Ile	Met	Gly	Tyr	Asp	Asp	Thr	
		100					105						110			
Arg	Asp	Arg	Gly	Leu	Phe	Glu	Asp	Ser	Ala	Met	Ser	Gln	Gln	Pro	Thr	
	115						120					125				
Val	Ser	Asp	Arg	Leu	Arg	Trp	Leu	Leu	Gln	Thr	Phe	Lys	Tyr	Gln	Lys	
	130					135					140					
Asn	Ile	Arg	Ile	His	Ala	Phe	Asn	Glu	Glu	Gly	Met	Glu	Pro	Tyr	Pro	
145					150					155					160	
His	Gly	Trp	Asp	Val	Trp	Ser	Asn	Gly	Ile	Lys	Ala	Phe	Met	Ala	Glu	
			165					170					175			
Lys	Gly	Ile	Gln	Pro	Ser	Trp	Ile	Tyr	Thr	Ser	Glu	Glu	Ala	Asp	Ala	
		180					185					190				
Pro	Gln	Tyr	Leu	Glu	His	Leu	Gly	Ile	Glu	Thr	Val	Leu	Val	Asp	Pro	
	195						200					205				
Glu	Arg	Thr	Phe	Met	Asn	Ile	Ser	Gly	Ala	Gln	Ile	Arg	Glu	Asn	Pro	
	210				215						220					
Phe	Arg	Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	Glu	Val	Lys	Pro	Phe	Phe	Val	
225					230					235					240	
Arg	Thr	Val	Ala	Ile	Leu	Gly	Gly	Glu	Ser	Ser	Gly	Lys	Ser	Thr	Leu	
			245					250					255			
Val	Asn	Lys	Leu	Ala	Asn	Ile	Phe	Asn	Thr	Thr	Ser	Ala	Trp	Glu	Tyr	
		260					265					270				
Gly	Arg	Asp	Tyr	Val	Phe	Ser	His	Leu	Gly	Gly	Asp	Glu	Ile	Ala	Leu	
		275					280					285				
Gln	Tyr	Ser	Asp	Tyr	Asp	Lys	Ile	Ala	Leu	Gly	His	Ala	Gln	Tyr	Ile	
	290				295						300					
Asp	Phe	Ala	Val	Lys	Tyr	Ala	Asn	Lys	Val	Ala	Phe	Ile	Asp	Thr	Asp	
305					310					315					320	
Phe	Val	Thr	Thr	Gln	Ala	Phe	Cys	Lys	Lys	Tyr	Glu	Gly	Arg	Glu	His	
			325					330					335			
Pro	Phe	Val	Gln	Ala	Leu	Ile	Asp	Glu	Tyr	Arg	Phe	Asp	Leu	Val	Ile	

PF59083SeqList PF59083.txt

340 345 350
 Leu Leu Glu Asn Asn Thr Pro Trp Val Ala Asp Gly Leu Arg Ser Leu
 355 360 365
 Gly Ser Ser Val Asp Arg Lys Ala Phe Gln Ser Leu Leu Val Glu Met
 370 375 380
 Leu Lys Glu Asn Asn Ile Phe Val His Val Lys Glu Ala Asp Tyr
 385 390 395 400
 Asp Gly Arg Phe Leu Arg Cys Val Glu Leu Val Lys Glu Met Met Gly
 405 410 415
 Glu Gln Gly

<210> 9856
 <211> 1257
 <212> DNA
 <213> Photorhabdus luminescens subsp

<220>
 <221> CDS
 <222> (1)..(1257)
 <223> transl_table=11

<400> 9856
 ttg att aaa cag gga gga gat atg ggg caa ttt gac tac ctt aaa gaa 48
 Met Ile Lys Gln Gly Gly Asp Met Gly Gln Phe Asp Tyr Leu Lys Glu
 1 5 10 15
 gcg att aaa cag aca ggt tat acg ttg caa cag gtt gcc gat gca agt 96
 Ala Ile Lys Gln Thr Gly Tyr Thr Leu Gln Gln Val Ala Asp Ala Ser
 20 25 30
 ggt atg acc aaa ggt tat ctt agc caa tta att aat gac aaa att aaa 144
 Gly Met Thr Lys Gly Tyr Leu Ser Gln Leu Ile Asn Asp Lys Ile Lys
 35 40 45
 agt cct agt gcc caa aaa ctg gcg gcg ctc cat cac tat ctg agg ttg 192
 Ser Pro Ser Ala Gln Lys Leu Ala Ala Leu His His Tyr Leu Arg Leu
 50 55 60
 caa tat cct gtg caa aat aaa act gtt gga gtg gta ttc ggc aaa ttc 240
 Gln Tyr Pro Val Gln Asn Lys Thr Val Gly Val Val Phe Gly Lys Phe
 65 70 75 80
 tat cca ttg cat act ggg cat atc tat ctg att caa cgg gcc tgt agt 288
 Tyr Pro Leu His Thr Gly His Ile Tyr Leu Ile Gln Arg Ala Cys Ser
 85 90 95
 cag gtg gat gag ttg cat att atc ctt tgc cat gat gag cct aga gat 336
 Gln Val Asp Glu Leu His Ile Ile Leu Cys His Asp Glu Pro Arg Asp
 100 105 110
 cgg gag cta ttt atg agt agt tcc atg tct cag caa ccc acg gtg agt 384
 Arg Glu Leu Phe Met Ser Ser Ser Met Ser Gln Gln Pro Thr Val Ser
 115 120 125
 gat cgc ttg cgc tgg ttg ctt caa aca ttt aag tat cag aaa aat att 432
 Asp Arg Leu Arg Trp Leu Leu Gln Thr Phe Lys Tyr Gln Lys Asn Ile
 130 135 140
 cat att cac tct ttt gat gaa cag gga att gaa ccc tat cca cat ggt 480
 His Ile His Ser Phe Asp Glu Gln Gly Ile Glu Pro Tyr Pro His Gly
 145 150 155 160
 tgg gat gtg tgg agt gat ggc atg aaa gcc ttt atg tca aag aaa ggc 528
 Trp Asp Val Trp Ser Asp Gly Met Lys Ala Phe Met Ser Lys Lys Gly
 165 170 175
 att cat ccc act tat ata tat tcc agc gaa act cag gat tct ccc cga 576
 Ile His Pro Thr Tyr Ile Tyr Ser Ser Glu Thr Gln Asp Ser Pro Arg
 180 185 190
 tat aaa gag cat tta gga att gag aca att ctt atc gat cca caa cgt 624
 Tyr Lys Glu His Leu Gly Ile Glu Thr Ile Leu Ile Asp Pro Gln Arg
 195 200 205
 tcg ttt atg aaa atc agt ggt cgg cat att cgc caa gat cca ttc cgt 672
 Ser Phe Met Lys Ile Ser Gly Arg His Ile Arg Gln Asp Pro Phe Arg
 210 215 220
 cat tgg gaa tat att cct acc gaa gtg aaa cct ttc ttt gtt cgt acc 720
 His Trp Glu Tyr Ile Pro Thr Glu Val Lys Pro Phe Phe Val Arg Thr
 225 230 235 240
 gta gcg att ctt ggt gga gaa tct agt ggt aaa tct aca tta gtt aac 768

PF59083SeqList PF59083.txt

Val	Ala	Ile	Leu	Gly	Gly	Glu	Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	
aaa	ttg	gca	aat	att	ttt	aat	acg	aca	agt	gct	tgg	gaa	tat	ggg	cgt	816
Lys	Leu	Ala	Asn	Ile	Phe	Asn	Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	
			260					265					270			
gat	tat	gtt	ttt	tct	cat	ctg	ggg	gga	gat	gag	atg	gcg	cta	caa	tat	864
Asp	Tyr	Val	Phe	Ser	His	Leu	Gly	Gly	Asp	Glu	Met	Ala	Leu	Gln	Tyr	
		275					280					285				
tcg	gac	tat	gac	aag	att	gca	ttg	gga	caa	gcc	caa	tat	att	gat	ttt	912
Ser	Asp	Tyr	Asp	Lys	Ile	Ala	Leu	Gly	Gln	Ala	Gln	Tyr	Ile	Asp	Phe	
	290					295					300					
gcc	gta	aaa	tat	gcg	aat	aag	gtt	aca	ttt	atc	gat	acc	gat	ttt	gtc	960
Ala	Val	Lys	Tyr	Ala	Asn	Lys	Val	Thr	Phe	Ile	Asp	Thr	Asp	Phe	Val	
305					310				315						320	
act	acc	caa	gca	ttc	tgt	aag	cga	tat	gaa	gga	cgt	gaa	cac	ccg	ttt	1008
Thr	Thr	Gln	Ala	Phe	Cys	Lys	Arg	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	
				325					330					335		
gtt	cag	gca	tta	att	gat	gaa	tac	cga	ttt	gat	ttg	gtc	att	cta	ctg	1056
Val	Gln	Ala	Leu	Ile	Asp	Glu	Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	
			340					345					350			
gaa	aac	aac	act	cct	tgg	gtt	gct	gac	ggg	ttg	cgt	agc	ctt	ggc	agc	1104
Glu	Asn	Asn	Thr	Pro	Trp	Val	Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	
		355					360					365				
gag	cag	gat	cgt	aaa	gcg	ttt	cag	caa	ctg	ctg	gag	gat	atg	ctg	aaa	1152
Glu	Gln	Asp	Arg	Lys	Ala	Phe	Gln	Gln	Leu	Leu	Glu	Asp	Met	Leu	Lys	
	370					375					380					
agt	aat	aat	att	gaa	tat	gtc	aat	gtg	gat	tca	ccc	gat	tat	gat	cag	1200
Ser	Asn	Asn	Ile	Glu	Tyr	Val	Asn	Val	Asp	Ser	Pro	Asp	Tyr	Asp	Gln	
385					390				395						400	
cgt	ttc	cta	cgt	tgt	att	gag	ctc	att	cag	caa	ctt	tta	gcg	gct	aat	1248
Arg	Phe	Leu	Arg	Cys	Ile	Glu	Leu	Ile	Gln	Gln	Leu	Leu	Ala	Ala	Asn	
				405					410					415		
cct	aaa	tga														1257
Pro	Lys															

<210> 9857

<211> 418

<212> PRT

<213> Photorhabdus luminescens subsp

<400> 9857

Met	Ile	Lys	Gln	Gly	Gly	Asp	Met	Gly	Gln	Phe	Asp	Tyr	Leu	Lys	Glu	
1				5					10					15		
Ala	Ile	Lys	Gln	Thr	Gly	Tyr	Thr	Leu	Gln	Gln	Val	Ala	Asp	Ala	Ser	
			20					25					30			
Gly	Met	Thr	Lys	Gly	Tyr	Leu	Ser	Gln	Leu	Ile	Asn	Asp	Lys	Ile	Lys	
		35					40					45				
Ser	Pro	Ser	Ala	Gln	Lys	Leu	Ala	Ala	Leu	His	His	Tyr	Leu	Arg	Leu	
	50					55					60					
Gln	Tyr	Pro	Val	Gln	Asn	Lys	Thr	Val	Gly	Val	Val	Phe	Gly	Lys	Phe	
65					70				75						80	
Tyr	Pro	Leu	His	Thr	Gly	His	Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Cys	Ser	
			85						90					95		
Gln	Val	Asp	Glu	Leu	His	Ile	Ile	Leu	Cys	His	Asp	Glu	Pro	Arg	Asp	
		100						105					110			
Arg	Glu	Leu	Phe	Met	Ser	Ser	Ser	Met	Ser	Gln	Gln	Pro	Thr	Val	Ser	
		115					120					125				
Asp	Arg	Leu	Arg	Trp	Leu	Leu	Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile	
	130					135					140					
His	Ile	His	Ser	Phe	Asp	Glu	Gln	Gly	Ile	Glu	Pro	Tyr	Pro	His	Gly	
145					150				155						160	
Trp	Asp	Val	Trp	Ser	Asp	Gly	Met	Lys	Ala	Phe	Met	Ser	Lys	Lys	Gly	
			165						170					175		
Ile	His	Pro	Thr	Tyr	Ile	Tyr	Ser	Ser	Glu	Thr	Gln	Asp	Ser	Pro	Arg	
			180					185					190			
Tyr	Lys	Glu	His	Leu	Gly	Ile	Glu	Thr	Ile	Leu	Ile	Asp	Pro	Gln	Arg	
		195					200					205				
Ser	Phe	Met	Lys	Ile	Ser	Gly	Arg	His	Ile	Arg	Gln	Asp	Pro	Phe	Arg	

PF59083SeqList PF59083.txt

```

210      215      220
His Trp Glu Tyr Ile Pro Thr Glu Val Lys Pro Phe Phe Val Arg Thr
225 Val Ala Ile Leu Gly Gly Glu Ser Ser Gly Lys Ser Thr Leu Val Asn
245
Lys Leu Ala Asn Ile Phe Asn Thr Thr Ser Ala Trp Glu Tyr Gly Arg
260
Asp Tyr Val Phe Ser His Leu Gly Gly Asp Glu Met Ala Leu Gln Tyr
275
Ser Asp Tyr Asp Lys Ile Ala Leu Gly Gln Ala Gln Tyr Ile Asp Phe
290
Ala Val Lys Tyr Ala Asn Lys Val Thr Phe Ile Asp Thr Asp Phe Val
305
Thr Thr Gln Ala Phe Cys Lys Arg Tyr Glu Gly Arg Glu His Pro Phe
325
Val Gln Ala Leu Ile Asp Glu Tyr Arg Phe Asp Leu Val Ile Leu Leu
340
Glu Asn Asn Thr Pro Trp Val Ala Asp Gly Leu Arg Ser Leu Gly Ser
355
Glu Gln Asp Arg Lys Ala Phe Gln Gln Leu Leu Glu Asp Met Leu Lys
370
Ser Asn Asn Ile Glu Tyr Val Asn Val Asp Ser Pro Asp Tyr Asp Gln
385
Arg Phe Leu Arg Cys Ile Glu Leu Ile Gln Gln Leu Leu Ala Ala Asn
405
Pro Lys

```

<210> 9858
 <211> 1254
 <212> DNA
 <213> Shigella flexneri

<220>
 <221> CDS
 <222> (1)..(1254)
 <223> transl_table=11

```

<400> 9858
atg aga gat acg gag gga gat atg tcg tca ttt gat tac ctg aaa act      48
Met Arg Asp Thr Glu Gly Asp Met Ser Ser Phe Asp Tyr Leu Lys Thr
1      5      10      15
gcc atc aag caa cag ggc tgc acg cta cag cag gta gct gat gcc agc      96
Ala Ile Lys Gln Gln Gly Cys Thr Leu Gln Gln Val Ala Asp Ala Ser
20      25      30
ggg atg acc aaa ggg tat tta agc cag tta ctg aat gcc aaa att aaa      144
Gly Met Thr Lys Gly Tyr Leu Ser Gln Leu Leu Asn Ala Lys Ile Lys
35      40      45
agc ccc agc gcg caa aag ctg gag gca ttg cac cgt ttt ttg ggg ctt      192
Ser Pro Ser Ala Gln Lys Leu Glu Ala Leu His Arg Phe Leu Gly Leu
50      55      60
gaa ttt ccc cgg cag aag aaa acc att ggt gtc gta ttc ggt aag ttc      240
Glu Phe Pro Arg Gln Lys Lys Thr Ile Gly Val Val Phe Gly Lys Phe
65      70      75
tac ccg ctg cat acc gga cat atc tac ctt atc cag cgc gcc tgt agc      288
Tyr Pro Leu His Thr Gly His Ile Tyr Leu Ile Gln Arg Ala Cys Ser
85      90      95
cag gtt gac gag ctg cat atc att atg ggt ttt gac gat acc cgc gac      336
Gln Val Asp Glu Leu His Ile Ile Met Gly Phe Asp Asp Thr Arg Asp
100      105      110
cgc gcg ttg ttt gaa gac agc gcc atg tcg cag cag ccc acg gtg ccg      384
Arg Ala Leu Phe Glu Asp Ser Ala Met Ser Gln Gln Pro Thr Val Pro
115      120      125
gat cgt ctg cgc tgg cta ttg caa acc ttt aaa tat cag aaa aat atc      432
Asp Arg Leu Arg Trp Leu Leu Gln Thr Phe Lys Tyr Gln Lys Asn Ile
130      135      140
cgt att cat gct ttc aac gaa gag ggc atg gag ccg tat ccg cat ggc      480
Arg Ile His Ala Phe Asn Glu Glu Gly Met Glu Pro Tyr Pro His Gly
145      150      155      160

```

PF59083SeqList PF59083.txt

tgg	gat	gtg	tgg	agc	aac	ggc	atc	aaa	aag	ttt	atg	gct	gaa	aag	ggg	528
Trp	Asp	Val	Trp	Ser	Asn	Gly	Ile	Lys	Lys	Phe	Met	Ala	Glu	Lys	Gly	
				165					170					175		
atc	cag	ccg	gac	ctg	atc	tac	acc	tcg	gaa	gaa	gcc	gat	gcg	cca	cag	576
Ile	Gln	Pro	Asp	Leu	Ile	Tyr	Thr	Ser	Glu	Glu	Ala	Asp	Ala	Pro	Gln	
			180					185					190			
tat	atg	gaa	cat	ctg	ggg	atc	gag	acg	gtg	ctg	gtc	gat	ccg	aaa	cgt	624
Tyr	Met	Glu	His	Leu	Gly	Ile	Glu	Thr	Val	Leu	Val	Asp	Pro	Lys	Arg	
		195				200					205					
acc	ttt	atg	agt	atc	agc	ggg	gcg	cag	atc	cg	gaa	aac	ccg	ttc	cg	672
Thr	Phe	Met	Ser	Ile	Ser	Gly	Ala	Gln	Ile	Arg	Glu	Asn	Pro	Phe	Arg	
	210					215					220					
tac	tgg	gaa	tat	att	cct	acc	gaa	gtg	aag	ccg	ttt	ttt	gtg	cgt	acc	720
Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	
	225				230					235					240	
gtg	gcg	atc	ctt	ggc	ggc	gag	tcg	agc	ggg	aaa	tcc	acc	ttg	gta	aac	768
Val	Ala	Ile	Leu	Gly	Gly	Glu	Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	
				245					250					255		
aaa	ctt	gcc	aat	atc	ttc	aac	acc	acc	agt	gcg	tgg	gaa	tat	ggc	cg	816
Lys	Leu	Ala	Asn	Ile	Phe	Asn	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg		
			260				265						270			
gat	tat	gtc	ttt	tca	cac	ctc	ggc	ggg	gat	gag	atc	gca	ttg	cag	tat	864
Asp	Tyr	Val	Phe	Ser	His	Leu	Gly	Gly	Asp	Glu	Ile	Ala	Leu	Gln	Tyr	
		275					280					285				
tcc	gac	tac	gat	aaa	atc	gcg	ttg	ggg	cac	gca	caa	tac	att	gat	ttt	912
Ser	Asp	Tyr	Asp	Lys	Ile	Ala	Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe	
	290					295					300					
gca	gtg	aaa	tac	gcc	aat	aaa	gtg	gcg	ttt	att	gac	acc	gat	ttt	gtc	960
Ala	Val	Lys	Tyr	Ala	Asn	Lys	Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	
	305				310					315					320	
act	acc	cag	gcg	ttc	tgc	aaa	aag	tac	gaa	ggg	cgt	gag	cat	ccg	ttc	1008
Thr	Thr	Gln	Ala	Phe	Cys	Lys	Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	
			325						330					335		
gtg	cag	gcg	ctg	att	gat	gaa	tac	cgt	ttc	gat	ctg	gtg	atc	ctg	ctg	1056
Val	Gln	Ala	Leu	Ile	Asp	Glu	Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	
			340				345						350			
gag	aac	aac	acg	ccg	tgg	gtg	gcg	gat	ggg	tta	cg	agc	ctc	ggc	agt	1104
Glu	Asn	Asn	Thr	Pro	Trp	Val	Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	
		355				360					365					
tcg	gtg	gat	cg	aaa	gag	ttc	cag	aac	ttg	ctg	gtg	gag	atg	ctg	gaa	1152
Ser	Val	Asp	Arg	Lys	Glu	Phe	Gln	Asn	Leu	Leu	Val	Glu	Met	Leu	Glu	
	370					375					380					
gag	aac	aat	atc	gaa	ttc	gtg	cgg	gtt	gaa	gag	gac	gat	tac	gac	agc	1200
Glu	Asn	Asn	Ile	Glu	Phe	Val	Arg	Val	Glu	Glu	Asp	Asp	Tyr	Asp	Ser	
	385				390					395					400	
cgt	ttc	ctg	cg	tgc	gtg	gag	ctg	gtg	cgg	gag	atg	atg	ggg	gag	caa	1248
Arg	Phe	Leu	Arg	Cys	Val	Glu	Leu	Val	Arg	Glu	Met	Met	Gly	Glu	Gln	
				405					410					415		
gga	taa															1254
Gly																

<210> 9859

<211> 417

<212> PRT

<213> Shigella flexneri

<400> 9859

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

PF59083SeqList PF59083.txt

85 90 95
 Gln Val Asp Glu Leu His Ile Ile Met Gly Phe Asp Asp Thr Arg Asp
 100 105 110
 Arg Ala Leu Phe Glu Asp Ser Ala Met Ser Gln Gln Pro Thr Val Pro
 115 120 125
 Asp Arg Leu Arg Trp Leu Leu Thr Phe Lys Tyr Gln Lys Asn Ile
 130 135 140
 Arg Ile His Ala Phe Asn Glu Glu Gly Met Glu Pro Tyr Pro His Gly
 145 150 155 160
 Trp Asp Val Trp Ser Asn Gly Ile Lys Lys Phe Met Ala Glu Lys Gly
 165 170 175
 Ile Gln Pro Asp Leu Ile Tyr Thr Ser Glu Glu Ala Asp Ala Pro Gln
 180 185 190
 Tyr Met Glu His Leu Gly Ile Glu Thr Val Leu Val Asp Pro Lys Arg
 195 200 205
 Thr Phe Met Ser Ile Ser Gly Ala Gln Ile Arg Glu Asn Pro Phe Arg
 210 215 220
 Tyr Trp Glu Tyr Ile Pro Thr Glu Val Lys Pro Phe Phe Val Arg Thr
 225 230 235 240
 Val Ala Ile Leu Gly Glu Ser Ser Gly Lys Ser Thr Leu Val Asn
 245 250 255
 Lys Leu Ala Asn Ile Phe Asn Thr Thr Ser Ala Trp Glu Tyr Gly Arg
 260 265 270
 Asp Tyr Val Phe Ser His Leu Gly Gly Asp Glu Ile Ala Leu Gln Tyr
 275 280 285
 Ser Asp Tyr Asp Lys Ile Ala Leu Gly His Ala Gln Tyr Ile Asp Phe
 290 295 300
 Ala Val Lys Tyr Ala Asn Lys Val Ala Phe Ile Asp Thr Asp Phe Val
 305 310 315 320
 Thr Thr Gln Ala Phe Cys Lys Lys Tyr Glu Gly Arg Glu His Pro Phe
 325 330 335
 Val Gln Ala Leu Ile Asp Glu Tyr Arg Phe Asp Leu Val Ile Leu Leu
 340 345 350
 Glu Asn Asn Thr Pro Trp Val Ala Asp Gly Leu Arg Ser Leu Gly Ser
 355 360 365
 Ser Val Asp Arg Lys Glu Phe Gln Asn Leu Leu Val Glu Met Leu Glu
 370 375 380
 Glu Asn Asn Ile Glu Phe Val Arg Val Glu Glu Asp Asp Tyr Asp Ser
 385 390 400
 Arg Phe Leu Arg Cys Val Glu Leu Val Arg Glu Met Met Gly Glu Gln
 405 410 415
 Gly

<210> 9860
 <211> 1254
 <212> DNA
 <213> Escherichia coli 06

<220>
 <221> CDS
 <222> (1)..(1254)
 <223> transl_table=11

<400> 9860
 atg aga gat acg gag gga gat atg tcg tca ttt gat tac ctg aaa act 48
 Met Arg Asp Thr Glu Gly Asp Met Ser Ser Phe Asp Tyr Leu Lys Thr
 1 5 10 15
 gcc att aag caa cag ggc tgc acg cta cag cag gta gct gat gcc agc 96
 Ala Ile Lys Gln Gln Gly Cys Thr Leu Gln Gln Val Ala Asp Ala Ser
 20 25 30
 ggt atg acc aaa ggg tat tta agc cag tta ctg aat gcc aaa att aaa 144
 Gly Met Thr Lys Gly Tyr Leu Ser Gln Leu Leu Asn Ala Lys Ile Lys
 35 40 45
 agc ccc agc gcg caa aaa ctg gag gca ttg cac cgt ttt ttg ggg ctt 192
 Ser Pro Ser Ala Gln Lys Leu Glu Ala Leu His Arg Phe Leu Gly Leu
 50 55 60
 gag ttt ccc cgg cag aag aaa acg atc ggt gtc gta ttc ggt aag ttt 240
 Glu Phe Pro Arg Gln Lys Lys Thr Ile Gly Val Val Phe Gly Lys Phe
 65 70 75 80 85 90 95
 Seite 10376

PF59083SeqList PF59083.txt

65					70					75					80	
tac	ccg	ctg	cat	act	gga	cat	atc	tac	ctt	atc	cag	cgc	gcc	tgt	agc	288
Tyr	Pro	Leu	His	Thr	Gly	His	Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Cys	Ser	
				85					90					95		
cag	gtt	gac	gag	ctg	cat	atc	att	atg	ggg	ttt	gac	gat	acc	cgc	gac	336
Gln	Val	Asp	Glu	Leu	His	Ile	Ile	Met	Gly	Phe	Asp	Asp	Thr	Arg	Asp	
			100					105					110			
cgc	gca	ttg	ttc	gaa	gac	agc	gcc	atg	tcg	cag	cag	cca	acc	gtg	ccg	384
Arg	Ala	Leu	Phe	Glu	Asp	Ser	Ala	Met	Ser	Gln	Gln	Pro	Thr	Val	Pro	
		115					120					125				
gat	cgt	ctg	cgc	tgg	tta	ttg	cag	acc	ttt	aag	tat	caa	aaa	aat	atc	432
Asp	Arg	Leu	Arg	Trp	Leu	Leu	Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile	
	130				135						140					
cgc	att	cat	gct	ttt	aac	gaa	gag	ggc	atg	gaa	ccg	tat	cca	cat	ggc	480
Arg	Ile	His	Ala	Phe	Asn	Glu	Glu	Gly	Met	Glu	Pro	Tyr	Pro	His	Gly	
	145				150					155					160	
tgg	gat	gtg	tgg	agc	aac	ggc	atc	aaa	aag	ttt	atg	gcc	gaa	aaa	ggc	528
Trp	Asp	Val	Trp	Ser	Asn	Gly	Ile	Lys	Lys	Phe	Met	Ala	Glu	Lys	Gly	
			165					170					175			
att	cag	ccg	gac	ctg	atc	tac	acc	tcg	gaa	gaa	gcc	gat	gcg	ccg	cag	576
Ile	Gln	Pro	Asp	Leu	Ile	Tyr	Thr	Ser	Glu	Glu	Ala	Asp	Ala	Pro	Gln	
			180					185					190			
tat	atg	gaa	cat	ctg	ggg	atc	gag	acg	gtg	ctg	gtc	gat	ccg	aag	cgt	624
Tyr	Met	Glu	His	Leu	Gly	Ile	Glu	Thr	Val	Leu	Val	Asp	Pro	Lys	Arg	
	195						200					205				
acc	ttt	atg	agt	atc	agc	ggg	cgc	cag	atc	cgc	gaa	aac	ccg	ttc	cgc	672
Thr	Phe	Met	Ser	Ile	Ser	Gly	Ala	Gln	Ile	Arg	Glu	Asn	Pro	Phe	Arg	
	210				215						220					
tac	tgg	gaa	tat	att	cct	acg	gaa	gtt	aag	ccg	ttc	ttt	gtg	cgt	acc	720
Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	
	225				230					235				240		
gtg	gcg	atc	ctt	ggc	ggc	gag	tcg	agc	ggg	aaa	tcc	acc	ctg	gta	aac	768
Val	Ala	Ile	Leu	Gly	Gly	Glu	Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	
			245					250					255			
aaa	ctt	gcc	aat	atc	ttc	aac	act	acc	agt	gca	tgg	gaa	tat	ggg	cgc	816
Lys	Leu	Ala	Asn	Ile	Phe	Asn	Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	
		260					265					270				
gat	tat	gtc	ttt	tca	cac	ctt	ggc	ggg	gat	gag	att	gcg	ttg	cag	tat	864
Asp	Tyr	Val	Phe	Ser	His	Leu	Gly	Gly	Asp	Glu	Ile	Ala	Leu	Gln	Tyr	
	275						280				285					
tcc	gac	tac	gat	aaa	atc	gcg	ctg	gga	cac	gcg	caa	tat	att	gat	ttt	912
Ser	Asp	Tyr	Asp	Lys	Ile	Ala	Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe	
	290				295					300						
gca	gtg	aaa	tat	gcc	aat	aaa	gtg	gcg	ttt	atc	gac	acc	gat	ttt	gtc	960
Ala	Val	Lys	Tyr	Ala	Asn	Lys	Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	
	305				310				315						320	
act	acc	cag	gcg	ttc	tgc	aaa	aag	tac	gaa	ggg	cgt	gag	cat	ccg	ttc	1008
Thr	Thr	Gln	Ala	Phe	Cys	Lys	Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	
			325					330					335			
gtg	cag	gcg	ttg	att	gat	gaa	tac	cgt	ttc	gat	ctg	gtg	atc	ctg	ctg	1056
Val	Gln	Ala	Leu	Ile	Asp	Glu	Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	
			340					345				350				
gag	aac	aac	acg	ccg	tgg	gtg	gcg	gat	ggg	tta	cgc	agc	ctc	ggc	agt	1104
Glu	Asn	Asn	Thr	Pro	Trp	Val	Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	
	355						360					365				
tcg	gtg	gat	cgc	aaa	gag	ttc	cag	aac	ttg	ctg	gtg	gag	atg	ctg	gaa	1152
Ser	Val	Asp	Arg	Lys	Glu	Phe	Gln	Asn	Leu	Leu	Val	Glu	Met	Leu	Glu	
	370				375					380						
gag	aac	aat	atc	gaa	ttc	gtg	cgg	gtt	gaa	gag	gac	gat	tac	gac	agc	1200
Glu	Asn	Asn	Ile	Glu	Phe	Val	Arg	Val	Glu	Glu	Asp	Asp	Tyr	Asp	Ser	
	385				390				395						400	
cgt	ttc	ctg	cgc	tgc	gtg	gag	ctg	gtg	cgg	gag	atg	atg	ggg	gag	caa	1248
Arg	Phe	Leu	Arg	Cys	Val	Glu	Leu	Val	Arg	Glu	Met	Met	Gly	Glu	Gln	
			405					410					415			
aga	taa															1254
Arg																

PF59083SeqList PF59083.txt

<211> 417

<212> PRT

<213> Escherichia coli 06

<400> 9861

```

Met Arg Asp Thr Glu Gly Asp Met Ser Ser Phe Asp Tyr Leu Lys Thr
1      5      10      15
Ala Ile Lys Gln Gln Gly Cys Thr Leu Gln Gln Val Ala Asp Ala Ser
      20      25      30
Gly Met Thr Lys Gly Tyr Leu Ser Gln Leu Leu Asn Ala Lys Ile Lys
      35      40      45
Ser Pro Ser Ala Gln Lys Leu Glu Ala Leu His Arg Phe Leu Gly Leu
      50      55      60
Glu Phe Pro Arg Gln Lys Thr Ile Gly Val Val Phe Gly Lys Phe
65      70      75      80
Tyr Pro Leu His Thr Gly His Ile Tyr Leu Ile Gln Arg Ala Cys Ser
      85      90      95
Gln Val Asp Glu Leu His Ile Ile Met Gly Phe Asp Asp Thr Arg Asp
      100      105      110
Arg Ala Leu Phe Glu Asp Ser Ala Met Ser Gln Gln Pro Thr Val Pro
      115      120      125
Asp Arg Leu Arg Trp Leu Leu Gln Thr Phe Lys Tyr Gln Lys Asn Ile
      130      135      140
Arg Ile His Ala Phe Asn Glu Glu Gly Met Glu Pro Tyr Pro His Gly
145      150      155      160
Trp Asp Val Trp Ser Asn Gly Ile Lys Lys Phe Met Ala Glu Lys Gly
      165      170      175
Ile Gln Pro Asp Leu Ile Tyr Thr Ser Glu Glu Ala Asp Ala Pro Gln
      180      185      190
Tyr Met Glu His Leu Gly Ile Glu Thr Val Leu Val Asp Pro Lys Arg
      195      200      205
Thr Phe Met Ser Ile Ser Gly Ala Gln Ile Arg Glu Asn Pro Phe Arg
      210      215      220
Tyr Trp Glu Tyr Ile Pro Thr Glu Val Lys Pro Phe Phe Val Arg Thr
225      230      235      240
Val Ala Ile Leu Gly Gly Glu Ser Ser Gly Lys Ser Thr Leu Val Asn
      245      250      255
Lys Leu Ala Asn Ile Phe Asn Thr Thr Ser Ala Trp Glu Tyr Gly Arg
      260      265      270
Asp Tyr Val Phe Ser His Leu Gly Asp Glu Ile Ala Leu Gln Tyr
      275      280      285
Ser Asp Tyr Asp Lys Ile Ala Leu Gly His Ala Gln Tyr Ile Asp Phe
      290      295      300
Ala Val Lys Tyr Ala Asn Lys Val Ala Phe Ile Asp Thr Asp Phe Val
305      310      315      320
Thr Thr Gln Ala Phe Cys Lys Lys Tyr Glu Gly Arg Glu His Pro Phe
      325      330      335
Val Gln Ala Leu Ile Asp Glu Tyr Arg Phe Asp Leu Val Ile Leu Leu
      340      345      350
Glu Asn Asn Thr Pro Trp Val Ala Asp Gly Leu Arg Ser Leu Gly Ser
      355      360      365
Ser Val Asp Arg Lys Glu Phe Gln Asn Leu Leu Val Glu Met Leu Glu
      370      375      380
Glu Asn Asn Ile Glu Phe Val Arg Val Glu Glu Asp Asp Tyr Asp Ser
385      390      395      400
Arg Phe Leu Arg Cys Val Glu Leu Val Arg Glu Met Met Gly Glu Gln
      405      410      415
Arg

```

<210> 9862

<211> 1254

<212> DNA

<213> Escherichia coli 0157

<220>

<221> CDS

<222> (1)..(1254)

<223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 9862
atg aga aat acg gag gga gat atg tcg tca ttt gat tac ctg aaa act   48
Met Arg Asn Thr Glu Gly Asp Met Ser Ser Phe Asp Tyr Leu Lys Thr
1 5 10 15
gcc atc aag caa cag ggc tgc acg cta cag cag gta gct gat gcc agc   96
Ala Ile Lys Gln Gln Gly Cys Thr Leu Gln Gln Val Ala Asp Ala Ser
20 25 30
ggt atg acc aaa ggg tat tta agc cag tta ctg aat gcc aaa atc aaa   144
Gly Met Thr Lys Gly Tyr Leu Ser Gln Leu Leu Asn Ala Lys Ile Lys
35 40 45
agc ccc agc gcg caa aag ctg gag gcg ttg cac cgt ttt ttg ggg ctt   192
Ser Pro Ser Ala Gln Lys Leu Glu Ala Leu His Arg Phe Leu Gly Leu
50 55 60
gag ttt ccc cgg cag aag aaa acg atc ggt gtc gta ttc ggt aag ttc   240
Glu Phe Pro Arg Gln Lys Lys Thr Ile Gly Val Val Phe Gly Lys Phe
65 70 75 80
tac cca ctg cat acc gga cat atc tac ctt atc cag cgc gcc tgt agc   288
Tyr Pro Leu His Thr Gly His Ile Tyr Leu Ile Gln Arg Ala Cys Ser
85 90 95
cag gtt gac gag ctg cat atc att atg ggt ttt gac gat acc cgt gac   336
Gln Val Asp Glu Leu His Ile Ile Met Gly Phe Asp Asp Thr Arg Asp
100 105 110
cgc gcg ttg ttc gaa gac agt gcc atg tcg cag cag ccg acc gtg ccg   384
Arg Ala Leu Phe Glu Asp Ser Ala Met Ser Gln Gln Pro Thr Val Pro
115 120 125
gat cgt ctg cgc tgg tta ttg caa act ttt aaa tat cag aaa aat att   432
Asp Arg Leu Arg Trp Leu Leu Gln Thr Phe Lys Tyr Gln Lys Asn Ile
130 135 140
cgc att cat gct ttc aac gaa gag ggc atg gag ccg tat ccg cac ggc   480
Arg Ile His Ala Phe Asn Glu Glu Gly Met Glu Pro Tyr Pro His Gly
145 150 155 160
tgg gat gtg tgg agc aac ggt atc aaa aag ttt atg gct gaa aag ggg   528
Trp Asp Val Trp Ser Asn Gly Ile Lys Lys Phe Met Ala Glu Lys Gly
165 170 175
atc cag ccg gat ctg atc tac acc tcg gaa gaa gcc gat gcg cca cag   576
Ile Gln Pro Asp Leu Ile Tyr Thr Ser Glu Glu Ala Asp Ala Pro Gln
180 185 190
tat atg gaa cat ctg ggg atc gag acg gtg ctg gtc gat ccg aaa cgt   624
Tyr Met Glu His Leu Gly Ile Glu Thr Val Leu Val Asp Pro Lys Arg
195 200 205
acc ttt atg agt atc agc ggt gcg cag atc cgc gaa aac ccg ttc cgc   672
Thr Phe Met Ser Ile Ser Gly Ala Gln Ile Arg Glu Asn Pro Phe Arg
210 215 220
tac tgg gaa tat att cct acc gaa gtg aag ccg ttt gtg cgt acc   720
Tyr Trp Glu Tyr Ile Pro Thr Glu Val Lys Pro Phe Phe Val Arg Thr
225 230 235 240
gtg gcg atc ctt ggc ggc gag tcg agc ggt aaa tcc acc ctg gta aac   768
Val Ala Ile Leu Gly Gly Glu Ser Ser Gly Lys Ser Thr Leu Val Asn
245 250 255
aaa ctt gcc aat atc ttc aac acc acc agt gcg tgg gaa tat ggc cgc   816
Lys Leu Ala Asn Ile Phe Asn Thr Thr Ser Ala Trp Glu Tyr Gly Arg
260 265 270
gat tat gtc ttt tca cac ctc ggc ggt gat gag atc gca ttg cag tat   864
Asp Tyr Val Phe Ser His Leu Gly Gly Asp Glu Ile Ala Leu Gln Tyr
275 280 285
tct gac tac gat aaa atc gcg ctg ggc cac gct caa tac att gat ttt   912
Ser Asp Tyr Asp Lys Ile Ala Leu Gly His Ala Gln Tyr Ile Asp Phe
290 295 300
gcg gtg aaa tat gcc aat gtt gca ttt atc gat acc gat ttt gtc   960
Ala Val Lys Tyr Ala Asn Lys Val Ala Phe Ile Asp Thr Asp Phe Val
305 310 315 320
acc act cag gcg ttc tgc aaa aag tac gaa ggg ccg gaa cat ccg ttc   1008
Thr Thr Gln Ala Phe Cys Lys Lys Tyr Glu Gly Arg Glu His Pro Phe
325 330 335
gtg cag gcg ctg att gat gaa tac cgt ttc gat ctg gtg atc ctg ctg   1056
Val Gln Ala Leu Ile Asp Glu Tyr Arg Phe Asp Leu Val Ile Leu Leu
340 345 350
gag aac aac acg ccg tgg gtg gtg gat ggt tta cgc agc ctc ggc agt   1104
350

```

PF59083SeqList PF59083.txt

Glu	Asn	Asn	Thr	Pro	Trp	Val	Val	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	
		355					360					365				
tcg	gtg	gat	cgt	aaa	gag	ttc	cag	aat	ctg	ctg	gtg	gag	atg	ctg	gaa	1152
Ser	Val	Asp	Arg	Lys	Glu	Phe	Gln	Asn	Leu	Leu	Val	Glu	Met	Leu	Glu	
	370					375					380					
gag	aac	aat	atc	gaa	ttt	gtg	cgg	gtt	gaa	gag	gaa	gat	tac	gac	agc	1200
Glu	Asn	Asn	Ile	Glu	Phe	Val	Arg	Val	Glu	Glu	Glu	Asp	Tyr	Asp	Ser	
385					390					395					400	
cgt	ttc	ctg	cgc	tgc	gtg	gag	ctg	gtg	cgg	gag	atg	atg	ggg	gag	cag	1248
Arg	Phe	Leu	Arg	Cys	Val	Glu	Leu	Val	Arg	Glu	Met	Met	Gly	Glu	Gln	
				405					410					415		
aga	taa															1254
Arg																

<210> 9863

<211> 417

<212> PRT

<213> Escherichia coli 0157

<400> 9863

Met	Arg	Asn	Thr	Glu	Gly	Asp	Met	Ser	Ser	Phe	Asp	Tyr	Leu	Lys	Thr	
1				5					10					15		
Ala	Ile	Lys	Gln	Gln	Gly	Cys	Thr	Leu	Gln	Gln	Val	Ala	Asp	Ala	Ser	
			20					25					30			
Gly	Met	Thr	Lys	Gly	Tyr	Leu	Ser	Gln	Leu	Leu	Asn	Ala	Lys	Ile	Lys	
		35					40					45				
Ser	Pro	Ser	Ala	Gln	Lys	Leu	Glu	Ala	Leu	His	Arg	Phe	Leu	Gly	Leu	
	50					55					60					
Glu	Phe	Pro	Arg	Gln	Lys	Lys	Thr	Ile	Gly	Val	Val	Phe	Gly	Lys	Phe	
65					70				75						80	
Tyr	Pro	Leu	His	Thr	Gly	His	Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Cys	Ser	
				85					90					95		
Gln	Val	Asp	Glu	Leu	His	Ile	Ile	Met	Gly	Phe	Asp	Asp	Thr	Arg	Asp	
			100					105					110			
Arg	Ala	Leu	Phe	Glu	Asp	Ser	Ala	Met	Ser	Gln	Gln	Pro	Thr	Val	Pro	
		115					120					125				
Asp	Arg	Leu	Arg	Trp	Leu	Leu	Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile	
	130					135					140					
Arg	Ile	His	Ala	Phe	Asn	Glu	Glu	Gly	Met	Glu	Pro	Tyr	Pro	His	Gly	
145					150					155					160	
Trp	Asp	Val	Trp	Ser	Asn	Gly	Ile	Lys	Lys	Phe	Met	Ala	Glu	Lys	Gly	
				165					170					175		
Ile	Gln	Pro	Asp	Leu	Ile	Tyr	Thr	Ser	Glu	Glu	Ala	Asp	Ala	Pro	Gln	
			180					185					190			
Tyr	Met	Glu	His	Leu	Gly	Ile	Glu	Thr	Val	Leu	Val	Asp	Pro	Lys	Arg	
		195					200					205				
Thr	Phe	Met	Ser	Ile	Ser	Gly	Ala	Gln	Ile	Arg	Glu	Asn	Pro	Phe	Arg	
	210					215					220					
Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	
225					230					235					240	
Val	Ala	Ile	Leu	Gly	Gly	Glu	Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	
				245					250					255		
Lys	Leu	Ala	Asn	Ile	Phe	Asn	Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	
			260					265					270			
Asp	Tyr	Val	Phe	Ser	His	Leu	Gly	Gly	Asp	Glu	Ile	Ala	Leu	Gln	Tyr	
		275					280					285				
Ser	Asp	Tyr	Asp	Lys	Ile	Ala	Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe	
	290					295					300					
Ala	Val	Lys	Tyr	Ala	Asn	Lys	Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	
305					310					315					320	
Thr	Thr	Gln	Ala	Phe	Cys	Lys	Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	
				325					330					335		
Val	Gln	Ala	Leu	Ile	Asp	Glu	Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	
			340					345					350			
Glu	Asn	Asn	Thr	Pro	Trp	Val	Val	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	
		355					360					365				
Ser	Val	Asp	Arg	Lys	Glu	Phe	Gln	Asn	Leu	Leu	Val	Glu	Met	Leu	Glu	
	370					375					380					

PF59083SeqList PF59083.txt

Glu Asn Asn Ile Glu Phe Val Arg Val Glu Glu Glu Asp Tyr Asp Ser
 385 390 395 400
 Arg Phe Leu Arg Cys Val Glu Leu Val Arg Glu Met Met Gly Glu Gln
 405 410 415
 Arg

<210> 9864
 <211> 1233
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1233)
 <223> transl_table=11

<400> 9864
 atg tcg tca ttt gat tac ctg aaa act gcc atc aag caa cag ggc tgc 48
 Met Ser Ser Phe Asp Tyr Leu Lys Thr Ala Ile Lys Gln Gln Gly Cys
 1 5 10 15
 acg cta cag cag gta gct gat gcc agc ggt atg acc aaa ggg tat tta 96
 Thr Leu Gln Gln Val Ala Asp Ala Ser Gly Met Thr Lys Gly Tyr Leu
 20 25 30
 agc cag tta ctg aat gcc aaa atc aaa agc ccc agc gcg caa aag ctg 144
 Ser Gln Leu Asn Ala Lys Ile Lys Ser Pro Ser Ala Gln Lys Leu
 35 40 45
 gag gcg ttg cac cgt ttt ttg ggg ctt gag ttt ccc cgg cag aag aaa 192
 Glu Ala Leu His Arg Phe Leu Gly Leu Glu Phe Pro Arg Gln Lys Lys
 50 55 60
 acg atc ggt gtc gta ttc ggt aag ttc tac cca ctg cat acc gga cat 240
 Thr Ile Gly Val Val Phe Gly Lys Phe Tyr Pro Leu His Thr Gly His
 65 70 75 80
 atc tac ctt atc cag cgc gcc tgt agc cag gtt gac gag ctg cat atc 288
 Ile Tyr Leu Ile Gln Arg Ala Cys Ser Gln Val Asp Glu Leu His Ile
 85 90 95
 att atg ggt ttt gac gat acc cgt gac cgc gcg ttg ttc gaa gac agt 336
 Ile Met Gly Phe Asp Asp Thr Arg Asp Arg Ala Leu Phe Glu Asp Ser
 100 105 110
 gcc atg tcg cag cag ccg acc gtg ccg gat cgt ctg cgt tgg tta ttg 384
 Ala Met Ser Gln Gln Pro Thr Val Pro Asp Arg Leu Arg Trp Leu Leu
 115 120 125
 caa act ttt aaa tat cag aaa aat att cgc att cat gct ttc aac gaa 432
 Gln Thr Phe Lys Tyr Gln Lys Asn Ile Arg Ile His Ala Phe Asn Glu
 130 135 140
 gag ggc atg gag ccg tat ccg cac ggc tgg gat gtg tgg agc aac ggc 480
 Glu Gly Met Glu Pro Tyr Pro His Gly Trp Asp Val Trp Ser Asn Gly
 145 150 155 160
 atc aaa aag ttt atg gct gaa aaa ggg atc cag ccg gat ctg atc tac 528
 Ile Lys Lys Phe Met Ala Glu Lys Gly Ile Gln Pro Asp Leu Ile Tyr
 165 170 175
 acc tcg gaa gaa gcc gat gcg cca cag tat atg gaa cat ctg ggg atc 576
 Thr Ser Glu Glu Ala Asp Ala Pro Gln Tyr Met Glu His Leu Gly Ile
 180 185 190
 gag acg gtg ctg gtc gat ccg aaa cgt acc ttt atg agt atc agc ggt 624
 Glu Thr Val Leu Val Asp Pro Lys Arg Thr Phe Met Ser Ile Ser Gly
 195 200 205
 gcg cag atc cgc gaa aac ccg ttc cgc tac tgg gaa tat att cct acc 672
 Ala Gln Ile Arg Glu Asn Pro Phe Arg Tyr Trp Glu Tyr Ile Pro Thr
 210 215 220
 gaa gtg aag ccg ttt ttt gtg cgt acc gtg gcg atc ctt ggc ggc gag 720
 Glu Val Lys Pro Phe Phe Val Arg Thr Val Ala Ile Leu Gly Gly Glu
 225 230 235 240
 tcg agc ggt aaa tcc acc ctg gta aac aaa ctt gcc aat atc ttc aac 768
 Ser Ser Gly Lys Ser Thr Leu Val Asn Lys Leu Ala Asn Ile Phe Asn
 245 250 255
 acc acc agt gcg tgg gaa tat ggc cgc gat tat gtc ttt tca cac ctc 816
 Thr Thr Ser Ala Trp Glu Tyr Gly Arg Asp Tyr Val Phe Ser His Leu
 260 265 270

PF59083SeqList PF59083.txt

ggc	ggt	gat	gag	atc	gca	tgt	cag	tat	tct	gac	tac	gat	aaa	atc	gcg	864
Gly	Gly	Asp	Glu	Ile	Ala	Leu	Gln	Tyr	Ser	Asp	Tyr	Asp	Lys	Ile	Ala	
		275					280					285				
ctg	ggc	cac	gct	caa	tac	att	gat	ttt	gcg	gtg	aaa	tat	gcc	aat	aaa	912
Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe	Ala	Val	Lys	Tyr	Ala	Asn	Lys	
	290					295					300					
gtg	gca	ttt	atc	gat	acc	gat	ttt	gtc	acc	act	cag	gcg	ttc	tgc	aaa	960
Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	Thr	Thr	Gln	Ala	Phe	Cys	Lys	
305					310					315					320	
aag	tac	gaa	ggg	cgg	gaa	cat	ccg	ttc	gtg	cag	gcg	ctg	att	gat	gaa	1008
Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	Val	Gln	Ala	Leu	Ile	Asp	Glu	
				325					330					335		
tac	cgt	ttc	gat	ctg	gtg	atc	ctg	ctg	gag	aac	aac	acg	ccg	tgg	gtg	1056
Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	Glu	Asn	Asn	Thr	Pro	Trp	Val	
			340						345					350		
gcg	gat	ggt	tta	cgc	agc	ctc	ggc	agt	tcg	gtg	gat	cgc	aaa	gag	ttc	1104
Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	Ser	Val	Asp	Arg	Lys	Glu	Phe	
		355					360						365			
cag	aac	ttg	ctg	gtg	gag	atg	ctc	gaa	gag	aac	aat	atc	gaa	ttt	gtg	1152
Gln	Asn	Leu	Leu	Val	Glu	Met	Leu	Glu	Glu	Asn	Asn	Ile	Glu	Phe	Val	
	370					375										
cgg	gtt	gaa	gag	gaa	gat	tac	gac	agt	cgt	ttc	ctg	cgc	tgc	gtg	gaa	1200
Arg	Val	Glu	Glu	Glu	Asp	Tyr	Asp	Ser	Arg	Phe	Leu	Arg	Cys	Val	Glu	
385					390					395					400	
ctg	gtg	cgg	gag	atg	atg	ggg	gag	cag	aga	taa						1233
Leu	Val	Arg	Glu	Met	Met	Gly	Glu	Gln	Arg							
				405					410							

<210> 9865

<211> 410

<212> PRT

<213> Escherichia coli

<400> 9865

Met	Ser	Ser	Phe	Asp	Tyr	Leu	Lys	Thr	Ala	Ile	Lys	Gln	Gln	Gly	Cys	
1				5					10					15		
Thr	Leu	Gln	Gln	Val	Ala	Asp	Ala	Ser	Gly	Met	Thr	Lys	Gly	Tyr	Leu	
			20					25					30			
Ser	Gln	Leu	Leu	Asn	Ala	Lys	Ile	Lys	Ser	Pro	Ser	Ala	Gln	Lys	Leu	
		35					40					45				
Glu	Ala	Leu	His	Arg	Phe	Leu	Gly	Leu	Glu	Phe	Pro	Arg	Gln	Lys	Lys	
	50					55				60						
Thr	Ile	Gly	Val	Val	Phe	Gly	Lys	Phe	Tyr	Pro	Leu	His	Thr	Gly	His	
65					70				75					80		
Ile	Tyr	Leu	Ile	Gln	Arg	Ala	Cys	Ser	Gln	Val	Asp	Glu	Leu	His	Ile	
			85						90					95		
Ile	Met	Gly	Phe	Asp	Asp	Thr	Arg	Asp	Arg	Ala	Leu	Phe	Glu	Asp	Ser	
			100					105					110			
Ala	Met	Ser	Gln	Gln	Pro	Thr	Val	Pro	Asp	Arg	Leu	Arg	Trp	Leu	Leu	
		115					120					125				
Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile	Arg	Ile	His	Ala	Phe	Asn	Glu	
	130					135					140					
Glu	Gly	Met	Glu	Pro	Tyr	Pro	His	Gly	Trp	Asp	Val	Trp	Ser	Asn	Gly	
145					150				155					160		
Ile	Lys	Lys	Phe	Met	Ala	Glu	Lys	Gly	Ile	Gln	Pro	Asp	Leu	Ile	Tyr	
			165						170					175		
Thr	Ser	Glu	Glu	Ala	Asp	Ala	Pro	Gln	Tyr	Met	Glu	His	Leu	Gly	Ile	
			180					185					190			
Glu	Thr	Val	Leu	Val	Asp	Pro	Lys	Arg	Thr	Phe	Met	Ser	Ile	Ser	Gly	
		195					200					205				
Ala	Gln	Ile	Arg	Glu	Asn	Pro	Phe	Arg	Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	
	210					215					220					
Glu	Val	Lys	Pro	Phe	Phe	Val	Arg	Thr	Val	Ala	Ile	Leu	Gly	Gly	Glu	
225					230					235					240	
Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	Lys	Leu	Ala	Asn	Ile	Phe	Asn	
				245					250					255		
Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	Asp	Tyr	Val	Phe	Ser	His	Leu	
			260					265					270			
Gly	Gly	Asp	Glu	Ile	Ala	Leu	Gln	Tyr	Ser	Asp	Tyr	Asp	Lys	Ile	Ala	

PF59083SeqList PF59083.txt

```

      275      280      285
Leu Gly His Ala Gln Tyr Ile Asp Phe Ala Val Lys Tyr Ala Asn Lys
  290      295      300
Val Ala Phe Ile Asp Thr Asp Phe Val Thr Thr Gln Ala Phe Cys Lys
  305      310      315
Lys Tyr Glu Gly Arg Glu His Pro Phe Val Gln Ala Leu Ile Asp Glu
      325      330      335
Tyr Arg Phe Asp Leu Val Ile Leu Leu Glu Asn Asn Thr Pro Trp Val
      340      345      350
Ala Asp Gly Leu Arg Ser Leu Gly Ser Ser Val Asp Arg Lys Glu Phe
      355      360      365
Gln Asn Leu Leu Val Glu Met Leu Glu Glu Asn Asn Ile Glu Phe Val
      370      375      380
Arg Val Glu Glu Glu Asp Tyr Asp Ser Arg Phe Leu Arg Cys Val Glu
  385      390      395      400
Leu Val Arg Glu Met Met Gly Glu Gln Arg
      405      410

```

<210> 9866
 <211> 1266
 <212> DNA
 <213> Haemophilus influenzae

<220>
 <221> CDS
 <222> (1)..(1266)
 <223> transl_table=11

```

<400> 9866
gtg ggc ttt acc acc ggt agg gaa ttt cac cct gcc ctg aga atg cga      48
Met Gly Phe Thr Thr Gly Arg Glu Phe His Pro Ala Leu Arg Met Arg
  1      5      10      15
gct aag tat aac gca aaa tac cta ggc act aaa tca gaa cgt gaa aaa      96
Ala Lys Tyr Asn Ala Lys Tyr Leu Gly Thr Lys Ser Glu Arg Glu Lys
      20      25      30
tat ttt cat tta gcc tac aat aaa cac act caa ttc tta cgc tat caa      144
Tyr Phe His Leu Ala Tyr Asn Lys His Thr Gln Phe Leu Arg Tyr Gln
      35      40      45
gag cag att atg tca aaa aca aaa gag aaa aaa gtc ggt gtc att ttc      192
Glu Gln Ile Met Ser Lys Lys Glu Lys Lys Val Gly Val Ile Phe
      50      55      60
ggg aaa ttt tat cct gta cac aca ggt cat ata aat atg att tat gaa      240
Gly Lys Phe Tyr Pro Val His Thr Gly His Ile Asn Met Ile Tyr Glu
      65      70      75      80
gcg ttc agt aaa gtc gat gaa cta cac gtt atc gtg tgt agt gac act      288
Ala Phe Ser Lys Val Asp Glu Leu His Val Ile Val Cys Ser Asp Thr
      85      90      95
gtg cgc gat ttg aaa tta ttt tac gat agt aaa atg aaa cgc atg cca      336
Val Arg Asp Leu Lys Leu Phe Tyr Asp Ser Lys Met Lys Arg Met Pro
      100      105      110
acc gtg caa gat cgt ttg cgt tgg atg cag caa att ttc aaa tat caa      384
Thr Val Gln Asp Arg Leu Arg Trp Met Gln Gln Ile Phe Lys Tyr Gln
      115      120      125
aaa aat cag att ttt att cat cat ttg gtt gaa gac ggt att ccg agt      432
Lys Asn Gln Ile Phe Ile His His Leu Val Glu Asp Gly Ile Pro Ser
      130      135      140
tat cca aac ggc tgg caa tct tgg agt gaa gca gtt aaa acc cta ttt      480
Tyr Pro Asn Gly Trp Gln Ser Trp Ser Glu Ala Val Lys Thr Leu Phe
      145      150      155      160
cat gaa aaa cat ttt gag cct tca atc gta ttt agt agc gaa cct caa      528
His Glu Lys His Phe Glu Pro Ser Ile Val Phe Ser Ser Glu Pro Gln
      165      170      175
gat aaa gcg cct tac gag aaa tac tta ggt tta gaa gtt tcg tta gtc      576
Asp Lys Ala Pro Tyr Glu Lys Tyr Leu Gly Leu Glu Val Ser Leu Val
      180      185      190
gat cct gac cgc act ttc ttt aat gtg tcc gcc acc aaa att cgc acc      624
Asp Pro Asp Arg Thr Phe Phe Asn Val Ser Ala Thr Lys Ile Arg Thr
      195      200      205
act cca ttc caa tat tgg aag ttt att ccg aaa gaa gct cgt cct ttc      672

```

PF59083SeqList PF59083.txt

Thr	Pro	Phe	Gln	Tyr	Trp	Lys	Phe	Ile	Pro	Lys	Glu	Ala	Arg	Pro	Phe	
210	210					215					220					
ttt	gcc	aaa	acg	gtg	gcg	att	tta	ggg	gga	gaa	agc	agt	ggg	aaa	agc	720
Phe	Ala	Lys	Thr	Val	Ala	Ile	Leu	Gly	Gly	Glu	Ser	Ser	Gly	Lys	Ser	
225					230					235					240	
gtg	cta	gtt	aat	aag	tta	gcc	gcc	gta	ttt	aat	acc	act	tct	gcg	tgg	768
Val	Leu	Val	Asn	Lys	Leu	Ala	Ala	Val	Phe	Asn	Thr	Thr	Ser	Ala	Trp	
				245					250					255		
gaa	tac	ggg	cgt	gaa	ttt	gta	ttt	gaa	aag	ctc	ggg	ggc	gac	gag	caa	816
Glu	Tyr	Gly	Arg	Glu	Phe	Val	Phe	Glu	Lys	Leu	Gly	Gly	Asp	Glu	Gln	
			260					265					270			
gcg	atg	caa	tat	tct	gac	tat	ccg	caa	atg	gcg	ctt	ggg	cat	caa	cga	864
Ala	Met	Gln	Tyr	Ser	Asp	Tyr	Pro	Gln	Met	Ala	Leu	Gly	His	Gln	Arg	
		275				280						285				
tac	att	gat	tat	gcc	gtg	cgc	cat	tct	cat	aaa	att	gca	ttt	att	gat	912
Tyr	Ile	Asp	Tyr	Ala	Val	Arg	His	Ser	His	Lys	Ile	Ala	Phe	Ile	Asp	
	290					295					300					
acg	gat	ttc	atc	acc	acg	caa	gca	ttc	tgc	att	caa	tat	gaa	gga	aaa	960
Thr	Asp	Phe	Ile	Thr	Thr	Gln	Ala	Phe	Cys	Ile	Gln	Tyr	Glu	Gly	Lys	
305					310					315					320	
gcc	cat	cca	ttt	tta	gac	tca	atg	att	aaa	gaa	tat	ccc	ttc	gat	gtc	1008
Ala	His	Pro	Phe	Leu	Asp	Ser	Met	Ile	Lys	Glu	Tyr	Pro	Phe	Asp	Val	
			325					330					335			
act	att	tta	ctt	aaa	aac	aat	act	gaa	tgg	gtg	gat	gat	ggc	ttg	cgt	1056
Thr	Ile	Leu	Leu	Lys	Asn	Asn	Thr	Glu	Trp	Val	Asp	Asp	Gly	Leu	Arg	
			340					345					350			
agc	tta	ggc	tca	caa	aaa	caa	cgc	caa	caa	ttt	caa	caa	cta	ctc	aaa	1104
Ser	Leu	Gly	Ser	Gln	Lys	Gln	Arg	Gln	Gln	Phe	Gln	Gln	Leu	Leu	Lys	
		355				360					365					
aaa	ctg	tta	gat	aaa	tat	aaa	ggt	cct	tat	ata	gag	att	gaa	tca	cca	1152
Lys	Leu	Leu	Asp	Lys	Tyr	Lys	Val	Pro	Tyr	Ile	Glu	Ile	Glu	Ser	Pro	
	370					375					380					
agt	tat	ctt	gat	cgc	tat	aac	caa	gtt	aaa	gca	gtc	att	gag	aaa	gtg	1200
Ser	Tyr	Leu	Asp	Arg	Tyr	Asn	Gln	Val	Lys	Ala	Val	Ile	Glu	Lys	Val	
385					390					395					400	
tta	aat	gaa	gag	gaa	atc	agt	gaa	tta	caa	aac	aca	acc	ttt	cct	ata	1248
Leu	Asn	Glu	Glu	Glu	Ile	Ser	Glu	Leu	Gln	Asn	Thr	Thr	Phe	Pro	Ile	
			405					410					415			
aaa	ggg	aca	tct	caa	tga											1266
Lys	Gly	Thr	Ser	Gln												
			420													

<210> 9867

<211> 421

<212> PRT

<213> Haemophilus influenzae

<400> 9867

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

PF59083SeqList PF59083.txt

```

      165      170      175
Asp Lys Ala Pro Tyr Glu Lys Tyr Leu Gly Leu Glu Val Ser Leu Val
      180      185      190
Asp Pro Asp Arg Thr Phe Phe Asn Val Ser Ala Thr Lys Ile Arg Thr
      195      200      205
Thr Pro Phe Gln Tyr Trp Lys Phe Ile Pro Lys Glu Ala Arg Pro Phe
      210      215      220
Phe Ala Lys Thr Val Ala Ile Leu Gly Gly Glu Ser Ser Gly Lys Ser
      225      230      235
Val Leu Val Asn Lys Leu Ala Ala Val Phe Asn Thr Thr Ser Ala Trp
      240      245      250
Glu Tyr Gly Arg Glu Phe Val Phe Glu Lys Leu Gly Gly Asp Glu Gln
      255      260      265
Ala Met Gln Tyr Ser Asp Tyr Pro Gln Met Ala Leu Gly His Gln Arg
      270      275      280
Tyr Ile Asp Tyr Ala Val Arg His Ser His Lys Ile Ala Phe Ile Asp
      285      290      295
Thr Asp Phe Ile Thr Thr Gln Ala Phe Cys Ile Gln Tyr Glu Gly Lys
      300      305      310
Ala His Pro Phe Leu Asp Ser Met Ile Lys Glu Tyr Pro Phe Asp Val
      315      320      325
Thr Ile Leu Leu Lys Asn Asn Thr Glu Trp Val Asp Asp Gly Leu Arg
      330      335      340
Ser Leu Gly Ser Gln Lys Gln Arg Gln Gln Phe Gln Gln Leu Leu Lys
      345      350      355
Lys Leu Leu Asp Lys Tyr Lys Val Pro Tyr Ile Glu Ile Glu Ser Pro
      360      365      370
Ser Tyr Leu Asp Arg Tyr Asn Gln Val Lys Ala Val Ile Glu Lys Val
      375      380      385
Leu Asn Glu Glu Glu Ile Ser Glu Leu Gln Asn Thr Thr Phe Pro Ile
      390      395      400
Lys Gly Thr Ser Gln
      405      410      415
      420

```

<210> 9868

<211> 1233

<212> DNA

<213> Salmonella typhimurium

<220>

<221> CDS

<222> (1)..(1233)

<223> transl_table=11

<400> 9868

```

atg tca tcg ttc gac tat ctc aaa acc gcg att aag cag caa ggt tgc      48
Met Ser Ser Phe Asp Tyr Leu Lys Thr Ala Ile Lys Gln Gln Gly Cys
  1      5      10      15
act ctg caa cag gtg gct gac gcc agc ggt atg acc aag gga tat ctg      96
Thr Leu Gln Val Ala Asp Ala Ser Gly Met Thr Lys Gly Tyr Leu
      20      25      30
agt cag tta ctt aac gcc aaa atc aaa agc ccc agc gcg caa aaa ctg      144
Ser Gln Leu Leu Asn Ala Lys Ile Lys Ser Pro Ser Ala Gln Lys Leu
      35      40      45
gag gcg cta cac cgt ttt ctc ggg ctg gag ttt ccc cgc cga cag aaa      192
Glu Ala Leu His Arg Phe Leu Gly Leu Glu Phe Pro Arg Arg Gln Lys
      50      55      60
aac att ggc gtg gtg ttc ggt aaa ttt tat cca ttg cat acc gga cac      240
Asn Ile Gly Val Val Phe Gly Lys Phe Tyr Pro Leu His Thr Gly His
      65      70      75
atc tac ttg atc cag cgc gcc tgt agc cag gtg gat gag ttg cac atc      288
Ile Tyr Leu Ile Gln Arg Ala Cys Ser Gln Val Asp Glu Leu His Ile
      80      85      90
att atg gga tat gac gat acg cgc gac cgc ggg ctg ttt gag gat agc      336
Ile Met Gly Tyr Asp Asp Thr Arg Asp Arg Gly Leu Phe Glu Asp Ser
      95      100      105
gcc atg tcg cag cag ccc acc gtg tcg gat cgc ctg cgc tgg tta ttg      384
Ala Met Ser Gln Gln Pro Thr Val Ser Asp Arg Leu Arg Trp Leu Leu
      110      115      120      125

```

PF59083SeqList PF59083.txt

caa	acc	ttc	aaa	tac	caa	aaa	aat	att	cgc	atc	cac	gcc	ttt	aat	gaa	432
Gln	Thr	Phe	Lys	Tyr	Gln	Lys	Asn	Ile	Arg	Ile	His	Ala	Phe	Asn	Glu	
	130					135					140					
gag	ggg	atg	gag	cct	tat	ccg	cat	ggc	tgg	gac	gtc	tgg	agc	aac	ggc	480
Glu	Gly	Met	Glu	Pro	Tyr	Pro	His	Gly	Trp	Asp	Val	Trp	Ser	Asn	Gly	
145					150					155					160	
att	aaa	gcg	ttt	atg	gca	gag	aag	gga	ata	cag	ccg	agc	tgg	atc	tac	528
Ile	Lys	Ala	Phe	Met	Ala	Glu	Lys	Gly	Ile	Gln	Pro	Ser	Trp	Ile	Tyr	
				165				170						175		
act	tcc	gaa	gag	gct	gat	gcg	ccg	cag	tat	ctt	gag	cat	tta	ggg	att	576
Thr	Ser	Glu	Glu	Ala	Asp	Ala	Pro	Gln	Tyr	Leu	Glu	His	Leu	Gly	Ile	
				180				185					190			
gag	acg	gtg	ctg	gtc	gat	cct	gaa	cgc	acg	ttt	atg	aat	atc	agt	ggg	624
Glu	Thr	Val	Leu	Val	Asp	Pro	Glu	Arg	Thr	Phe	Met	Asn	Ile	Ser	Gly	
		195					200					205				
gcg	caa	atc	cgc	gaa	aat	ccg	ttt	cgt	tac	tgg	gaa	tat	att	cct	acc	672
Ala	Gln	Ile	Arg	Glu	Asn	Pro	Phe	Arg	Tyr	Trp	Glu	Tyr	Ile	Pro	Thr	
	210					215					220					
gaa	gtg	aag	ccg	ttt	ttc	gtg	cgt	acc	gtc	gcg	att	ctg	ggc	ggg	gaa	720
Glu	Val	Lys	Pro	Phe	Val	Val	Arg	Thr	Val	Ala	Ile	Leu	Gly	Gly	Glu	
225					230					235					240	
tca	agc	ggc	aag	tct	acg	ctg	gtc	aat	aag	ctc	gcc	aat	att	ttt	aat	768
Ser	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	Lys	Leu	Ala	Asn	Ile	Phe	Asn	
				245				250						255		
acc	acc	agc	gcc	tgg	gaa	tat	ggc	cgc	gac	tat	gtc	ttt	tcg	cat	ctg	816
Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	Asp	Tyr	Val	Phe	Ser	His	Leu	
			260					265					270			
ggc	ggc	gat	gag	atg	gcg	tta	cag	tat	tcc	gac	tac	gat	aaa	att	gcg	864
Gly	Gly	Asp	Glu	Met	Ala	Leu	Gln	Tyr	Ser	Asp	Tyr	Asp	Lys	Ile	Ala	
		275					280					285				
ctg	ggc	cat	gcg	caa	tat	att	gat	ttc	gca	gtg	aaa	tat	gcg	aat	aaa	912
Leu	Gly	His	Ala	Gln	Tyr	Ile	Asp	Phe	Ala	Val	Lys	Tyr	Ala	Asn	Lys	
	290					295					300					
gtg	gcg	ttt	atc	gat	acc	gat	ttc	gtc	acc	acc	cag	gca	ttt	tgc	aaa	960
Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Val	Thr	Thr	Gln	Ala	Phe	Cys	Lys	
305					310					315					320	
aaa	tac	gaa	gga	cgc	gag	cat	ccc	ttt	gtc	cag	gcg	ctg	atc	gac	gag	1008
Lys	Tyr	Glu	Gly	Arg	Glu	His	Pro	Phe	Val	Gln	Ala	Leu	Ile	Asp	Glu	
				325				330						335		
tat	cgc	ttc	gac	ctg	gtg	att	ttg	ctg	gag	aat	aat	acg	ccg	tgg	gta	1056
Tyr	Arg	Phe	Asp	Leu	Val	Ile	Leu	Leu	Glu	Asn	Asn	Thr	Pro	Trp	Val	
				340				345					350			
gct	gac	gga	ctg	cga	agc	ctg	ggc	agt	tca	gtg	gat	cgc	aaa	gcg	ttc	1104
Ala	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Ser	Ser	Val	Asp	Arg	Lys	Ala	Phe	
		355					360					365				
cag	aac	ctg	ctg	gtc	gag	atg	ctg	aaa	gag	aac	aac	att	gag	ttc	gtt	1152
Gln	Asn	Leu	Leu	Val	Glu	Met	Leu	Lys	Glu	Asn	Asn	Ile	Glu	Phe	Val	
	370					375					380					
cac	gtt	aaa	gag	gct	gat	tac	gat	ggc	cgc	ttt	ttg	cgc	tgt	gtg	gaa	1200
His	Val	Lys	Glu	Ala	Asp	Tyr	Asp	Gly	Arg	Phe	Leu	Arg	Cys	Val	Glu	
385					390					395					400	
ctg	gtg	aaa	gag	atg	atg	ggc	gag	cag	gga	taa						1233
Leu	Val	Lys	Glu	Met	Met	Gly	Glu	Gln	Gly							
				405					410							

<210> 9869

<211> 410

<212> PRT

<213> Salmonella typhimurium

<400> 9869

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

PF59083SeqList PF59083.txt

Asn Ile Gly Val Val Phe Gly Lys Phe Tyr Pro Leu His Thr Gly His
 65 70 75 80
 Ile Tyr Leu Ile Gln Arg Ala Cys Ser Gln Val Asp Glu Leu His Ile
 85 90 95
 Ile Met Gly Tyr Asp Asp Thr Arg Asp Arg Gly Leu Phe Glu Asp Ser
 100 105 110
 Ala Met Ser Gln Gln Pro Thr Val Ser Asp Arg Leu Arg Trp Leu Leu
 115 120 125
 Gln Thr Phe Lys Tyr Gln Lys Asn Ile Arg Ile His Ala Phe Asn Glu
 130 135 140
 Glu Gly Met Glu Pro Tyr Pro His Gly Trp Asp Val Trp Ser Asn Gly
 145 150 155 160
 Ile Lys Ala Phe Met Ala Glu Lys Gly Ile Gln Pro Ser Trp Ile Tyr
 165 170 175
 Thr Ser Glu Glu Ala Asp Ala Pro Gln Tyr Leu Glu His Leu Gly Ile
 180 185 190
 Glu Thr Val Leu Val Asp Pro Glu Arg Thr Phe Met Asn Ile Ser Gly
 195 200 205
 Ala Gln Ile Arg Glu Asn Pro Phe Arg Tyr Trp Glu Tyr Ile Pro Thr
 210 215 220
 Glu Val Lys Pro Phe Phe Val Arg Thr Val Ala Ile Leu Gly Gly Glu
 225 230 235 240
 Ser Ser Gly Lys Ser Thr Leu Val Asn Lys Leu Ala Asn Ile Phe Asn
 245 250 255
 Thr Thr Ser Ala Trp Glu Tyr Gly Arg Asp Tyr Val Phe Ser His Leu
 260 265 270
 Gly Gly Asp Glu Met Ala Leu Gln Tyr Ser Asp Tyr Asp Lys Ile Ala
 275 280 285
 Leu Gly His Ala Gln Tyr Ile Asp Phe Ala Val Lys Tyr Ala Asn Lys
 290 295 300
 Val Ala Phe Ile Asp Thr Asp Phe Val Thr Thr Gln Ala Phe Cys Lys
 305 310 315 320
 Lys Tyr Glu Gly Arg Glu His Pro Phe Val Gln Ala Leu Ile Asp Glu
 325 330 335
 Tyr Arg Phe Asp Leu Val Ile Leu Leu Glu Asn Asn Thr Pro Trp Val
 340 345 350
 Ala Asp Gly Leu Arg Ser Leu Gly Ser Ser Val Asp Arg Lys Ala Phe
 355 360 365
 Gln Asn Leu Leu Val Glu Met Leu Lys Glu Asn Asn Ile Glu Phe Val
 370 375 380
 His Val Lys Glu Ala Asp Tyr Asp Gly Arg Phe Leu Arg Cys Val Glu
 385 390 395 400
 Leu Val Lys Glu Met Met Gly Glu Gln Gly
 405 410

<210> 9870
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 9870
 atgagatata cggagggaga tatg

24

<210> 9871
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 9871
 ttatctctgc tccccatca tc

22

<210> 9872

<211> 395
<212> PRT
<213> Artificial sequence

<220>
<223> consensus sequence

<220>
<221> Variant
<222> (2)..(3)
<223> Xaa in position 2 to 3 is any amino acid

<220>
<221> Variant
<222> (5)..(5)
<223> Xaa in position 5 is any amino acid

<220>
<221> Variant
<222> (8)..(11)
<223> Xaa in position 8 to 11 is any amino acid

<220>
<221> Variant
<222> (14)..(27)
<223> Xaa in position 14 to 27 is any amino acid

<220>
<221> Variant
<222> (29)..(30)
<223> Xaa in position 29 to 30 is any amino acid

<220>
<221> Variant
<222> (32)..(33)
<223> Xaa in position 32 to 33 is any amino acid

<220>
<221> Variant
<222> (36)..(37)
<223> Xaa in position 36 to 37 is any amino acid

<220>
<221> Variant
<222> (38)..(38)
<223> Xaa in position 38 is any or no amino acid

<220>
<221> Variant
<222> (42)..(42)
<223> Xaa in position 42 is any amino acid

<220>
<221> Variant
<222> (46)..(46)
<223> Xaa in position 46 is any amino acid

<220>
<221> Variant
<222> (49)..(49)
<223> Xaa in position 49 is any amino acid

<220>
<221> Variant
<222> (53)..(54)
<223> Xaa in position 53 to 54 is any amino acid

<220>
<221> Variant

<222> (56)..(60)
<223> Xaa in position 56 to 60 is any amino acid

<220>
<221> Variant
<222> (61)..(63)
<223> Xaa in position 61 to 63 is any or no amino acid

<220>
<221> Variant
<222> (65)..(66)
<223> Xaa in position 65 to 66 is any amino acid

<220>
<221> Variant
<222> (69)..(69)
<223> Xaa in position 69 is any amino acid

<220>
<221> Variant
<222> (76)..(76)
<223> Xaa in position 76 is any amino acid

<220>
<221> Variant
<222> (82)..(83)
<223> Xaa in position 82 to 83 is any amino acid

<220>
<221> Variant
<222> (85)..(86)
<223> Xaa in position 85 to 86 is any amino acid

<220>
<221> Variant
<222> (88)..(88)
<223> Xaa in position 88 is any amino acid

<220>
<221> Variant
<222> (90)..(90)
<223> Xaa in position 90 is any amino acid

<220>
<221> Variant
<222> (96)..(96)
<223> Xaa in position 96 is any amino acid

<220>
<221> Variant
<222> (98)..(100)
<223> Xaa in position 98 to 100 is any amino acid

<220>
<221> Variant
<222> (102)..(103)
<223> Xaa in position 102 to 103 is any amino acid

<220>
<221> Variant
<222> (106)..(107)
<223> Xaa in position 106 to 107 is any amino acid

<220>
<221> Variant
<222> (110)..(111)
<223> Xaa in position 110 to 111 is any amino acid

<220>

```

<221> Variant
<222> (113)..(113)
<223> Xaa in position 113 is any amino acid

<220>
<221> Variant
<222> (115)..(117)
<223> Xaa in position 115 to 117 is any amino acid

<220>
<221> Variant
<222> (121)..(121)
<223> Xaa in position 121 is any amino acid

<220>
<221> Variant
<222> (127)..(128)
<223> Xaa in position 127 to 128 is any amino acid

<220>
<221> Variant
<222> (130)..(130)
<223> Xaa in position 130 is any amino acid

<220>
<221> Variant
<222> (137)..(137)
<223> Xaa in position 137 is any amino acid

<220>
<221> Variant
<222> (139)..(139)
<223> Xaa in position 139 is any amino acid

<220>
<221> Variant
<222> (142)..(144)
<223> Xaa in position 142 to 144 is any amino acid

<220>
<221> Variant
<222> (146)..(146)
<223> Xaa in position 146 is any amino acid

<220>
<221> Variant
<222> (148)..(150)
<223> Xaa in position 148 to 150 is any amino acid

<220>
<221> Variant
<222> (153)..(153)
<223> Xaa in position 153 is any amino acid

<220>
<221> Variant
<222> (156)..(157)
<223> Xaa in position 156 to 157 is any amino acid

<220>
<221> Variant
<222> (160)..(162)
<223> Xaa in position 160 to 162 is any amino acid

<220>
<221> Variant
<222> (164)..(167)
<223> Xaa in position 164 to 167 is any amino acid

```

<220>
<221> Variant
<222> (170)..(172)
<223> Xaa in position 170 to 172 is any amino acid

<220>
<221> Variant
<222> (174)..(178)
<223> Xaa in position 174 to 178 is any amino acid

<220>
<221> Variant
<222> (181)..(182)
<223> Xaa in position 181 to 182 is any amino acid

<220>
<221> Variant
<222> (184)..(186)
<223> Xaa in position 184 to 186 is any amino acid

<220>
<221> Variant
<222> (188)..(190)
<223> Xaa in position 188 to 190 is any amino acid

<220>
<221> Variant
<222> (192)..(193)
<223> Xaa in position 192 to 193 is any amino acid

<220>
<221> Variant
<222> (195)..(196)
<223> Xaa in position 195 to 196 is any amino acid

<220>
<221> Variant
<222> (198)..(198)
<223> Xaa in position 198 is any amino acid

<220>
<221> Variant
<222> (201)..(201)
<223> Xaa in position 201 is any amino acid

<220>
<221> Variant
<222> (203)..(203)
<223> Xaa in position 203 is any amino acid

<220>
<221> Variant
<222> (205)..(207)
<223> Xaa in position 205 to 207 is any amino acid

<220>
<221> Variant
<222> (209)..(211)
<223> Xaa in position 209 to 211 is any amino acid

<220>
<221> Variant
<222> (214)..(215)
<223> Xaa in position 214 to 215 is any amino acid

<220>
<221> Variant
<222> (218)..(218)
<223> Xaa in position 218 is any amino acid

<220>
 <221> Variant
 <222> (221)..(222)
 <223> Xaa in position 221 to 222 is any amino acid

<220>
 <221> Variant
 <222> (225)..(225)
 <223> Xaa in position 225 is any amino acid

<220>
 <221> Variant
 <222> (228)..(228)
 <223> Xaa in position 228 is any amino acid

<220>
 <221> Variant
 <222> (232)..(233)
 <223> Xaa in position 232 to 233 is any amino acid

<220>
 <221> Variant
 <222> (235)..(235)
 <223> Xaa in position 235 is any amino acid

<220>
 <221> Variant
 <222> (247)..(247)
 <223> Xaa in position 247 is any amino acid

<220>
 <221> Variant
 <222> (254)..(255)
 <223> Xaa in position 254 to 255 is any amino acid

<220>
 <221> Variant
 <222> (267)..(268)
 <223> Xaa in position 267 to 268 is any amino acid

<220>
 <221> Variant
 <222> (271)..(272)
 <223> Xaa in position 271 to 272 is any amino acid

<220>
 <221> Variant
 <222> (278)..(278)
 <223> Xaa in position 278 is any amino acid

<220>
 <221> Variant
 <222> (280)..(280)
 <223> Xaa in position 280 is any amino acid

<220>
 <221> Variant
 <222> (286)..(288)
 <223> Xaa in position 286 to 288 is any amino acid

<220>
 <221> Variant
 <222> (293)..(294)
 <223> Xaa in position 293 to 294 is any amino acid

<220>
 <221> Variant
 <222> (298)..(298)

<223> Xaa in position 298 is any amino acid

<220>

<221> Variant

<222> (301)..(302)

<223> Xaa in position 301 to 302 is any amino acid

<220>

<221> Variant

<222> (304)..(304)

<223> Xaa in position 304 is any amino acid

<220>

<221> Variant

<222> (314)..(314)

<223> Xaa in position 314 is any amino acid

<220>

<221> Variant

<222> (321)..(322)

<223> Xaa in position 321 to 322 is any amino acid

<220>

<221> Variant

<222> (326)..(327)

<223> Xaa in position 326 to 327 is any amino acid

<220>

<221> Variant

<222> (331)..(334)

<223> Xaa in position 331 to 334 is any amino acid

<220>

<221> Variant

<222> (336)..(336)

<223> Xaa in position 336 is any amino acid

<220>

<221> Variant

<222> (339)..(339)

<223> Xaa in position 339 is any amino acid

<220>

<221> Variant

<222> (342)..(343)

<223> Xaa in position 342 to 343 is any amino acid

<220>

<221> Variant

<222> (347)..(347)

<223> Xaa in position 347 is any amino acid

<220>

<221> Variant

<222> (351)..(351)

<223> Xaa in position 351 is any amino acid

<220>

<221> Variant

<222> (354)..(354)

<223> Xaa in position 354 is any amino acid

<220>

<221> Variant

<222> (362)..(365)

<223> Xaa in position 362 to 365 is any amino acid

<220>

<221> Variant

PF59083SeqList PF59083.txt

<222> (367)..(368)

<223> Xaa in position 367 to 368 is any amino acid

<220>

<221> Variant

<222> (371)..(371)

<223> Xaa in position 371 is any amino acid

<220>

<221> Variant

<222> (374)..(376)

<223> Xaa in position 374 to 376 is any amino acid

<220>

<221> Variant

<222> (378)..(391)

<223> Xaa in position 378 to 391 is any amino acid

<220>

<221> Variant

<222> (393)..(394)

<223> Xaa in position 393 to 394 is any amino acid

<400> 9872

Met	Xaa	Xaa	Phe	Xaa	Tyr	Leu	Xaa	Xaa	Xaa	Xaa	Lys	Gln	Xaa	Xaa	Xaa
1				5					10				15		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Xaa	Xaa	Tyr	Xaa
			20					25					30		
Xaa	Gln	Leu	Xaa	Xaa	Xaa	Lys	Ile	Lys	Xaa	Pro	Ser	Ala	Xaa	Lys	Leu
		35					40					45			
Xaa	Ala	Leu	His	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys
	50					55				60					
Xaa	Xaa	Gly	Val	Xaa	Phe	Gly	Lys	Phe	Tyr	Pro	Xaa	His	Thr	Gly	His
65					70				75						80
Ile	Xaa	Xaa	Ile	Xaa	Ala	Xaa	Ser	Xaa	Val	Asp	Glu	Leu	His	Xaa	
				85				90					95		
Ile	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Arg	Asp	Xaa	Xaa	Leu	Phe	Xaa	Xaa	Ser
			100					105				110			
Xaa	Met	Xaa	Xaa	Xaa	Pro	Thr	Val	Xaa	Asp	Arg	Leu	Arg	Trp	Xaa	Xaa
	115					120					125				
Gln	Xaa	Phe	Lys	Tyr	Gln	Lys	Asn	Xaa	Ile	Xaa	Ile	His	Xaa	Xaa	Xaa
	130					135					140				
Glu	Xaa	Gly	Xaa	Xaa	Xaa	Tyr	Pro	Xaa	Gly	Trp	Xaa	Xaa	Trp	Ser	Xaa
145					150					155					160
Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Glu	Lys	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa
				165				170					175		
Xaa	Xaa	Ser	Glu	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Leu	Xaa
			180					185					190		
Xaa	Glu	Xaa	Xaa	Leu	Xaa	Asp	Pro	Xaa	Arg	Xaa	Phe	Xaa	Xaa	Xaa	Ser
	195					200					205				
Xaa	Xaa	Xaa	Ile	Arg	Xaa	Xaa	Pro	Phe	Xaa	Tyr	Trp	Xaa	Xaa	Ile	Pro
	210				215						220				
Xaa	Glu	Val	Xaa	Pro	Phe	Phe	Xaa	Xaa	Thr	Xaa	Ala	Ile	Leu	Gly	Gly
225					230					235				240	
Glu	Ser	Ser	Gly	Lys	Ser	Xaa	Leu	Val	Asn	Lys	Leu	Ala	Xaa	Xaa	Phe
				245					250				255		
Asn	Thr	Thr	Ser	Ala	Trp	Glu	Tyr	Gly	Arg	Xaa	Xaa	Val	Phe	Xaa	Xaa
			260					265					270		
Leu	Gly	Gly	Asp	Glu	Xaa	Ala	Xaa	Gln	Tyr	Ser	Asp	Tyr	Xaa	Xaa	Xaa
		275					280					285			
Ala	Leu	Gly	His	Xaa	Xaa	Tyr	Ile	Asp	Xaa	Ala	Val	Xaa	Xaa	Ala	Xaa
	290					295					300				
Lys	Val	Ala	Phe	Ile	Asp	Thr	Asp	Phe	Xaa	Thr	Thr	Gln	Ala	Phe	Cys
305					310					315					320
Xaa	Xaa	Tyr	Glu	Gly	Xaa	Xaa	His	Pro	Phe	Xaa	Xaa	Xaa	Xaa	Ile	Xaa
				325					330					335	
Glu	Tyr	Xaa	Phe	Asp	Xaa	Xaa	Ile	Leu	Leu	Xaa	Asn	Asn	Thr	Xaa	Trp
			340					345					350		
Val	Xaa	Asp	Gly	Leu	Arg	Ser	Leu	Gly	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa

PF59083SeqList PF59083.txt
 355 360 365
 Phe Gln Xaa Leu Leu Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa
 370 375 380
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Arg
 385 390 395

<210> 9873
 <211> 59
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is any amino acid

<220>
 <221> Variant
 <222> (5)..(5)
 <223> Xaa in position 5 is Asp, Glu or Lys

<220>
 <221> Variant
 <222> (6)..(6)
 <223> Xaa in position 6 is Phe or Tyr

<220>
 <221> Variant
 <222> (9)..(9)
 <223> Xaa in position 9 is any amino acid

<220>
 <221> Variant
 <222> (11)..(11)
 <223> Xaa in position 11 is Ala or Val

<220>
 <221> Variant
 <222> (12)..(12)
 <223> Xaa in position 12 is Lys or Arg

<220>
 <221> Variant
 <222> (16)..(16)
 <223> Xaa in position 16 is Ala or Val

<220>
 <221> Variant
 <222> (17)..(17)
 <223> Xaa in position 17 is Lys or Arg

<220>
 <221> Variant
 <222> (19)..(19)
 <223> Xaa in position 19 is Ile or Val

<220>
 <221> Variant
 <222> (30)..(30)
 <223> Xaa in position 30 is Ser or Thr

<220>
 <221> Variant
 <222> (31)..(31)
 <223> Xaa in position 31 is Thr or Val

PF59083SeqList PF59083.txt

```

<220>
<221> Variant
<222> (38)..(38)
<223> Xaa in position 38 is Ala, Asn or Thr

<220>
<221> Variant
<222> (39)..(39)
<223> Xaa in position 39 is Ile or Val

<220>
<221> Variant
<222> (51)..(51)
<223> Xaa in position 51 is Asp or Glu

<220>
<221> Variant
<222> (52)..(52)
<223> Xaa in position 52 is Phe or Tyr

<220>
<221> Variant
<222> (55)..(55)
<223> Xaa in position 55 is Asp, Glu or Ser

<220>
<221> Variant
<222> (56)..(56)
<223> Xaa in position 56 is His or Lys

<400> 9873
Phe Xaa Tyr Trp Xaa Xaa Ile Pro Xaa Glu Xaa Xaa Pro Phe Phe Xaa
1      5      10      15
Xaa Thr Xaa Ala Ile Leu Gly Gly Glu Ser Ser Gly Lys Xaa Xaa Leu
20      25      30
Val Asn Lys Leu Ala Xaa Xaa Phe Asn Thr Thr Ser Ala Trp Glu Tyr
35      40      45
Gly Arg Xaa Xaa Val Phe Xaa Xaa Leu Gly Gly
50      55

<210> 9874
<211> 60
<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
<221> Variant
<222> (2)..(2)
<223> Xaa in position 2 is any amino acid

<220>
<221> Variant
<222> (5)..(5)
<223> Xaa in position 5 is any amino acid

<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is any or no amino acid

<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is any or no amino acid

```

```

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is Ile or Val

<220>
<221> Variant
<222> (20)..(21)
<223> Xaa in position 20 to 21 is any amino acid

<220>
<221> Variant
<222> (25)..(25)
<223> Xaa in position 25 is Lys or Arg

<220>
<221> Variant
<222> (26)..(26)
<223> Xaa in position 26 is any amino acid

<220>
<221> Variant
<222> (30)..(30)
<223> Xaa in position 30 is Leu or Val

<220>
<221> Variant
<222> (31)..(31)
<223> Xaa in position 31 is Asp or Gln

<220>
<221> Variant
<222> (32)..(32)
<223> Xaa in position 32 is Ala or Ser

<220>
<221> Variant
<222> (33)..(33)
<223> Xaa in position 33 is Leu or Met

<220>
<221> Variant
<222> (34)..(34)
<223> Xaa in position 34 is Ile or Val

<220>
<221> Variant
<222> (35)..(35)
<223> Xaa in position 35 is Asp or Lys

<220>
<221> Variant
<222> (38)..(38)
<223> Xaa in position 38 is any amino acid

<220>
<221> Variant
<222> (41)..(41)
<223> Xaa in position 41 is Leu or Val

<220>
<221> Variant
<222> (42)..(42)
<223> Xaa in position 42 is Thr or Val

<220>
<221> Variant
<222> (46)..(46)

```

<223> Xaa in position 46 is Glu or Asn

<220>

<221> Variant

<222> (50)..(50)

<223> Xaa in position 50 is any amino acid

<220>

<221> Variant

<222> (53)..(53)

<223> Xaa in position 53 is Ala, Asp or Val

<400> 9874

Ala	Xaa	Lys	Val	Xaa	Xaa	Ile	Xaa	Asp	Thr	Asp	Phe	Xaa	Thr	Thr	Gln
1				5					10					15	
Ala	Phe	Cys	Xaa	Xaa	Tyr	Glu	Gly	Xaa	Xaa	His	Pro	Phe	Xaa	Xaa	Xaa
		20					25						30		
Xaa	Xaa	Xaa	Glu	Tyr	Xaa	Phe	Asp	Xaa	Xaa	Ile	Leu	Leu	Xaa	Asn	Asn
		35					40					45			
Thr	Xaa	Trp	Val	Xaa	Asp	Gly	Leu	Arg	Ser	Leu	Gly				
	50					55					60				

<210> 9875

<211> 60

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (3)..(3)

<223> Xaa in position 3 is Ile or Val

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Leu or Val

<220>

<221> Variant

<222> (16)..(16)

<223> Xaa in position 16 is any amino acid

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is Leu or Met

<220>

<221> Variant

<222> (19)..(19)

<223> Xaa in position 19 is any amino acid

<220>

<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is Glu or Arg

<220>

<221> Variant

<222> (22)..(22)

<223> Xaa in position 22 is any amino acid

<220>

<221> Variant

<222> (24)..(24)

<223> Xaa in position 24 is any amino acid

<220>
<221> Variant
<222> (30)..(31)
<223> Xaa in position 30 to 31 is Ile or Val

<220>
<221> Variant
<222> (32)..(32)
<223> Xaa in position 32 is Leu, Met or Val

<220>
<221> Variant
<222> (33)..(33)
<223> Xaa in position 33 is Cys or Gly

<220>
<221> Variant
<222> (34)..(34)
<223> Xaa in position 34 is any amino acid

<220>
<221> Variant
<222> (36)..(36)
<223> Xaa in position 36 is Asp, Glu or Thr

<220>
<221> Variant
<222> (37)..(37)
<223> Xaa in position 37 is any amino acid

<220>
<221> Variant
<222> (40)..(41)
<223> Xaa in position 40 to 41 is any amino acid

<220>
<221> Variant
<222> (44)..(44)
<223> Xaa in position 44 is any amino acid

<220>
<221> Variant
<222> (45)..(45)
<223> Xaa in position 45 is Asp, Asn or Ser

<220>
<221> Variant
<222> (47)..(47)
<223> Xaa in position 47 is any amino acid

<220>
<221> Variant
<222> (49)..(49)
<223> Xaa in position 49 is any amino acid

<220>
<221> Variant
<222> (50)..(50)
<223> Xaa in position 50 is Gln or Arg

<220>
<221> Variant
<222> (51)..(51)
<223> Xaa in position 51 is any amino acid

<220>
<221> Variant

PF59083SeqList PF59083.txt

<222> (55)..(55)

<223> Xaa in position 55 is Pro, Gln or Ser

<400> 9875

Gly	Val	Xaa	Phe	Gly	Lys	Phe	Tyr	Pro	Xaa	His	Thr	Gly	His	Ile	Xaa
1				5				10					15		
Xaa	Ile	Xaa	Xaa	Ala	Xaa	Ser	Xaa	Val	Asp	Glu	Leu	His	Xaa	Xaa	Xaa
			20				25					30			
Xaa	Xaa	Asp	Xaa	Xaa	Arg	Asp	Xaa	Xaa	Leu	Phe	Xaa	Xaa	Ser	Xaa	Met
		35					40					45			
Xaa	Xaa	Xaa	Pro	Thr	Val	Xaa	Asp	Arg	Leu	Arg	Trp				
	50					55				60					

<210> 9876

<211> 57

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (2)..(2)

<223> Xaa in position 2 is any amino acid

<220>

<221> Variant

<222> (4)..(4)

<223> Xaa in position 4 is any amino acid

<220>

<221> Variant

<222> (5)..(5)

<223> Xaa in position 5 is any or no amino acid

<220>

<221> Variant

<222> (7)..(7)

<223> Xaa in position 7 is any or no amino acid

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is any amino acid

<220>

<221> Variant

<222> (13)..(13)

<223> Xaa in position 13 is Asp, Glu, Gln or Arg

<220>

<221> Variant

<222> (14)..(14)

<223> Xaa in position 14 is Ala, Ser or Val

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is any amino acid

<220>

<221> Variant

<222> (18)..(18)

<223> Xaa in position 18 is Ala or Gly

<220>

<221> Variant


```

<222> (19)..(21)
<223> Xaa in position 19 to 21 is any amino acid

<220>
<221> Variant
<222> (22)..(22)
<223> Xaa in position 22 is Phe or Leu

<220>
<221> Variant
<222> (23)..(23)
<223> Xaa in position 23 is Phe or Met

<220>
<221> Variant
<222> (24)..(24)
<223> Xaa in position 24 is any amino acid

<220>
<221> Variant
<222> (25)..(25)
<223> Xaa in position 25 is Glu or Lys

<220>
<221> Variant
<222> (27)..(27)
<223> Xaa in position 27 is any amino acid

<220>
<221> Variant
<222> (28)..(28)
<223> Xaa in position 28 is Phe or Ile

<220>
<221> Variant
<222> (29)..(29)
<223> Xaa in position 29 is any amino acid

<220>
<221> Variant
<222> (31)..(31)
<223> Xaa in position 31 is Asp, Glu, Asn, Ser or Thr

<220>
<221> Variant
<222> (32)..(32)
<223> Xaa in position 32 is any amino acid

<220>
<221> Variant
<222> (33)..(33)
<223> Xaa in position 33 is Ile or Val

<220>
<221> Variant
<222> (34)..(34)
<223> Xaa in position 34 is Phe or Tyr

<220>
<221> Variant
<222> (35)..(35)
<223> Xaa in position 35 is Ser or Thr

<220>
<221> Variant
<222> (38)..(38)
<223> Xaa in position 38 is any amino acid

<220>

```

```

<221> Variant
<222> (39)..(39)
<223> Xaa in position 39 is Ala or Gln

<220>
<221> Variant
<222> (41)..(41)
<223> Xaa in position 41 is any amino acid

<220>
<221> Variant
<222> (42)..(42)
<223> Xaa in position 42 is Ala, Leu or Pro

<220>
<221> Variant
<222> (43)..(43)
<223> Xaa in position 43 is any amino acid

<220>
<221> Variant
<222> (45)..(45)
<223> Xaa in position 45 is any amino acid

<220>
<221> Variant
<222> (46)..(46)
<223> Xaa in position 46 is Glu or Lys

<220>
<221> Variant
<222> (47)..(47)
<223> Xaa in position 47 is His or Tyr

<220>
<221> Variant
<222> (48)..(48)
<223> Xaa in position 48 is Phe or Leu

<220>
<221> Variant
<222> (49)..(49)
<223> Xaa in position 49 is Asp, Gly or Asn

<220>
<221> Variant
<222> (50)..(50)
<223> Xaa in position 50 is Ile or Leu

<220>
<221> Variant
<222> (51)..(51)
<223> Xaa in position 51 is Asp or Glu

<220>
<221> Variant
<222> (52)..(52)
<223> Xaa in position 52 is Ala, Thr or Val

<220>
<221> Variant
<222> (53)..(53)
<223> Xaa in position 53 is any amino acid

<220>
<221> Variant
<222> (55)..(55)
<223> Xaa in position 55 is Ile or Val

```

PF59083SeqList PF59083.txt

<400> 9876

Glu Xaa Gly Xaa Xaa Pro Xaa Tyr Pro Xaa Gly Trp Xaa Xaa Trp Ser
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Pro Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Ser Glu Xaa Xaa Asp Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Leu Xaa Asp Pro
 50 55

<210> 9877

<211> 23

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (2)..(2)

<223> Xaa in position 2 is any or no amino acid

<220>

<221> Variant

<222> (4)..(5)

<223> Xaa in position 4 to 5 is any amino acid

<220>

<221> Variant

<222> (6)..(6)

<223> Xaa in position 6 is any or no amino acid

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Asn or Ser

<220>

<221> Variant

<222> (14)..(14)

<223> Xaa in position 14 is Ala, Gln or Thr

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is Ala, Glu, Ser or Thr

<220>

<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is His, Lys or Arg

<220>

<221> Variant

<222> (22)..(22)

<223> Xaa in position 22 is any amino acid

<400> 9877

Gln Xaa Leu Xaa Xaa Xaa Lys Ile Lys Xaa Pro Ser Ala Xaa Lys Leu
 1 5 10 15
 Xaa Ala Leu His Xaa Xaa Leu
 20

<210> 9878

<211> 40

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (2)..(3)

<223> Xaa in position 2 to 3 is any amino acid

<220>

<221> Variant

<222> (6)..(6)

<223> Xaa in position 6 is any amino acid

<220>

<221> Variant

<222> (9)..(10)

<223> Xaa in position 9 to 10 is any amino acid

<220>

<221> Variant

<222> (11)..(11)

<223> Xaa in position 11 is Leu or Met

<220>

<221> Variant

<222> (13)..(13)

<223> Xaa in position 13 is any amino acid

<220>

<221> Variant

<222> (14)..(14)

<223> Xaa in position 14 is Glu or Lys

<220>

<221> Variant

<222> (15)..(16)

<223> Xaa in position 15 to 16 is any amino acid

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is Ile or Val

<220>

<221> Variant

<222> (18)..(18)

<223> Xaa in position 18 is Glu or Pro

<220>

<221> Variant

<222> (19)..(19)

<223> Xaa in position 19 is Phe or Tyr

<220>

<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is Ile or Val

<220>

<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is any amino acid

<220>

<221> Variant

<222> (22)..(22)

<223> Xaa in position 22 is Ile or Val

```

<220>
<221> Variant
<222> (23)..(23)
<223> Xaa in position 23 is Asp, Glu or Lys

<220>
<221> Variant
<222> (24)..(24)
<223> Xaa in position 24 is Glu or Ser

<220>
<221> Variant
<222> (25)..(25)
<223> Xaa in position 25 is any amino acid

<220>
<221> Variant
<222> (26)..(26)
<223> Xaa in position 26 is Asp or Ser

<220>
<221> Variant
<222> (28)..(28)
<223> Xaa in position 28 is any amino acid

<220>
<221> Variant
<222> (29)..(29)
<223> Xaa in position 29 is Ala, Asp, Glu, Gly or Ser

<220>
<221> Variant
<222> (31)..(33)
<223> Xaa in position 31 to 33 is any amino acid

<220>
<221> Variant
<222> (34)..(34)
<223> Xaa in position 34 is any or no amino acid

<220>
<221> Variant
<222> (36)..(36)
<223> Xaa in position 36 is Glu or Lys

<220>
<221> Variant
<222> (37)..(37)
<223> Xaa in position 37 is any amino acid

<220>
<221> Variant
<222> (38)..(38)
<223> Xaa in position 38 is Ile or Val

<220>
<221> Variant
<222> (39)..(39)
<223> Xaa in position 39 is any amino acid

<220>
<221> Variant
<222> (40)..(40)
<223> Xaa in position 40 is Glu or Gln

<400> 9878
Arg Xaa Xaa Phe Gln Xaa Leu Leu Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa
1          5          10          15
Seite 10405

```

PF59083SeqList PF59083.txt

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Arg Xaa Xaa
 20 25 30
 Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa
 35 40

<210> 9879
 <211> 22
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is any amino acid

<220>
 <221> Variant
 <222> (8)..(8)
 <223> Xaa in position 8 is Asp or Pro

<220>
 <221> Variant
 <222> (9)..(9)
 <223> Xaa in position 9 is any amino acid

<220>
 <221> Variant
 <222> (10)..(10)
 <223> Xaa in position 10 is Ile or Met

<220>
 <221> Variant
 <222> (15)..(15)
 <223> Xaa in position 15 is any or no amino acid

<220>
 <221> Variant
 <222> (17)..(17)
 <223> Xaa in position 17 is any or no amino acid

<220>
 <221> Variant
 <222> (21)..(21)
 <223> Xaa in position 21 is Phe or Tyr

<400> 9879
 Ala Xaa Gln Tyr Ser Asp Tyr Xaa Xaa Xaa Ala Leu Gly His Xaa Gln
 1 5 10 15
 Xaa Tyr Ile Asp Xaa Ala
 20

<210> 9880
 <211> 23
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (3)..(4)
 <223> Xaa in position 3 to 4 is any or no amino acid

```

<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is any amino acid

<220>
<221> Variant
<222> (7)..(8)
<223> Xaa in position 7 to 8 is any or no amino acid

<220>
<221> Variant
<222> (10)..(11)
<223> Xaa in position 10 to 11 is any amino acid

<220>
<221> Variant
<222> (12)..(12)
<223> Xaa in position 12 is Gly, Asn or Ser

<220>
<221> Variant
<222> (13)..(14)
<223> Xaa in position 13 to 14 is any amino acid

<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is Leu or Val

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is Asn or Gln

<220>
<221> Variant
<222> (17)..(17)
<223> Xaa in position 17 is Asp, Glu or Gln

<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is Ile, Leu or Val

<220>
<221> Variant
<222> (19)..(19)
<223> Xaa in position 19 is Ala or Cys

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is Ala, Asp, Glu, Gln or Thr

<220>
<221> Variant
<222> (21)..(21)
<223> Xaa in position 21 is any amino acid

<220>
<221> Variant
<222> (22)..(22)
<223> Xaa in position 22 is Ala, Cys or Ser

<220>
<221> Variant
<222> (23)..(23)
<223> Xaa in position 23 is Gly or Asn

```

PF59083SeqList PF59083.txt

<400> 9880
 Tyr Leu Xaa Xaa Lys Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20

<210> 9881
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is Ser, Thr or Val

<220>
 <221> Variant
 <222> (4)..(4)
 <223> Xaa in position 4 is Phe or Met

<220>
 <221> Variant
 <222> (5)..(5)
 <223> Xaa in position 5 is any amino acid

<220>
 <221> Variant
 <222> (6)..(6)
 <223> Xaa in position 6 is Ile or Val

<220>
 <221> Variant
 <222> (8)..(8)
 <223> Xaa in position 8 is Ala or Gly

<220>
 <221> Variant
 <222> (9)..(10)
 <223> Xaa in position 9 to 10 is any amino acid

<220>
 <221> Variant
 <222> (13)..(13)
 <223> Xaa in position 13 is any amino acid

<220>
 <221> Variant
 <222> (14)..(14)
 <223> Xaa in position 14 is Ala, Asp, Glu, Asn or Thr

<400> 9881
 Arg Xaa Phe Xaa Xaa Ser Xaa Xaa Xaa Ile Arg Xaa Xaa
 1 5 10

<210> 9882
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

PF59083SeqList PF59083.txt

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is any amino acid

<400> 9882
 Gln Xaa Phe Lys Tyr Gln Lys Asn
 1 5

<210> 9883
 <211> 564
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>
 <221> CDS
 <222> (1)..(564)

<400> 9883
 atg cta cct tta tat ctt tta aca aat gcg aag gga caa caa atg caa 48
 Met Leu Pro Leu Tyr Leu Leu Thr Asn Ala Lys Gly Gln Gln Met Gln
 1 5 10 15
 ata gaa ttg aaa aac ggt gaa att ata caa ggg ata ttg acc aac gta 96
 Ile Glu Leu Lys Asn Gly Glu Ile Ile Gln Gly Ile Leu Thr Asn Val
 20 25 30
 gat aac tgg atg aac ctt act tta tct aat gta acc gaa tat agt gaa 144
 Asp Asn Trp Met Asn Leu Thr Leu Ser Asn Val Thr Glu Tyr Ser Glu
 35 40 45
 gaa agc gca att aat tca gaa gac aat gct gag agc agt aaa gcc gta 192
 Glu Ser Ala Ile Asn Ser Glu Asp Asn Ala Glu Ser Ser Lys Ala Val
 50 55 60
 aaa ttg aac gaa att tat att aga ggg act ttt atc aag ttt atc aaa 240
 Lys Leu Asn Glu Ile Tyr Ile Arg Gly Thr Phe Ile Lys Phe Ile Lys
 65 70 75 80
 ttg caa gat aat ata att gac aag gtc aag cag caa att aac tcc aac 288
 Leu Gln Asp Asn Ile Ile Asp Lys Val Lys Gln Gln Ile Asn Ser Asn
 85 90 95
 aat aac tct aat agt aac ggc cct ggg cat aaa aga tac tac aac aat 336
 Asn Asn Ser Asn Ser Asn Gly Pro Gly His Lys Arg Tyr Tyr Asn Asn
 100 105 110
 agg gat tca aac aac aat aga ggt aac tac aac aga aga aat aat aat 384
 Arg Asp Ser Asn Asn Asn Arg Gly Asn Tyr Asn Arg Arg Asn Asn Asn
 115 120 125
 aac ggc aac agc aac cgc cgt cca tac tct caa aac cgt caa tac aac 432
 Asn Gly Asn Ser Asn Arg Arg Pro Tyr Ser Gln Asn Arg Gln Tyr Asn
 130 135 140
 aac agc aac agc agt aac att aac aac agt atc aac agt atc aat agc 480
 Asn Ser Asn Ser Ser Asn Ile Asn Asn Ser Ile Asn Ser Ile Asn Ser
 145 150 155 160
 aac aac caa aat atg aac aat ggt tta ggt ggg tcc gcc caa cat cat 528
 Asn Asn Gln Asn Met Asn Asn Gly Leu Gly Gly Ser Ala Gln His His
 165 170 175
 ttt aac agc tct tct cca caa aag gtc gaa ttt taa 564
 Phe Asn Ser Ser Ser Pro Gln Lys Val Glu Phe
 180 185

<210> 9884
 <211> 187
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 9884
 Met Leu Pro Leu Tyr Leu Leu Thr Asn Ala Lys Gly Gln Gln Met Gln
 1 5 10 15
 Ile Glu Leu Lys Asn Gly Glu Ile Ile Gln Gly Ile Leu Thr Asn Val
 20 25 30
 Asp Asn Trp Met Asn Leu Thr Leu Ser Asn Val Thr Glu Tyr Ser Glu
 35 40 45
 Glu Ser Ala Ile Asn Ser Glu Asp Asn Ala Glu Ser Ser Lys Ala Val
 50 55 60
 Seite 10409

PF59083SeqList PF59083.txt

50 55 60
 Lys Leu Asn Glu Ile Tyr Ile Arg Gly Thr Phe Ile Lys Phe Ile Lys
 65 70 75 80
 Leu Gln Asp Asn Ile Ile Asp Lys Val Lys Gln Gln Ile Asn Ser Asn
 85 90 95
 Asn Asn Ser Asn Ser Asn Gly Pro Gly His Lys Arg Tyr Tyr Asn Asn
 100 105 110
 Arg Asp Ser Asn Asn Asn Arg Gly Asn Tyr Asn Arg Arg Asn Asn Asn
 115 120 125
 Asn Gly Asn Ser Asn Arg Arg Pro Tyr Ser Gln Asn Arg Gln Tyr Asn
 130 135 140
 Asn Ser Asn Ser Ser Asn Ile Asn Asn Ser Ile Asn Ser Ile Asn Ser
 145 150 155 160
 Asn Asn Gln Asn Met Asn Asn Gly Leu Gly Gly Ser Ala Gln His His
 165 170 175
 Phe Asn Ser Ser Pro Gln Lys Val Glu Phe
 180 185

<210> 9885

<211> 507

<212> DNA

<213> *Eremothecium gossypii*

<220>

<221> CDS

<222> (1)..(507)

<400> 9885

atg ctg ccg cta tac ctg ttg acg aac gcc aag ggc cag aag ctc ttt	48
Met Leu Pro Leu Tyr Leu Leu Thr Asn Ala Lys Gly Gln Lys Leu Phe	
1 5 10 15	
ata gag ctc aag aac ggc gag acg atc gag ggg gag ctt gtg aat gtt	96
Ile Glu Leu Lys Asn Gly Glu Thr Ile Glu Gly Glu Leu Val Asn Val	
20 25 30	
gat aac tgg atg aac ctg aca ctg cag agc gtg gtg cat gca ggg agc	144
Asp Asn Trp Met Asn Leu Thr Leu Gln Ser Val Val His Ala Gly Ser	
35 40 45	
gac caa aca ctg caa ctt ccg gag ata tat gtg cgg ggt tcc ttc atc	192
Asp Gln Thr Leu Gln Leu Pro Glu Ile Tyr Val Arg Gly Ser Phe Ile	
50 55 60	
aag tat ata cgg ctt cag gac gac atc atc gag aag gtg aag cag cag	240
Lys Tyr Ile Arg Leu Gln Asp Asp Ile Ile Glu Lys Val Lys Gln Gln	
65 70 75 80	
ctg aac agc ggc aaa gac ggc agc ggc agc aac gga cag cag cgg gac	288
Leu Asn Ser Gly Lys Asp Gly Ser Gly Ser Asn Gly Gln Gln Arg Asp	
85 90 95	
cgc gac ggc aga agg tac aac ggc aga cga gaa ggc aat gcg ggc ggg	336
Arg Asp Gly Arg Arg Tyr Asn Gly Arg Arg Glu Gly Asn Ala Gly Gly	
100 105 110	
cgc ttc ggc aac cag gag cac cag cgg aag cgc ggg gga ggc ttt cag	384
Arg Phe Gly Asn Gln Glu His Gln Arg Lys Arg Gly Gly Gly Phe Gln	
115 120 125	
cgg cgc gac ggg cag tac ggc ggc agc agg cgc ggg cgg tcc ggc caa	432
Arg Arg Asp Gly Gln Tyr Gly Gly Ser Arg Arg Gly Arg Ser Gly Gln	
130 135 140	
tcg gga ggc gcc ggc ttt gtc cag tac caa cag tct cag cag tgg cag	480
Ser Gly Gly Ala Gly Phe Val Gln Tyr Gln Gln Ser Gln Gln Trp Gln	
145 150 155 160	
tcg tcc gca tcg caa gtc cag tcc tga	507
Ser Ser Ala Ser Gln Val Gln Ser	
165	

<210> 9886

<211> 168

<212> PRT

<213> *Eremothecium gossypii*

<400> 9886

Met Leu Pro Leu Tyr Leu Leu Thr Asn Ala Lys Gly Gln Lys Leu Phe

PF59083SeqList PF59083.txt

```

1           5           10           15
Ile Glu Leu Lys Asn Gly Glu Thr Ile Glu Gly Glu Leu Val Asn Val
      20           25           30
Asp Asn Trp Met Asn Leu Thr Leu Gln Ser Val Val His Ala Gly Ser
      35           40           45
Asp Gln Thr Leu Gln Leu Pro Glu Ile Tyr Val Arg Gly Ser Phe Ile
      50           55           60
Lys Tyr Ile Arg Leu Gln Asp Asp Ile Ile Glu Lys Val Lys Gln Gln
65           70           75           80
Leu Asn Ser Gly Lys Asp Gly Ser Gly Ser Asn Gly Gln Gln Arg Asp
      85           90           95
Arg Asp Gly Arg Arg Tyr Asn Gly Arg Arg Glu Gly Asn Ala Gly Gly
      100          105          110
Arg Phe Gly Asn Gln Glu His Gln Arg Lys Arg Gly Gly Gly Phe Gln
      115          120          125
Arg Arg Asp Gly Gln Tyr Gly Gly Ser Arg Arg Gly Arg Ser Gly Gln
      130          135          140
Ser Gly Gly Ala Gly Phe Val Gln Tyr Gln Gln Ser Gln Gln Trp Gln
145          150          155          160
Ser Ser Ala Ser Gln Val Gln Ser
      165

```

<210> 9887
 <211> 711
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (116)..(505)

<400> 9887
 ctgaatccaa caaggtttct cctgtctttg tttagggttt tgttctgttt ctcttcctct 60

attggttctc ccgcacgggt tctttaccga tctctaaatc tactgattgg agaag atg 118
 Met 1

ctt cct ctt tcg cta ctc aag act gct caa gga cat ccc atg ctt gtg 166
 Leu Pro Leu Ser Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu Val

gag ctc aag aat gga gag aca tac aat ggg cat tta gta aat tgc gat 214
 Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys Asp

acg tgg atg aac atc cat ctg cgt gaa gtt atc tgc aca tca aag gat 262
 Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Lys Asp

gga gac agg ttt tgg agg atg ccg gaa tgt tat atc cgt ggt aac act 310
 Gly Asp Arg Phe Trp Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn Thr

atc aag tac ctt cgt gtt cca gat gag gtg att gat aaa gta cag gag 358
 Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp Lys Val Gln Glu

gag aag acc cgc aca gat agg aaa cca cca ggg gtt gga cgt gga aga 406
 Glu Lys Thr Arg Thr Asp Arg Lys Pro Pro Gly Val Gly Arg Gly Arg

gga cgt ggt atg gat gat gga ggg gcc aga gga cga ggc cga gga gct 454
 Gly Arg Gly Met Asp Asp Gly Gly Ala Arg Gly Arg Gly Arg Gly Ala

cca atg gct aag atg agt ggc aac aga gga gca ggg cgt ggg cgt ggt 502
 Pro Met Ala Lys Met Ser Gly Asn Arg Gly Ala Gly Arg Gly Arg Gly

tga tgattcaaca actttgaacg acaaaactct gtgttttcta gctggctcct 555

cttgctgctg ctgctgttgt tgcactagtt tgattatatt ggaaggggat aaaattgctt 615

ttacaatgtg atttgactgt ttttttttct tcatgtatcg tttttcatgc tatattccat 675

PF59083SeqList PF59083.txt

tcagtgattg ttaaattctat ccaaaaaaaaa aaaaaa 711

<210> 9888
<211> 129
<212> PRT
<213> Brassica napus

<400> 9888
Met Leu Pro Leu Ser Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu
1 5 10 15
Val Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys
20 25 30
Asp Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Lys
35 40 45
Asp Gly Asp Arg Phe Trp Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn
50 55 60
Thr Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp Lys Val Gln
65 70 75 80
Glu Glu Lys Thr Arg Thr Asp Arg Lys Pro Pro Gly Val Gly Arg Gly
85 90 95
Arg Gly Arg Gly Met Asp Asp Gly Gly Ala Arg Gly Arg Gly Arg Gly
100 105 110
Ala Pro Met Ala Lys Met Ser Gly Asn Arg Gly Ala Gly Arg Gly Arg
115 120 125
Gly

<210> 9889
<211> 681
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (131)..(520)

<400> 9889
ggtaaccgga ttctgaaaat atttcgccgc ctccgtccgt cgtcttcgat ctctttcttt 60

tggtgaagag gaagccaatc ttctggtagc aagggttcttc acggatctct aaatcttttg 120

attcgagaag atg ctt cct ctt tcg ctg ctc aag act gct caa ggg cat 169
Met Leu Pro Leu Ser Leu Leu Lys Thr Ala Gln Gly His
1 5 10

ccc atg ctt gtg gag ctc aag aat gga gag acg tac aat ggg cat tta 217
Pro Met Leu Val Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu
15 20 25

gtg aat tgt gat acg tgg atg aac att cat ctg cgt gaa gtc atc tgc 265
Val Asn Cys Asp Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys
30 35 40 45

aca tca aag gac gga gac agg ttt tgg agg atg ccg gag tgt tat atc 313
Thr Ser Lys Asp Gly Asp Arg Phe Trp Arg Met Pro Glu Cys Tyr Ile
50 55 60

cgc ggt aac act atc aag tac ctt cga gtt cca gat gag gtg att gat 361
Arg Gly Asn Thr Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp
65 70 75

aaa gta cag gag gag aag acc cgc aca gat aga aaa cca cca ggg gtt 409
Lys Val Gln Glu Glu Lys Thr Arg Thr Asp Arg Lys Pro Pro Gly Val
80 85 90

gga cgt ggg aga gga cgt ggt gtg gat gat gga ggg gcc aga ggc cgt 457
Gly Arg Gly Arg Gly Arg Gly Val Asp Asp Gly Gly Ala Arg Gly Arg
95 100 105

ggt cga gga gct cca atg gcg aag atg agt ggc aac aga gga gca ggt 505

PF59083SeqList PF59083.txt

Gly Arg Gly Ala Pro Met Ala Lys Met Ser Gly Asn Arg Gly Ala Gly
 110 115 120 125
 cgt ggc cgt ggt tga tgcaagaact tatataaaga ctgcctgctg ctgcactcgc 560
 Arg Gly Arg Gly

attttaagag ttctcttggt tgtttaaatt tcatctttga gctaatatat aaaactaaac 620

attgtgcgct gaatatataa aattcgagct gttataagct tttccctaaa aaaaaaaaaa 680

a 681

<210> 9890
 <211> 129
 <212> PRT
 <213> Brassica napus

<400> 9890
 Met Leu Pro Leu Ser Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu
 1 5 10 15
 Val Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys
 20 25 30
 Asp Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Lys
 35 40 45
 Asp Gly Asp Arg Phe Trp Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn
 50 55 60
 Thr Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp Lys Val Gln
 65 70 75 80
 Glu Glu Lys Thr Arg Thr Asp Arg Lys Pro Pro Gly Val Gly Arg Gly
 85 90 95
 Arg Gly Arg Gly Val Asp Asp Gly Gly Ala Arg Gly Arg Gly Arg Gly
 100 105 110
 Ala Pro Met Ala Lys Met Ser Gly Asn Arg Gly Ala Gly Arg Gly Arg
 115 120 125
 Gly

<210> 9891
 <211> 763
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (98)..(547)

<400> 9891
 ggaacacaag agaggtctga ttaatactag ttttctgtaa aatcgcaaag aaacacacag 60

ttagcaccgt caacctctgc aaccaccgat tccaacc atg ctt ccc ctt tcc ctt 115
 Met Leu Pro Leu Ser Leu
 1 5

ctc aag act gcc caa ggc cac ccc atg ctg gtg gaa ctg aaa aat ggg 163
 Leu Lys Thr Ala Gln Gly His Pro Met Leu Val Glu Leu Lys Asn Gly
 10 15 20

gag act tat aac ggg cac ttg gtt aat tgt gat aca tgg atg aac atc 211
 Glu Thr Tyr Asn Gly His Leu Val Asn Cys Asp Thr Trp Met Asn Ile
 25 30 35

cat ctc cga gaa gtc att tgt acc tct aaa gat gga gat aga ttt tgg 259
 His Leu Arg Glu Val Ile Cys Thr Ser Lys Asp Gly Asp Arg Phe Trp
 40 45 50

cgt atg cct gag tgc tac att cgt ggc aat acc att aag tac ctt cgg 307
 Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn Thr Ile Lys Tyr Leu Arg
 55 60 65 70

gtt cct gat gag gtt att gac aaa gtc cag gaa aca aag agc cgt 355
 Seite 10413

PF59083SeqList PF59083.txt

```

Val Pro Asp Glu Val Ile Asp Lys Val Gln Glu Glu Thr Lys Ser Arg
      75      80      85
act gat cgc aaa ccc cct ggt gtg gga cgt gga agg gga aga ggt agg 403
Thr Asp Arg Lys Pro Pro Gly Val Gly Arg Gly Arg Gly Arg Gly Arg
      90      95      100
gat gat ggt cct ggt gga cgt caa cct aaa gga att ggg cga ggt att 451
Asp Asp Gly Pro Gly Gly Arg Gln Pro Lys Gly Ile Gly Arg Gly Ile
      105      110      115
gat gag ggt gga gct aaa gga caa gga gga cga ggc cgg ggt ggt cca 499
Asp Glu Gly Gly Ala Lys Gly Gln Gly Gly Arg Gly Arg Gly Gly Pro
      120      125      130
ggt gga aaa ccc agt gga aac aga ggt gca ggg cga ggt aga ggt tga 547
Gly Gly Lys Pro Ser Gly Asn Arg Gly Ala Gly Arg Gly Arg Gly
      135      140      145
tttgggtgct gatatggaac tacagatggg ccagttgctg ctttttagagg cattggtgcc 607

cattcaaac atttagtggt tgtgttatgt ttcctgtgca ttatttgatt ttaggtttcc 667

aattgttttc ctgcatttat agtcacaaaa atggtgatat tatggacctc ataaaaaatc 727

ttctatgccac acatcgtttt ccaaaaaaaaa aaaaaa 763

```

<210> 9892
 <211> 149
 <212> PRT
 <213> Glycine max

```

<400> 9892
Met Leu Pro Leu Ser Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu
1      5      10      15
Val Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys
      20      25      30
Asp Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Lys
      35      40      45
Asp Gly Asp Arg Phe Trp Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn
      50      55      60
Thr Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp Lys Val Gln
      65      70      75      80
Glu Glu Thr Lys Ser Arg Thr Asp Arg Lys Pro Pro Gly Val Gly Arg
      85      90      95
Gly Arg Gly Arg Gly Arg Asp Asp Gly Pro Gly Gly Arg Gln Pro Lys
      100      105      110
Gly Ile Gly Arg Gly Ile Asp Glu Gly Gly Ala Lys Gly Gln Gly Gly
      115      120      125
Arg Gly Arg Gly Gly Pro Gly Gly Lys Pro Ser Gly Asn Arg Gly Ala
      130      135      140
Gly Arg Gly Arg Gly
145

```

<210> 9893
 <211> 435
 <212> DNA
 <213> Unknown

<220>
 <223> Unidentified

<220>
 <221> CDS
 <222> (1)..(432)

```

<400> 9893
atg ctt ccc ctc tcg ctc ctc aag acc gcc cag ggg cat ccc atg ctc 48
Met Leu Pro Leu Ser Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu
      10414
Seite 10414

```

PF59083SeqList PF59083.txt

1	5	10	15	
gtg gag ctc aag aac ggc gag acc tac aat ggg cac ttg gtg aac tgc				96
Val Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys				
20	25	30		
gac acg tgg atg aac atc cac ctc cgg gag gtt att tgc acc tct aag				144
Asp Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Lys				
35	40	45		
gat ggt gat aag ttt tgg agg atg ccg gag tgc tat att cgt ggt aac				192
Asp Gly Asp Lys Phe Trp Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn				
50	55	60		
acg atc aag tat ctt cgg gtt cct gat gag gtg att gac aag gtt caa				240
Thr Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp Lys Val Gln				
65	70	75		
gag gaa act tct aag agt aga tca gat agg aag cca cca ggt gtt ggt				288
Glu Glu Thr Ser Lys Ser Arg Ser Asp Arg Lys Pro Pro Gly Val Gly				
85	90	95		
cgt gga aga gga aga gga gat ata ggc act aaa cct gga ggc aga ggc				336
Arg Gly Arg Gly Arg Gly Asp Ile Gly Thr Lys Pro Gly Gly Arg Gly				
100	105	110		
att ggt cgt ggc caa gat gat ggc aaa ggc ggt ggc cgt gga agg ggc				384
Ile Gly Arg Gly Gln Asp Asp Gly Lys Gly Gly Gly Arg Gly Arg Gly				
115	120	125		
gga att gga agt aaa ggt ggc aac aaa ggc gga cgt ggt cgt ggg taa				432
Gly Ile Gly Ser Lys Gly Gly Asn Lys Gly Gly Arg Gly Arg Gly				
130	135	140		
gac				435

<210> 9894
 <211> 143
 <212> PRT
 <213> Unknown

<220>
 <223> Unidentified

<400> 9894
Met Leu Pro Leu Ser Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu
1 5 10 15
Val Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys
20 25 30
Asp Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Lys
35 40 45
Asp Gly Asp Lys Phe Trp Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn
50 55 60
Thr Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp Lys Val Gln
65 70 75
Glu Glu Thr Ser Lys Ser Arg Ser Asp Arg Lys Pro Pro Gly Val Gly
85 90 95
Arg Gly Arg Gly Arg Gly Asp Ile Gly Thr Lys Pro Gly Gly Arg Gly
100 105 110
Ile Gly Arg Gly Gln Asp Asp Gly Lys Gly Gly Gly Arg Gly Arg Gly
115 120 125
Gly Ile Gly Ser Lys Gly Gly Asn Lys Gly Gly Arg Gly Arg Gly
130 135 140

<210> 9895
 <211> 838
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (54)..(500)

<400> 9895	
gttttctttg aaacgcacag cttcaatcac cgaccacacc acccatcaac gac atg	56
	Met

PF59083SeqList PF59083.txt

ctt cct ctt tcc ctt ctc aag act gcc caa ggc cac cct atg ttg gtg	1	104
Leu Pro Leu Ser 5 Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu Val	10 15	
gaa ctg aaa aat ggg gag aca tat aac ggg cat ttg gtt aat tgc gac	20 25 30	152
Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys Asp	35 40 45	
aca tgg atg aac atc cat ctg cga gaa gtc att tgt aca tct aaa gac	50 55 60	200
Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Lys Asp	65 70 75	
gga gat aga ttt tgg agg atg cct gaa tgc tac ata cga ggc aat aca	80 85 90	248
Gly Asp Arg Phe Trp Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn Thr	95 100 105	
atc aag tac ctt cga gta cct gat gag gtt att gat aaa gtt caa gaa	110 115 120	296
Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp Lys Val Gln Glu	125 130 135	
gaa acc aag agc cgt gca gat cgc aaa cca cct ggt gtt ggg cgt gga	140 145 150	344
Glu Thr Lys Ser Arg Ala Asp Arg Lys Pro Pro Gly Val Gly Arg Gly	155 160 165	
agg gga aga ggc aga gag gaa ggt cct ggt ggg cgc cca aca aaa gga	170 175 180	392
Arg Gly Arg Gly Arg Glu Glu Gly Pro Gly Gly Arg Pro Thr Lys Gly	185 190 195	
att ggg cgt ggt ctt gat gat ggt ggt gct agg gga gct gga gga agc	200 205 210	440
Ile Gly Arg Gly Leu Asp Asp Gly Gly Ala Arg Gly Ala Gly Gly Ser	215 220 225	
cga ggc agg ggt ggt ccc agt gga aag cct ggt gga aac aga ggg cgt	230 235 240	488
Arg Gly Arg Gly Gly Pro Ser Gly Lys Pro Gly Gly Asn Arg Gly Arg	245 250 255	
ggg aga ggt tga ttctaacaag tgacaggaac tacttaaatgt gtatcggtag		540
Gly Arg Gly		
caacttcact gccagtgtta cctgtgcatc cttgccttgg ctttttagctt ccagtgtttt		600
tcttgtgtta tgagcacaaa aatgttagtg ctattatatt actcgaggaa agtttctctg		660
ccagactgcc cccgtctccc ttttaatatatt cccaacagca aacttgcctt ttccctttct		720
ttccttccaa tgaaaagtaa tgatggcgca atgcgtgaaa tacttaactc aaccttgata		780
tatttagaga tgtaatttg acaattgtat atttggcacc aagcaaaaaa aaaaaaaa		838

<210> 9896
 <211> 148
 <212> PRT
 <213> Glycine max

<400> 9896
 Met Leu Pro Leu Ser 5 Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu
 1 10 15
 Val Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys
 20 25 30
 Asp Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Lys
 35 40 45
 Asp Gly Asp Arg Phe Trp Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn
 50 55 60
 Thr Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp Lys Val Gln
 65 70 75 80
 Glu Glu Thr Lys Ser Arg Ala Asp Arg Lys Pro Pro Gly Val Gly Arg
 85 90 95
 Gly Arg Gly Arg Gly Arg Glu Glu Gly Pro Gly Gly Arg Pro Thr Lys
 100 105 110
 Gly Ile Gly Arg Gly Leu Asp Asp Gly Gly Ala Arg Gly Ala Gly Gly
 115 120 125

PF59083SeqList PF59083.txt

Ser Arg Gly Arg Gly Gly Pro Ser Gly Lys Pro Gly Gly Asn Arg Gly
 130 135 140
 Arg Gly Arg Gly
 145

<210> 9897
 <211> 450
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(450)

<400> 9897
 atg ctg ccc ctt tcc ctt ctc aag act gcc caa ggc cac cct atg cta 48
 Met Leu Pro Leu Ser Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu
 1 5 10 15
 gtg gaa ctg aaa aat ggg gag act tat aac ggg cac ttg gtt aat tgt 96
 Val Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys
 20 25 30
 gat aca tgg atg aac att cat ctc cga gaa gtc att tgt acc tct aaa 144
 Asp Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Lys
 35 40 45
 gat gga gat aga ttt tgg cgt atg ccc gag tgc tac att cgc ggc aat 192
 Asp Gly Asp Arg Phe Trp Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn
 50 55 60
 acc ata aag tac ctt cgg gtt cct gat gag gtt att gac aaa gtc cag 240
 Thr Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp Lys Val Gln
 65 70 75 80
 gaa gaa aca aag agc cgc act gat cgc aaa ccc cct ggt gtg gga cgt 288
 Glu Glu Thr Lys Ser Arg Thr Asp Arg Lys Pro Pro Gly Val Gly Arg
 85 90 95
 gga aga gga aga ggt agg gag gat ggt cct ggt gga cgt caa cca aaa 336
 Gly Arg Gly Arg Gly Arg Glu Asp Gly Pro Gly Gly Arg Gln Pro Lys
 100 105 110
 gga att ggg cgt ggc ctt gat gaa ggt gga cct aaa gga caa gga gga 384
 Gly Ile Gly Arg Gly Leu Asp Glu Gly Gly Pro Lys Gly Gln Gly Gly
 115 120 125
 cga ggt agg ggt ggt ccc ggt gga aag cct ggt gga aac aga ggt gga 432
 Arg Gly Arg Gly Gly Pro Gly Gly Lys Pro Gly Gly Asn Arg Gly Gly
 130 135 140
 ggg cga ggt aga ggt tga 450
 Gly Arg Gly Arg Gly
 145

<210> 9898
 <211> 149
 <212> PRT
 <213> Glycine max

<400> 9898
 Met Leu Pro Leu Ser Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu
 1 5 10 15
 Val Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys
 20 25 30
 Asp Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Lys
 35 40 45
 Asp Gly Asp Arg Phe Trp Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn
 50 55 60
 Thr Ile Lys Tyr Leu Arg Val Pro Asp Glu Val Ile Asp Lys Val Gln
 65 70 75 80
 Glu Glu Thr Lys Ser Arg Thr Asp Arg Lys Pro Pro Gly Val Gly Arg
 85 90 95
 Gly Arg Gly Arg Gly Arg Glu Asp Gly Pro Gly Gly Arg Gln Pro Lys
 100 105 110
 Gly Ile Gly Arg Gly Leu Asp Glu Gly Gly Pro Lys Gly Gln Gly Gly
 115 120 125
 Arg Gly Arg Gly Gly Pro Gly Gly Lys Pro Gly Gly Asn Arg Gly Gly

130
Gly Arg Gly Arg Gly
145

135

140

<210> 9899
<211> 441
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(441)

<400> 9899

atg	ctt	ccc	ctc	tcg	ctc	ctc	aag	acc	gcc	cag	ggg	cac	ccc	atg	ctc	48
Met	Leu	Pro	Leu	Ser	Leu	Leu	Lys	Thr	Ala	Gln	Gly	His	Pro	Met	Leu	
1				5					10					15		
gtg	gag	ctg	aag	aat	ggt	gag	aca	tac	aac	ggg	cat	ctg	gtc	aat	tgc	96
Val	Glu	Leu	Lys	Asn	Gly	Glu	Thr	Tyr	Asn	Gly	His	Leu	Val	Asn	Cys	
			20					25					30			
gac	acg	tgg	atg	aac	atc	cat	ctt	agg	gag	gtt	att	tgc	acc	tca	aag	144
Asp	Thr	Trp	Met	Asn	Ile	His	Leu	Arg	Glu	Val	Ile	Cys	Thr	Ser	Lys	
		35					40					45				
gac	ggt	gac	aag	ttt	tgg	agg	atg	cca	gag	tgt	tac	att	cgc	ggg	aac	192
Asp	Gly	Asp	Lys	Phe	Trp	Arg	Met	Pro	Glu	Cys	Tyr	Ile	Arg	Gly	Asn	
	50					55					60					
acc	att	aag	tat	ctt	cga	gtt	cct	gat	gag	gtg	att	gac	aag	gtt	cag	240
Thr	Ile	Lys	Tyr	Leu	Arg	Val	Pro	Asp	Glu	Val	Ile	Asp	Lys	Val	Gln	
	65				70				75					80		
gag	gaa	act	tct	aaa	agc	cga	tca	gat	agg	aag	cca	cca	ggt	gtt	ggc	288
Glu	Glu	Thr	Ser	Lys	Ser	Arg	Ser	Asp	Arg	Lys	Pro	Pro	Gly	Val	Gly	
				85					90					95		
cgt	gga	aga	gga	agg	ggg	gac	gtc	ggt	gct	aaa	cct	gga	ggc	aga	ggc	336
Arg	Gly	Arg	Gly	Arg	Gly	Asp	Val	Gly	Ala	Lys	Pro	Gly	Gly	Arg	Gly	
			100					105					110			
att	gga	cgc	ggc	caa	gat	gat	gga	ggt	aga	ggc	agt	ggt	ggc	cgt	gga	384
Ile	Gly	Arg	Gly	Gln	Asp	Asp	Gly	Gly	Arg	Gly	Ser	Gly	Gly	Arg	Gly	
		115					120					125				
agg	ggt	gga	gtt	ggt	gcc	aaa	ggt	ggt	aac	aaa	ggt	ggg	ggc	cgt	ggt	432
Arg	Gly	Gly	Val	Gly	Ala	Lys	Gly	Gly	Asn	Lys	Gly	Gly	Gly	Arg	Gly	
	130					135					140					
cgt	ggc	tga														441
Arg	Gly															
145																

<210> 9900
<211> 146
<212> PRT
<213> Zea mays

<400> 9900

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

Arg Gly
145

<210> 9901
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 9901
atgctacctt tataatctttt aacaaatg

28

<210> 9902
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 9902
ttaaaattcg accttttgtg gagaag

26

<210> 9903
<211> 172
<212> PRT
<213> Artificial sequence

<220>
<223> consensus sequence

<220>
<221> Variant
<222> (48)..(57)
<223> Xaa in position 48 to 57 is any amino acid

<220>
<221> Variant
<222> (62)..(62)
<223> Xaa in position 62 is any amino acid

<220>
<221> Variant
<222> (93)..(93)
<223> Xaa in position 93 is any amino acid

<220>
<221> Variant
<222> (94)..(94)
<223> Xaa in position 94 is any or no amino acid

<220>
<221> Variant
<222> (98)..(98)
<223> Xaa in position 98 is any amino acid

<220>
<221> Variant
<222> (113)..(124)
<223> Xaa in position 113 to 124 is any amino acid

<220>
<221> Variant
<222> (125)..(126)
<223> Xaa in position 125 to 126 is any or no amino acid

PF59083SeqList PF59083.txt

```

<220>
<221> Variant
<222> (128)..(128)
<223> Xaa in position 128 is any amino acid

<220>
<221> Variant
<222> (129)..(129)
<223> Xaa in position 129 is any or no amino acid

<220>
<221> Variant
<222> (131)..(131)
<223> Xaa in position 131 is any amino acid

<220>
<221> Variant
<222> (133)..(136)
<223> Xaa in position 133 to 136 is any amino acid

<220>
<221> Variant
<222> (137)..(140)
<223> Xaa in position 137 to 140 is any or no amino acid

<220>
<221> Variant
<222> (145)..(148)
<223> Xaa in position 145 to 148 is any amino acid

<220>
<221> Variant
<222> (150)..(150)
<223> Xaa in position 150 is any amino acid

<220>
<221> Variant
<222> (151)..(162)
<223> Xaa in position 151 to 162 is any or no amino acid

<220>
<221> Variant
<222> (165)..(165)
<223> Xaa in position 165 is any amino acid

<220>
<221> Variant
<222> (167)..(167)
<223> Xaa in position 167 is any amino acid

<220>
<221> Variant
<222> (168)..(168)
<223> Xaa in position 168 is any or no amino acid

<220>
<221> Variant
<222> (171)..(171)
<223> Xaa in position 171 is any amino acid

<400> 9903
Met Leu Pro Leu Ser Leu Leu Lys Thr Ala Gln Gly His Pro Met Leu
1      5      10      15
Val Glu Leu Lys Asn Gly Glu Thr Tyr Asn Gly His Leu Val Asn Cys
20      25      30
Asp Thr Trp Met Asn Ile His Leu Arg Glu Val Ile Cys Thr Ser Xaa
35      40      45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Asp Gly Asp Xaa Phe Trp
50      55      60

```

PF59083SeqList PF59083.txt

```

Arg Met Pro Glu Cys Tyr Ile Arg Gly Asn Thr Ile Lys Tyr Leu Arg
65      70      75      80
Val Pro Asp Glu Val Ile Asp Lys Val Gln Glu Glu Xaa Xaa Lys Ser
      85      90      95
Arg Xaa Asp Arg Lys Pro Pro Gly Val Gly Arg Gly Arg Gly Arg Gly
100      105      110
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
115      120      125
Xaa Asp Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Gly Arg Gly
130      135      140
Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145      150      155      160
Xaa Xaa Gly Asn Xaa Gly Xaa Xaa Arg Gly Xaa Gly
      165      170

```

<210> 9904
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<400> 9904
 Glu Leu Lys Asn Gly Glu
 1 5

<210> 9905
 <211> 690
 <212> DNA
 <213> SACCHAROMYCES CEREVISIAE

<220>
 <221> CDS
 <222> (1)..(690)

<400> 9905

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

PF59083SeqList PF59083.txt

Ser	Gln	Ser	Ser	Ile	Thr	Ala	Pro	Gln	Asn	Ser	Pro	Ser	Asn	Leu	Arg	
				165				170						175		
gat	tgg	ttg	gcc	cca	tta	aat	gca	tat	gat	agt	gac	gat	gtt	cca	gtt	576
Asp	Trp	Leu	Ala	Pro	Leu	Asn	Ala	Tyr	Asp	Ser	Asp	Asp	Val	Pro	Val	
			180					185					190			
cca	aag	tat	tcg	cca	aat	gat	aaa	gtc	agt	gta	ccg	tcg	gaa	gac	aaa	624
Pro	Lys	Tyr	Ser	Pro	Asn	Asp	Lys	Val	Ser	Val	Pro	Ser	Glu	Asp	Lys	
		195					200					205				
caa	gaa	ctt	gaa	caa	aaa	aga	cta	caa	cag	tta	gaa	agc	gat	cct	ccc	672
Gln	Glu	Leu	Glu	Gln	Lys	Arg	Leu	Gln	Gln	Leu	Glu	Ser	Asp	Pro	Pro	
	210					215					220					
cct	tgt	gat	gac	tat	taa											690
Pro	Cys	Asp	Asp	Tyr												
225																

<210> 9906

<211> 229

<212> PRT

<213> SACCHAROMYCES CEREVISIAE

<400> 9906

Met	Asp	Pro	Met	Glu	Thr	Phe	Arg	Lys	Asp	Ile	Cys	Gln	Ser	Ile	Ser	
1				5					10					15		
Pro	Ile	Tyr	Ile	Asn	Pro	Glu	Thr	Leu	Gln	Phe	Gln	Ser	Arg	Val	Tyr	
			20					25					30			
Leu	Lys	Val	Pro	Leu	Asp	Ala	Phe	Ser	Thr	Leu	Thr	Thr	Val	Gly	Lys	
		35				40						45				
Phe	Phe	Ser	Phe	Gln	Tyr	Tyr	Ile	Glu	Val	Met	Val	Asn	Leu	Ser	Lys	
	50				55					60						
Lys	Asn	Val	Val	Tyr	Thr	Glu	Ser	Asn	Arg	Ile	Ile	Gly	Thr	Pro	Ile	
65				70						75				80		
Gly	Glu	Gln	Asn	Gly	Leu	Gly	Val	Glu	Asn	Asn	Ile	Asn	Arg	Ile	Gln	
			85					90						95		
Arg	Lys	Met	Leu	Arg	Met	Val	Asn	Pro	Glu	Thr	Leu	Glu	Asn	Asp	Ser	
			100					105					110			
Glu	Gly	Tyr	Glu	Ser	Ser	Ile	Phe	Phe	Lys	Asp	Met	Val	Asn	Val	Glu	
		115					120					125				
Lys	Leu	Lys	Arg	Leu	Arg	Asn	Val	Thr	Gly	Met	Ser	Ile	Glu	Thr	Val	
	130					135					140					
Ile	Gly	Thr	Thr	Arg	Ser	Glu	Gln	Gln	Gln	Ser	Asp	Ala	Ser	Ile	Pro	
145				150						155					160	
Ser	Gln	Ser	Ser	Ile	Thr	Ala	Pro	Gln	Asn	Ser	Pro	Ser	Asn	Leu	Arg	
				165				170						175		
Asp	Trp	Leu	Ala	Pro	Leu	Asn	Ala	Tyr	Asp	Ser	Asp	Asp	Val	Pro	Val	
			180					185					190			
Pro	Lys	Tyr	Ser	Pro	Asn	Asp	Lys	Val	Ser	Val	Pro	Ser	Glu	Asp	Lys	
		195					200					205				
Gln	Glu	Leu	Glu	Gln	Lys	Arg	Leu	Gln	Gln	Leu	Glu	Ser	Asp	Pro	Pro	
	210					215					220					
Pro	Cys	Asp	Asp	Tyr												
225																

<210> 9907

<211> 1539

<212> DNA

<213> Saccharomyces pastorianus

<220>

<221> CDS

<222> (1)..(1539)

<400> 9907

atg	ctg	gcc	cat	aac	aac	gtc	cgg	caa	ttt	cgc	att	gac	ata	aac	gag	48
Met	Leu	Ala	His	Asn	Asn	Val	Arg	Gln	Phe	Arg	Ile	Asp	Ile	Asn	Glu	
1				5					10					15		
ccg	cac	agt	gtg	tgg	aag	ccc	gat	gaa	tgc	ata	acc	ggg	gag	aca	gtc	96
Pro	His	Ser	Val	Trp	Lys	Pro	Asp	Glu	Cys	Ile	Thr	Gly	Glu	Thr	Val	
			20					25					30			
atc	gac	atc	aag	aga	gac	atc	act	aat	gtg	gcc	att	aag	ctc	tct	ctg	144

PF59083SeqList PF59083.txt																
Ile	Asp	Ile	Lys	Arg	Asp	Ile	Thr	Asn	Val	Ala	Ile	Lys	Leu	Ser	Leu	
gtg	tgt	gag	gta	cga	gtg	aag	acc	ggc	aat	agt	cca	acc	tcc	aag	aat	192
Val	Cys	Glu	Val	Arg	Val	Lys	Thr	Gly	Asn	Ser	Pro	Thr	Ser	Lys	Asn	
aaa	aga	gta	gag	aag	att	tta	gaa	aag	tca	acc	ttt	ctt	tac	ggg	caa	240
Lys	Arg	Val	Glu	Lys	Ile	Leu	Glu	Lys	Ser	Thr	Phe	Leu	Tyr	Gly	Gln	
65					70				75						80	
gag	tac	ata	aag	gca	gct	ccc	gcg	gag	aaa	aaa	ccg	gcc	atc	gac	aag	288
Glu	Tyr	Ile	Lys	Ala	Ala	Pro	Ala	Glu	Lys	Lys	Pro	Ala	Ile	Asp	Lys	
				85					90					95		
tct	acc	gtt	ctc	aac	ggt	cta	agc	aag	ggc	gaa	cac	aga	ttc	ccc	ttc	336
Ser	Thr	Val	Leu	Asn	Gly	Leu	Ser	Lys	Gly	Glu	His	Arg	Phe	Pro	Phe	
			100					105					110			
aga	ata	aaa	ata	cca	agg	ggc	aag	ggc	atg	ttg	agc	tcc	atc	aaa	ttc	384
Arg	Ile	Lys	Ile	Pro	Arg	Gly	Lys	Gly	Met	Leu	Ser	Ser	Ile	Lys	Phe	
		115					120					125				
gaa	aga	ggc	tcc	atc	gca	tac	ttc	ctg	aac	tgc	acc	ttg	gag	tcc	ctt	432
Glu	Arg	Gly	Ser	Ile	Ala	Tyr	Phe	Leu	Asn	Cys	Thr	Leu	Glu	Ser	Leu	
	130					135					140					
aat	aac	gtt	aat	gct	ctg	aaa	cca	gag	gcg	agg	tgc	gaa	cgt	gag		480
Asn	Asn	Val	Asn	Ala	Leu	Lys	Lys	Pro	Glu	Ala	Arg	Cys	Glu	Arg	Glu	
145				150					155						160	
ttc	tcg	gtc	ata	gtg	ccc	ttg	gac	gtc	tcg	agg	ctg	ccc	aaa	cag	aag	528
Phe	Ser	Val	Ile	Val	Pro	Leu	Asp	Val	Ser	Arg	Leu	Pro	Lys	Gln	Lys	
			165					170						175		
acc	aag	acg	gtg	gtg	ctg	cag	tcc	gca	tcc	atg	gtc	caa	aac	aaa	aag	576
Thr	Lys	Thr	Val	Val	Leu	Gln	Ser	Ala	Ser	Met	Val	Gln	Asn	Lys	Lys	
			180					185					190			
ggc	aaa	tcc	tcg	gag	gac	gca	tcc	tcc	tac	aca	caa	tta	acc	cat		624
Gly	Lys	Ser	Ser	Glu	Asp	Ala	Ser	Ser	Ser	Tyr	Thr	Gln	Leu	Thr	His	
		195					200					205				
aag	tcc	aac	aat	tcc	aat	tct	tcc	agc	agt	acg	gta	aac	tcc	tcc	aag	672
Lys	Ser	Asn	Asn	Ser	Asn	Ser	Ser	Ser	Ser	Thr	Val	Asn	Ser	Ser	Lys	
	210					215					220					
aca	tcc	tcc	cca	cca	aac	aca	gtg	acc	ata	tcc	gtc	gac	ata	ccg		720
Thr	Ser	Ser	Pro	Pro	Asn	Lys	Thr	Val	Thr	Ile	Ser	Val	Asp	Ile	Pro	
225					230				235						240	
cac	gcc	ggg	ttc	gtg	atc	ggc	gag	acg	atc	ccc	atc	gac	gtg	aag	atc	768
His	Ala	Gly	Phe	Val	Ile	Gly	Glu	Thr	Ile	Pro	Ile	Asp	Val	Lys	Ile	
			245					250						255		
gaa	cac	tat	aaa	ccc	ttc	tac	cac	cca	gcg	ggc	ctc	acc	acc	acc	ttg	816
Glu	His	Tyr	Lys	Pro	Phe	Tyr	His	Pro	Ala	Gly	Leu	Thr	Thr	Thr	Leu	
			260					265					270			
gtg	aga	atc	agg	gtg	ggc	ggt	gcg	ggc	aaa	gac	gac	ccc	atg	gag		864
Val	Arg	Ile	Cys	Arg	Val	Gly	Gly	Ala	Gly	Lys	Asp	Asp	Pro	Met	Glu	
		275				280						285				
act	ttt	aga	aag	gac	atc	tgc	cag	agt	atc	tcc	cct	ata	tac	atc	aat	912
Thr	Phe	Arg	Lys	Asp	Ile	Cys	Gln	Ser	Ile	Ser	Pro	Ile	Tyr	Ile	Asn	
	290					295					300					
cct	gaa	acg	ctc	cag	ttc	cag	ccc	aga	att	cat	ttg	aaa	gtg	ccc	cta	960
Pro	Glu	Thr	Leu	Gln	Phe	Gln	Pro	Arg	Ile	His	Leu	Lys	Val	Pro	Leu	
305					310					315					320	
gac	gca	ttt	tcg	aca	ctc	acc	tcc	gtg	agc	aag	ttc	ttc	tcc	ttc	caa	1008
Asp	Ala	Phe	Ser	Thr	Leu	Thr	Ser	Val	Ser	Lys	Phe	Phe	Ser	Phe	Gln	
				325				330						335		
tac	tac	atc	gaa	gtc	atg	gtc	aat	ttg	tcc	aag	aaa	aac	gtg	gtc	tat	1056
Tyr	Tyr	Ile	Glu	Val	Met	Val	Asn	Leu	Ser	Lys	Lys	Asn	Val	Val	Tyr	
			340					345					350			
acg	gaa	tcc	aac	agg	gta	gta	gga	acc	ccc	gtc	gag	gag	cag	aac	ggc	1104
Thr	Glu	Ser	Asn	Arg	Val	Val	Gly	Thr	Pro	Val	Glu	Glu	Gln	Asn	Gly	
		355					360					365				
tcg	ggc	gta	gaa	cac	aac	atc	aac	cgc	att	caa	agg	aaa	atg	cta	cgc	1152
Ser	Gly	Val	Glu	His	Asn	Ile	Asn	Arg	Ile	Gln	Arg	Lys	Met	Leu	Arg	
	370					375					380					
atg	gtc	aat	cca	gaa	act	ttg	gaa	aac	gtc	tcc	gag	ggc	tat	gaa	tcc	1200
Met	Val	Asn	Pro	Glu	Thr	Leu	Glu	Asn	Val	Ser	Glu	Gly	Tyr	Glu	Ser	
385					390					395					400	
agt	ata	ttc	ttc	aaa	gac	atg	gtc	aac	gta	gaa	aaa	ctg	aaa	agg	ctc	1248

PF59083SeqList PF59083.txt

Ser	Ile	Phe	Phe	Lys	Asp	Met	Val	Asn	Val	Glu	Lys	Leu	Lys	Arg	Leu	
				405					410					415		
aga	aac	gtc	aca	ggc	atg	tcc	atc	gaa	act	gtc	ata	gga	acg	aca	aga	1296
Arg	Asn	Val	Thr	Gly	Met	Ser	Ile	Glu	Thr	Val	Ile	Gly	Thr	Thr	Arg	
			420					425					430			
tcc	gag	cag	caa	cag	tac	gat	acg	aac	ctc	cct	cgc	cag	ccc	gcc	acc	1344
Ser	Glu	Gln	Gln	Gln	Tyr	Asp	Thr	Asn	Leu	Pro	Arg	Gln	Pro	Ala	Thr	
		435					440					445				
act	acc	gcg	caa	gat	cca	gta	ccg	gac	ttg	aga	gac	tgg	cta	gcc	cca	1392
Thr	Thr	Ala	Gln	Asp	Pro	Val	Pro	Asp	Leu	Arg	Asp	Trp	Leu	Ala	Pro	
		450				455					460					
ctg	aat	gca	tac	gaa	tgc	gac	gat	gtc	ccc	gtt	cca	aag	tat	tcc	ccc	1440
Leu	Asn	Ala	Tyr	Glu	Cys	Asp	Asp	Val	Pro	Val	Pro	Lys	Tyr	Ser	Pro	
465					470			475							480	
aat	gat	aga	gtt	aac	gta	gcg	tcg	gaa	gac	aag	cag	gag	ctg	gag	caa	1488
Asn	Asp	Arg	Val	Asn	Val	Ala	Ser	Glu	Asp	Lys	Gln	Glu	Leu	Glu	Gln	
				485				490						495		
aaa	aga	cta	caa	caa	cta	gaa	agt	gac	cct	ccg	tcc	tgt	gat	gac	tat	1536
Lys	Arg	Leu	Gln	Gln	Leu	Glu	Ser	Asp	Pro	Pro	Ser	Cys	Asp	Asp	Tyr	
			500					505					510			
tag																1539

<210> 9908

<211> 512

<212> PRT

<213> Saccharomyces pastorianus

<400> 9908

Met	Leu	Ala	His	Asn	Asn	Val	Arg	Gln	Phe	Arg	Ile	Asp	Ile	Asn	Glu	
1				5					10					15		
Pro	His	Ser	Val	Trp	Lys	Pro	Asp	Glu	Cys	Ile	Thr	Gly	Glu	Thr	Val	
			20					25					30			
Ile	Asp	Ile	Lys	Arg	Asp	Ile	Thr	Asn	Val	Ala	Ile	Lys	Leu	Ser	Leu	
		35				40						45				
Val	Cys	Glu	Val	Arg	Val	Lys	Thr	Gly	Asn	Ser	Pro	Thr	Ser	Lys	Asn	
	50					55				60						
Lys	Arg	Val	Glu	Lys	Ile	Leu	Glu	Lys	Ser	Thr	Phe	Leu	Tyr	Gly	Gln	
65				70					75						80	
Glu	Tyr	Ile	Lys	Ala	Ala	Pro	Ala	Glu	Lys	Lys	Pro	Ala	Ile	Asp	Lys	
			85					90						95		
Ser	Thr	Val	Leu	Asn	Gly	Leu	Ser	Lys	Gly	Glu	His	Arg	Phe	Pro	Phe	
		100						105					110			
Arg	Ile	Lys	Ile	Pro	Arg	Gly	Lys	Gly	Met	Leu	Ser	Ser	Ile	Lys	Phe	
		115				120						125				
Glu	Arg	Gly	Ser	Ile	Ala	Tyr	Phe	Leu	Asn	Cys	Thr	Leu	Glu	Ser	Leu	
	130				135			140								
Asn	Asn	Val	Asn	Ala	Leu	Lys	Lys	Pro	Glu	Ala	Arg	Cys	Glu	Arg	Glu	
145				150					155						160	
Phe	Ser	Val	Ile	Val	Pro	Leu	Asp	Val	Ser	Arg	Leu	Pro	Lys	Gln	Lys	
			165					170						175		
Thr	Lys	Thr	Val	Val	Leu	Gln	Ser	Ala	Ser	Met	Val	Gln	Asn	Lys	Lys	
		180						185					190			
Gly	Lys	Ser	Ser	Glu	Asp	Ala	Ser	Ser	Ser	Tyr	Thr	Gln	Leu	Thr	His	
		195				200						205				
Lys	Ser	Asn	Asn	Ser	Asn	Ser	Ser	Ser	Ser	Thr	Val	Asn	Ser	Ser	Lys	
	210				215						220					
Thr	Ser	Ser	Pro	Pro	Asn	Lys	Thr	Val	Thr	Ile	Ser	Val	Asp	Ile	Pro	
225					230				235						240	
His	Ala	Gly	Phe	Val	Ile	Gly	Glu	Thr	Ile	Pro	Ile	Asp	Val	Lys	Ile	
			245					250						255		
Glu	His	Tyr	Lys	Pro	Phe	Tyr	His	Pro	Ala	Gly	Leu	Thr	Thr	Thr	Leu	
		260						265					270			
Val	Arg	Ile	Cys	Arg	Val	Gly	Gly	Ala	Gly	Lys	Asp	Asp	Pro	Met	Glu	
		275				280					285					
Thr	Phe	Arg	Lys	Asp	Ile	Cys	Gln	Ser	Ile	Ser	Pro	Ile	Tyr	Ile	Asn	
	290				295						300					
Pro	Glu	Thr	Leu	Gln	Phe	Gln	Pro	Arg	Ile	His	Leu	Lys	Val	Pro	Leu	

PF59083SeqList PF59083.txt

```

305          310          315          320
Asp Ala Phe Ser Thr Leu Thr Ser Val Ser Lys Phe Phe Ser Phe Gln
Tyr Tyr Ile Glu Val Met Val Asn Leu Ser Lys Lys Asn Val Val Tyr
Thr Glu Ser Asn Arg Val Val Gly Thr Pro Val Glu Glu Gln Asn Gly
Ser Gly Val Glu His Asn Ile Asn Arg Ile Gln Arg Lys Met Leu Arg
Met Val Asn Pro Glu Thr Leu Glu Asn Val Ser Glu Gly Tyr Glu Ser
385 Ser Ile Phe Phe Lys Asp Met Val Asn Val Glu Lys Leu Lys Arg Leu
Arg Asn Val Thr Gly Met Ser Ile Glu Thr Val Ile Gly Thr Thr Arg
Ser Glu Gln Gln Gln Tyr Asp Thr Asn Leu Pro Arg Gln Pro Ala Thr
Thr Thr Ala Gln Asp Pro Val Pro Asp Leu Arg Asp Trp Leu Ala Pro
Leu Asn Ala Tyr Glu Cys Asp Asp Val Pro Val Pro Lys Tyr Ser Pro
465 Asn Asp Arg Val Asn Val Ala Ser Glu Asp Lys Gln Glu Leu Glu Gln
Lys Arg Leu Gln Gln Leu Glu Ser Asp Pro Pro Ser Cys Asp Asp Tyr
500          505          510

```

<210> 9909
 <211> 2592
 <212> DNA
 <213> Gibberella zeae PH-1

<220>
 <221> CDS
 <222> (1)..(2592)

```

<400> 9909
atg cct ttg gca aca cgt ctg gga atg ggt cgc cgc tcg aga tct tct      48
Met Pro Leu Ala Thr Arg Leu Gly Met Gly Arg Arg Ser Arg Ser Ser
1          5          10          15
ccc acg ctc tct aac gtt aca gaa gct cct ggt cct acc aac tcg acg      96
Pro Thr Leu Ser Asn Val Thr Glu Ala Pro Gly Pro Thr Asn Ser Thr
20          25          30
gct ccc gac act cct aat aac atc gcg aca tcc tct ccg gcc gag tct      144
Ala Pro Asp Thr Pro Asn Asn Ile Ala Thr Ser Ser Pro Ala Glu Ser
35          40          45
gcc gcc tcc tcc acc tct cac gcc cca acg gcg acg tca ccc acg gca      192
Ala Gly Ser Ser Thr Ser His Ala Pro Thr Ala Thr Ser Pro Thr Ala
50          55          60
tct gcc acc tct tct acg cgc cca ggt ttc ctt tcg cgc ttc agc ctc      240
Ser Ala Thr Ser Ser Thr Arg Pro Gly Phe Leu Ser Arg Phe Ser Leu
65          70          75          80
cca ctc tct cta cct ttg cgc aat cga aac cgc aac gtc acc gac ttt      288
Pro Leu Ser Leu Pro Leu Arg Asn Arg Asn Arg Asn Val Thr Asp Phe
85          90          95
cat att cgt gcc gaa gaa ccc cac cgt cga tat agc gct gcc gac aat      336
His Ile Arg Ala Glu Glu Pro His Arg Arg Tyr Ser Ala Gly Asp Asn
100          105          110
gtt cgt gga gct gtc gtc atc gtc atc gtg aaa ccg gtt cga att act      384
Val Arg Gly Ala Val Val Ile Val Ile Val Lys Pro Val Arg Ile Thr
115          120          125
cat ctt acc gta tca ctg cat ggg tat gtg cgt gtg ctt aaa gat cca      432
His Leu Thr Val Ser Leu His Gly Tyr Val Arg Val Leu Lys Asp Pro
130          135          140
acc tcg gtc gcc aag gcg caa gga act gtt gtg tta ccg caa aac ggc      480
Thr Ser Val Ala Lys Ala Gln Gly Thr Val Val Leu Pro Gln Asn Gly
145          150          155          160
gat gcg gca cgg cca aga tat cac gga aac ggt ctt gca agt ctt ttc      528
Asp Ala Ala Arg Pro Arg Tyr His Gly Asn Gly Leu Ala Ser Leu Phe
165          170          175

```

PF59083SeqList PF59083.txt

caa	gac	gaa	caa	gtg	ttg	agt	ggc	gag	gga	cgg	ctg	gag	cca	ggc	aga	576
Gln	Asp	Glu	Gln	Val	Leu	Ser	Gly	Glu	Gly	Arg	Leu	Glu	Pro	Gly	Arg	
			180					185					190			
tat	gag	ttc	ggg	ttc	gac	ctt	ttg	ttt	ccc	gac	aag	gga	ttg	cca	agc	624
Tyr	Glu	Phe	Gly	Phe	Asp	Leu	Leu	Phe	Pro	Asp	Lys	Gly	Leu	Pro	Ser	
			195				200					205				
agt	att	gat	ttc	gag	cga	gga	acg	gtt	tcc	tac	atg	gtt	aca	gcg	acg	672
Ser	Ile	Asp	Phe	Glu	Arg	Gly	Thr	Val	Ser	Tyr	Met	Val	Thr	Ala	Thr	
	210					215					220					
cta	acg	cga	cca	acc	tca	att	gcc	cca	acg	tca	tgc	gaa	agg	aaa		720
Leu	Thr	Arg	Pro	Thr	Ser	Ile	Ala	Pro	Thr	Ser	Ser	Cys	Glu	Arg	Lys	
225					230					235					240	
gta	ata	ctg	gta	gaa	aac	gtg	gat	gtt	ggg	tta	cta	cac	act	ccc	aga	768
Val	Ile	Leu	Val	Glu	Asn	Val	Asp	Val	Gly	Leu	Leu	His	Thr	Pro	Arg	
				245				250						255		
ccg	cgc	acc	atc	ttt	ctc	gaa	cca	atc	tcg	aag	cga	aac	cga	agg	aga	816
Pro	Arg	Thr	Ile	Phe	Leu	Glu	Pro	Ile	Ser	Lys	Arg	Asn	Arg	Arg	Arg	
			260					265					270			
aag	tct	atg	gtg	ata	gac	aag	tca	cct	gcc	gcc	cac	tcc	gag	gtc	aac	864
Lys	Ser	Met	Val	Ile	Asp	Lys	Ser	Pro	Ala	Ala	His	Ser	Glu	Val	Asn	
		275					280					285				
gaa	gtc	aac	gct	ggg	cat	gaa	ttg	aca	gaa	aca	ccg	aca	gaa	gac	tac	912
Glu	Val	Asn	Ala	Gly	His	Glu	Leu	Thr	Glu	Thr	Pro	Thr	Glu	Asp	Tyr	
	290					295					300					
cgt	gaa	cac	acc	aca	gat	ccg	agg	agt	ccg	ata	caa	agt	gat	ttg	cga	960
Arg	Glu	His	Thr	Thr	Asp	Pro	Arg	Ser	Pro	Ile	Gln	Ser	Asp	Leu	Arg	
305					310					315					320	
agc	gaa	gtc	agc	ggg	gac	agt	ggg	gtc	agc	aac	agc	aca	agc	ttg	agc	1008
Ser	Glu	Val	Ser	Gly	Asp	Ser	Gly	Val	Ser	Asn	Ser	Thr	Ser	Leu	Ser	
				325				330						335		
aga	ccg	gaa	gtc	gca	cta	tcc	caa	gta	ggg	aca	ctc	aca	tca	gcc	aag	1056
Arg	Pro	Glu	Val	Ala	Leu	Ser	Gln	Val	Gly	Thr	Leu	Thr	Ser	Ala	Lys	
			340					345					350			
caa	caa	gcg	gta	gac	aag	aag	acg	atc	acg	gcg	acg	gtt	gag	ctg	ctc	1104
Gln	Gln	Ala	Val	Asp	Lys	Lys	Thr	Ile	Thr	Ala	Thr	Val	Glu	Leu	Leu	
		355					360					365				
aaa	ggg	ggg	tgc	tta	cca	ggc	gat	gcc	atc	tct	gtg	cga	gtc	aca	gtt	1152
Lys	Gly	Gly	Cys	Leu	Pro	Gly	Asp	Ala	Ile	Ser	Val	Arg	Val	Thr	Val	
	370					375					380					
cag	cac	acc	aag	cgg	gtc	aag	agc	atg	acg	gga	gtg	att	gtg	acg	cta	1200
Gln	His	Thr	Lys	Arg	Val	Lys	Ser	Met	Thr	Gly	Val	Ile	Val	Thr	Leu	
385					390					395					400	
ctc	aga	caa	ggc	aaa	atc	gac	agc	aat	ccg	cca	aaa	gct	ttt	ttc	gac	1248
Leu	Arg	Gln	Gly	Lys	Ile	Asp	Ser	Asn	Pro	Pro	Lys	Ala	Phe	Phe	Asp	
			405						410				415			
gaa	tct	atg	agc	cag	gaa	gac	ata	gct	cgt	att	gat	aag	gaa	gag	gtg	1296
Glu	Ser	Met	Ser	Gln	Glu	Asp	Ile	Ala	Arg	Ile	Asp	Lys	Glu	Glu	Val	
		420					425					430				
ttc	cca	cga	tca	aga	aca	ggg	ctc	ggg	gga	ttg	tcc	ttg	tca	tct	tcg	1344
Phe	Pro	Arg	Ser	Arg	Thr	Gly	Leu	Gly	Gly	Leu	Ser	Leu	Ser	Ser	Ser	
		435				440						445				
agt	tcg	aca	agc	ata	ttc	cgc	aag	gac	ctc	gat	cag	aac	ata	gca	cct	1392
Ser	Ser	Thr	Ser	Ile	Phe	Arg	Lys	Asp	Leu	Asp	Gln	Asn	Ile	Ala	Pro	
	450					455					460					
ctc	att	att	gat	ccc	aac	act	atg	caa	aca	tca	gtc	act	gtc	act	gtt	1440
Leu	Ile	Ile	Asp	Pro	Asn	Thr	Met	Gln	Thr	Ser	Val	Thr	Val	Thr	Val	
					470					475					480	
aag	ctg	ccc	gat	gat	tca	ttc	cca	aca	atc	aag	ggg	gtt	cct	ggg	gag	1488
Lys	Leu	Pro	Asp	Asp	Ser	Phe	Pro	Thr	Ile	Lys	Gly	Val	Pro	Gly	Glu	
				485					490					495		
atg	atc	agc	ttc	aag	tac	gtg	gtt	gag	gtg	gtt	gtc	gac	ctg	ggg	gga	1536
Met	Ile	Ser	Phe	Lys	Tyr	Val	Val	Glu	Val	Val	Val	Asp	Leu	Gly	Gly	
			500				505					510				
aga	ttg	tcg	aat	cag	atg	caa	aca	ggg	cca	gcg	aga	ttc	gga	ccc	tat	1584
Arg	Leu	Ser	Asn	Gln	Met	Gln	Thr	Gly	Pro	Ala	Arg	Phe	Gly	Pro	Tyr	
		515				520						525				
ggg	cat	gga	agc	aca	gac	aac	aat	acg	tac	ggg	cca	agg	agg	gga	gca	1632
Gly	His	Gly	Ser	Thr	Asp	Asn	Asn	Thr	Tyr	Gly	Pro	Arg	Arg	Gly	Ala	
	530					535					540					

PF59083SeqList PF59083.txt

aat	atc	gca	gac	act	tcg	cag	atg	cgc	cac	gaa	aag	ggg	gta	atc	gcg	1680
Asn	Ile	Ala	Asp	Thr	Ser	Gln	Met	Arg	His	Glu	Lys	Gly	Val	Ile	Ala	
545					550					555					560	
gta	tca	atg	gag	aca	gtc	gtg	ggg	acc	tcg	gat	tcg	tca	cgc	ggg	agg	1728
Val	Ser	Met	Glu	Thr	Val	Val	Gly	Thr	Ser	Asp	Ser	Ser	Arg	Gly	Arg	
				565					570					575		
aaa	aag	tcg	agg	gcg	tcg	ccg	aca	tca	cga	agc	gtg	cag	att	ctc	gaa	1776
Lys	Lys	Ser	Arg	Ala	Ser	Pro	Thr	Ser	Arg	Ser	Val	Gln	Ile	Leu	Glu	
			580					585					590			
agc	gac	gaa	gag	gat	atg	atg	gga	caa	gag	cca	aac	tac	ggc	gaa	ggg	1824
Ser	Asp	Glu	Glu	Asp	Met	Met	Gly	Gln	Glu	Pro	Asn	Tyr	Gly	Glu	Gly	
			595				600						605			
cct	tcc	ctc	gaa	tac	tat	tca	ggg	aac	gga	cca	ctt	tct	cct	act	ggg	1872
Pro	Ser	Leu	Glu	Tyr	Tyr	Ser	Gly	Asn	Gly	Pro	Leu	Ser	Pro	Thr	Gly	
			610			615					620					
tat	ttc	tct	ccc	cac	acc	aat	ggg	agt	cga	ctt	cct	tcg	att	ccc	tca	1920
Tyr	Phe	Ser	Pro	His	Thr	Asn	Gly	Ser	Arg	Leu	Pro	Ser	Ile	Pro	Ser	
625					630					635					640	
cat	cca	cca	cag	cct	tac	tca	caa	gta	cct	ccc	ttg	caa	gct	tcg	tcg	1968
His	Pro	Pro	Gln	Pro	Tyr	Ser	Gln	Val	Pro	Pro	Leu	Gln	Ala	Ser	Ser	
				645					650					655		
cat	tcg	cgt	ggc	ttc	tct	ggg	tca	agt	acc	aac	ggg	ttt	ggg	tct	tcc	2016
His	Ser	Arg	Gly	Phe	Ser	Gly	Ser	Ser	Thr	Asn	Gly	Phe	Gly	Ser	Ser	
			660					665					670			
tca	gca	gcg	cct	tcg	tat	att	ccc	cct	ccc	gag	ata	ccg	aat	ccg	aat	2064
Ser	Ala	Ala	Pro	Ser	Tyr	Ile	Pro	Pro	Pro	Glu	Ile	Pro	Asn	Pro	Asn	
			675				680					685				
aat	cta	tca	gaa	aaa	gaa	aga	att	cgg	cag	gcc	gag	ata	cgg	cta	cta	2112
Asn	Leu	Ser	Glu	Lys	Glu	Arg	Ile	Arg	Gln	Ala	Glu	Ile	Arg	Leu	Leu	
			690			695				700						
cca	agc	caa	cct	cca	gtg	gca	ggg	cca	tca	aca	agt	tca	aac	cag	gat	2160
Pro	Ser	Gln	Pro	Pro	Val	Ala	Gly	Pro	Ser	Thr	Ser	Ser	Asn	Gln	Asp	
705					710					715					720	
gat	gaa	gat	ata	tac	gac	gca	gag	gac	acg	cct	cgg	gtc	ccg	gat	ctg	2208
Asp	Glu	Asp	Ile	Tyr	Asp	Ala	Glu	Asp	Thr	Pro	Arg	Val	Pro	Asp	Leu	
				725					730					735		
gat	gcc	gga	ttt	gat	ctg	agt	gta	cct	agt	gcc	ccc	agt	gcc	ccc	gag	2256
Asp	Ala	Gly	Phe	Asp	Leu	Ser	Val	Pro	Ser	Ala	Pro	Ser	Ala	Pro	Glu	
			740					745					750			
gca	ggc	ccc	tca	gca	cca	aca	gag	gac	gac	gtc	gag	tta	gca	gca	gtg	2304
Ala	Gly	Pro	Ser	Ala	Pro	Thr	Glu	Asp	Asp	Val	Glu	Leu	Ala	Ala	Val	
			755				760					765				
ccg	ccg	tct	ggg	gtc	gtg	gaa	gat	aag	cag	gaa	atc	gaa	aga	cgg	cgg	2352
Pro	Pro	Ser	Gly	Val	Val	Glu	Asp	Lys	Gln	Glu	Ile	Glu	Arg	Arg	Arg	
			770			775										
ctg	ctg	gac	gaa	gcc	agt	gct	ccc	ccg	gac	gtc	ccc	gag	gat	atg	cag	2400
Leu	Leu	Asp	Glu	Ala	Ser	Ala	Pro	Pro	Asp	Val	Pro	Glu	Asp	Met	Gln	
					790					795					800	
cga	aga	aga	att	gac	ggc	cct	tca	acg	gaa	gtg	gac	acc	gga	gct	gaa	2448
Arg	Arg	Arg	Ile	Asp	Gly	Pro	Ser	Thr	Glu	Val	Asp	Thr	Gly	Ala	Glu	
				805					810					815		
gcc	agt	gca	ccg	agc	gca	ccg	agc	gca	ccg	agt	gca	cct	tta	gtt	gat	2496
Ala	Ser	Ala	Pro	Ser	Ala	Pro	Ser	Ala	Pro	Ser	Ala	Pro	Leu	Val	Asp	
			820					825					830			
gat	tat	gat	gag	ttt	cct	gga	tac	ggc	gca	gga	cct	tcc	agt			2544
Asp	Tyr	Asp	Glu	Phe	Pro	Gly	Tyr	Gly	Ser	Gly	Ala	Gly	Pro	Ser	Ser	
			835				840					845				
ggc	tcg	aga	cac	ggg	ggg	gga	gag	cag	tta	cct	gcg	tac	caa	aga		2589
Gly	Ser	Arg	His	Gly	Gly	Gly	Glu	Gln	Leu	Pro	Ala	Tyr	Gln	Arg		
						855					860					
taa																2592

<210> 9910
 <211> 863
 <212> PRT
 <213> Gibberella zeae PH-1

PF59083SeqList PF59083.txt

<400> 9910

```

Met Pro Leu Ala Thr Arg Leu Gly Met Gly Arg Arg Ser Arg Ser Ser
1      5      10      15
Pro Thr Leu Ser Asn Val Thr Glu Ala Pro Gly Pro Thr Asn Ser Thr
20      25      30
Ala Pro Asp Thr Pro Asn Asn Ile Ala Thr Ser Ser Pro Ala Glu Ser
35      40      45
Ala Gly Ser Ser Thr Ser His Ala Pro Thr Ala Thr Ser Pro Thr Ala
50      55      60
Ser Ala Thr Ser Ser Thr Arg Pro Gly Phe Leu Ser Arg Phe Ser Leu
65      70      75      80
Pro Leu Ser Leu Pro Leu Arg Asn Arg Asn Arg Asn Val Thr Asp Phe
85      90      95
His Ile Arg Ala Glu Glu Pro His Arg Arg Tyr Ser Ala Gly Asp Asn
100     105     110
Val Arg Gly Ala Val Val Ile Val Ile Val Lys Pro Val Arg Ile Thr
115     120     125
His Leu Thr Val Ser Leu His Gly Tyr Val Arg Val Leu Lys Asp Pro
130     135     140
Thr Ser Val Ala Lys Ala Gln Gly Thr Val Val Leu Pro Gln Asn Gly
145     150     155     160
Asp Ala Ala Arg Pro Arg Tyr His Gly Asn Gly Leu Ala Ser Leu Phe
165     170     175
Gln Asp Glu Gln Val Leu Ser Gly Glu Gly Arg Leu Glu Pro Gly Arg
180     185     190
Tyr Glu Phe Gly Phe Asp Leu Leu Phe Pro Asp Lys Gly Leu Pro Ser
195     200     205
Ser Ile Asp Phe Glu Arg Gly Thr Val Ser Tyr Met Val Thr Ala Thr
210     215     220
Leu Thr Arg Pro Thr Ser Ile Ala Pro Thr Ser Ser Cys Glu Arg Lys
225     230     235     240
Val Ile Leu Val Glu Asn Val Asp Val Gly Leu Leu His Thr Pro Arg
245     250     255
Pro Arg Thr Ile Phe Leu Glu Pro Ile Ser Lys Arg Asn Arg Arg Arg
260     265     270
Lys Ser Met Val Ile Asp Lys Ser Pro Ala Ala His Ser Glu Val Asn
275     280     285
Glu Val Asn Ala Gly His Glu Leu Thr Glu Thr Pro Thr Glu Asp Tyr
290     295     300
Arg Glu His Thr Thr Asp Pro Arg Ser Pro Ile Gln Ser Asp Leu Arg
305     310     315     320
Ser Glu Val Ser Gly Asp Ser Gly Val Ser Asn Ser Thr Ser Leu Ser
325     330     335
Arg Pro Glu Val Ala Leu Ser Gln Val Gly Thr Leu Thr Ser Ala Lys
340     345     350
Gln Gln Ala Val Asp Lys Lys Thr Ile Thr Ala Thr Val Glu Leu Leu
355     360     365
Lys Gly Gly Cys Leu Pro Gly Asp Ala Ile Ser Val Arg Val Thr Val
370     375     380
Gln His Thr Lys Arg Val Lys Ser Met Thr Gly Val Ile Val Thr Leu
385     390     395     400
Leu Arg Gln Gly Lys Ile Asp Ser Asn Pro Pro Lys Ala Phe Phe Asp
405     410     415
Glu Ser Met Ser Gln Glu Asp Ile Ala Arg Ile Asp Lys Glu Glu Val
420     425     430
Phe Pro Arg Ser Arg Thr Gly Leu Gly Gly Leu Ser Leu Ser Ser Ser
435     440     445
Ser Ser Thr Ser Ile Phe Arg Lys Asp Leu Asp Gln Asn Ile Ala Pro
450     455     460
Leu Ile Ile Asp Pro Asn Thr Met Gln Thr Ser Val Thr Val Thr Val
465     470     475     480
Lys Leu Pro Asp Asp Ser Phe Pro Thr Ile Lys Gly Val Pro Gly Glu
485     490     495
Met Ile Ser Phe Lys Tyr Val Val Glu Val Val Val Asp Leu Gly Gly
500     505     510
Arg Leu Ser Asn Gln Met Gln Thr Gly Pro Ala Arg Phe Gly Pro Tyr
515     520     525
Gly His Gly Ser Thr Asp Asn Asn Thr Tyr Gly Pro Arg Arg Gly Ala
530     535     540

```

PF59083SeqList PF59083.txt

Asn Ile Ala Asp Thr Ser Gln Met Arg His Glu Lys Gly Val Ile Ala
545 550 555 560
Val Ser Met Glu Thr Val Val Gly Thr Ser Asp Ser Ser Arg Gly Arg
565 570 575
Lys Lys Ser Arg Ala Ser Pro Thr Ser Arg Ser Val Gln Ile Leu Glu
580 585 590
Ser Asp Glu Glu Asp Met Met Gly Gln Glu Pro Asn Tyr Gly Glu Gly
595 600 605
Pro Ser Leu Glu Tyr Tyr Ser Gly Asn Gly Pro Leu Ser Pro Thr Gly
610 615 620
Tyr Phe Ser Pro His Thr Asn Gly Ser Arg Leu Pro Ser Ile Pro Ser
625 630 635 640
His Pro Pro Gln Pro Tyr Ser Gln Val Pro Pro Leu Gln Ala Ser Ser
645 650 655
His Ser Arg Gly Phe Ser Gly Ser Ser Thr Asn Gly Phe Gly Ser Ser
660 665 670
Ser Ala Ala Pro Ser Tyr Ile Pro Pro Pro Glu Ile Pro Asn Pro Asn
675 680 685
Asn Leu Ser Glu Lys Glu Arg Ile Arg Gln Ala Glu Ile Arg Leu Leu
690 695 700
Pro Ser Gln Pro Pro Val Ala Gly Pro Ser Thr Ser Ser Asn Gln Asp
705 710 715 720
Asp Glu Asp Ile Tyr Asp Ala Glu Asp Thr Pro Arg Val Pro Asp Leu
725 730 735
Asp Ala Gly Phe Asp Leu Ser Val Pro Ser Ala Pro Ser Ala Pro Glu
740 745 750
Ala Gly Pro Ser Ala Pro Thr Glu Asp Asp Val Glu Leu Ala Ala Val
755 760 765
Pro Pro Ser Gly Val Val Glu Asp Lys Gln Glu Ile Glu Arg Arg Arg
770 775 780
Leu Leu Asp Glu Ala Ser Ala Pro Pro Asp Val Pro Glu Asp Met Gln
785 790 795 800
Arg Arg Arg Ile Asp Gly Pro Ser Thr Glu Val Asp Thr Gly Ala Glu
805 810 815
Ala Ser Ala Pro Ser Ala Pro Ser Ala Pro Leu Val Asp
820 825 830
Asp Tyr Asp Glu Phe Pro Gly Tyr Gly Ser Gly Ala Gly Pro Ser Ser
835 840 845
Gly Ser Arg His Gly Gly Gly Glu Gln Leu Pro Ala Tyr Gln Arg
850 855 860

<210> 9911
<211> 2252
<212> DNA
<213> Pichia stipitis

<220>
<221> CDS
<222> (87)..(2198)

<400> 9911
tcaacatcgc cgctactaca tgcctccagt acaccatttt aaagctcccc tactccctaa 60

gcacatataa gcacacctaa accatc atg agg cgt gcc gta ctg aaa atc atc 113
Met Arg Arg Ala Val Leu Lys Ile Ile
1 5

ccc acg ccg aag ttt ctc tct ggt tct acc gag cca ctc cac tct tcc 161
Pro Thr Pro Lys Phe Leu Ser Gly Ser Thr Glu Pro Leu His Ser Ser
10 15 20 25

aac ttt cgc ata gac ttc aac tcc gtg gcc gat ttt tac atc cag ctc 209
Asn Phe Arg Ile Asp Phe Asn Ser Val Ala Asp Phe Tyr Ile Gln Leu
30 35 40

gat aaa ccg cat aag aca tgg ctc cct ggc gat gaa gtg ccc ggc aaa 257
Asp Lys Pro His Lys Thr Trp Leu Pro Gly Asp Glu Val Pro Gly Lys
45 50 55

atc att ctt atc tcc aag aag aat ctc gcc aac atc gtc atc act ttg 305
Ile Ile Leu Ile Ser Lys Lys Asn Leu Ala Asn Ile Val Ile Thr Leu
60 65 70

PF59083SeqList PF59083.txt

tca	tta	ata	ggg	tat	gtg	aaa	atc	aac	gct	ctg	tcg	cac	tcc	aaa	ttg	353
Ser	Leu	Ile	Gly	Tyr	Val	Lys	Ile	Asn	Ala	Leu	Ser	His	Ser	Lys	Leu	
	75					80					85					
aga	cct	ata	aaa	cac	agc	ttg	ttt	gac	cac	acg	ata	aag	atc	tat	gga	401
Arg	Pro	Ile	Lys	His	Ser	Leu	Phe	Asp	His	Thr	Ile	Lys	Ile	Tyr	Gly	
	90				95					100					105	
gat	ggc	cta	ctg	cca	gaa	gct	ctg	ggg	tct	gta	agc	gaa	gca	gac	ttc	449
Asp	Gly	Leu	Leu	Pro	Glu	Ala	Leu	Gly	Ser	Val	Ser	Glu	Ala	Asp	Phe	
				110				115						120		
acc	aac	ggc	ttg	tac	aag	ggc	gag	cac	gtc	ttt	cct	ttc	atc	gtc	aag	497
Thr	Asn	Gly	Leu	Tyr	Lys	Gly	Glu	His	Val	Phe	Pro	Phe	Ile	Val	Lys	
			125					130					135			
ctt	cct	aac	aaa	aga	gta	ttt	acc	tct	atc	gat	ttc	ggg	aag	ggg	tcc	545
Leu	Pro	Asn	Lys	Arg	Val	Phe	Thr	Ser	Ile	Asp	Phe	Gly	Lys	Gly	Ser	
			140				145					150				
atc	agc	tac	ata	ttg	aga	gcc	tct	cta	gga	aat	tca	agc	tca	tac	aca	593
Ile	Ser	Tyr	Ile	Leu	Arg	Ala	Ser	Leu	Gly	Asn	Ser	Ser	Ser	Tyr	Thr	
	155					160					165					
acc	aca	ggc	gca	tca	act	aca	tca	ata	tca	act	tct	tca	aac	tcg	atc	641
Thr	Thr	Gly	Ala	Ser	Thr	Thr	Ser	Ile	Ser	Thr	Ser	Ser	Asn	Ser	Ile	
	170				175					180					185	
cag	cct	act	tcc	tcc	atc	ttt	gcc	aaa	aca	aag	tcg	ttg	aaa	att	ctc	689
Gln	Pro	Thr	Ser	Ser	Ile	Phe	Ala	Lys	Thr	Lys	Ser	Leu	Lys	Ile	Leu	
				190				195						200		
cag	aat	ccc	tca	act	tct	gaa	aaa	ctt	att	cac	tta	gta	aac	ccc		737
Gln	Asn	Pro	Ser	Tyr	Thr	Glu	Lys	Leu	Ile	His	Leu	Val	Asn	Pro		
			205				210					215				
ata	gac	gta	act	act	ctt	aca	cct	ccc	aaa	ccg	aag	cgc	ttg	atc	ttg	785
Ile	Asp	Val	Thr	Thr	Leu	Thr	Pro	Pro	Lys	Pro	Lys	Arg	Leu	Ile	Leu	
		220					225					230				
aaa	gat	cca	cgc	act	caa	cat	tcc	aag	aag	ttg	tct	cga	acc	caa	tct	833
Lys	Asp	Pro	Arg	Thr	Gln	His	Ser	Lys	Lys	Leu	Ser	Arg	Thr	Gln	Ser	
	235					240					245					
tca	act	tct	aca	atc	aac	aca	atc	aat	aca	atc	aac	aca	tat	tcc	act	881
Ser	Thr	Ser	Thr	Ile	Asn	Thr	Ile	Asn	Thr	Ile	Asn	Thr	Tyr	Ser	Thr	
	250				255					260					265	
gtt	tct	tcc	aat	aat	tca	gac	acc	tac	gaa	gct	cct	aat	gct	act	gga	929
Val	Ser	Ser	Asn	Asn	Ser	Asp	Thr	Tyr	Glu	Ala	Pro	Asn	Ala	Thr	Gly	
				270				275						280		
acc	aac	act	aat	ggc	tct	aat	aac	cca	ctt	ccc	aag	ccc	aat	gta	gtg	977
Thr	Asn	Thr	Asn	Gly	Ser	Asn	Asn	Pro	Ser	Pro	Lys	Pro	Asn	Val	Val	
			285					290					295			
ttg	cct	ggg	tta	gat	aaa	tct	tct	ata	aag	cca	gag	acg	att	aaa	gtc	1025
Leu	Pro	Gly	Leu	Asp	Lys	Ser	Ser	Ile	Lys	Pro	Glu	Thr	Ile	Lys	Val	
		300					305					310				
tgt	ctt	gag	att	cct	caa	cga	ggc	tat	ttg	cgt	gga	gaa	ttg	ata	ccg	1073
Cys	Leu	Glu	Ile	Pro	Gln	Arg	Gly	Tyr	Leu	Arg	Gly	Glu	Leu	Ile	Pro	
	315					320					325					
att	aaa	ctc	tcg	atc	agc	cac	ctc	aag	aag	atc	cag	gac	ttg	cat	gga	1121
Ile	Lys	Leu	Ser	Ile	Ser	His	Leu	Lys	Lys	Ile	Gln	Asp	Leu	His	Gly	
					335					340					345	
att	ata	att	acc	ctt	gta	aga	gtc	tgt	aga	ttg	gat	aac	ggc	aca	gag	1169
Ile	Ile	Ile	Thr	Leu	Val	Arg	Val	Cys	Arg	Leu	Asp	Asn	Gly	Thr	Glu	
				350					355					360		
tcc	ttt	ttt	gag	tcg	ttc	aga	aag	gat	ctt	caa	caa	ctg	gtt	ctt	ccc	1217
Ser	Phe	Phe	Glu	Ser	Phe	Arg	Lys	Asp	Leu	Gln	Gln	Leu	Val	Leu	Pro	
			365					370					375			
att	ttc	gta	gat	cct	gtg	acc	ttc	cag	tct	gaa	atc	aat	acc	agt	gtt	1265
Ile	Phe	Val	Asp	Pro	Val	Thr	Phe	Gln	Ser	Glu	Ile	Asn	Thr	Ser	Val	
		380					385					390				
cga	gtc	cca	gca	gat	gcc	ttt	ccg	act	att	ctg	gga	tgt	ccg	ttg	gta	1313
Arg	Val	Pro	Ala	Asp	Ala	Phe	Pro	Thr	Ile	Leu	Gly	Cys	Pro	Leu	Val	
	395				400						405					
tct	ttc	cag	tac	ttt	att	gaa	gtt	ttg	gtg	aac	ttg	tca	gga	aaa	tcg	1361
Ser	Phe	Gln	Tyr	Phe	Ile	Glu	Val	Leu	Val	Asn	Leu	Ser	Gly	Lys	Ser	
				415						420					425	
cta	gtc	tta	gac	aac	gat	gct	cct	aca	gat	cac	cat	tca	gca	acc	aag	1409
Leu	Val	Leu	Asp	Asn	Asp	Ala	Pro	Thr	Asp	His	His	Ser	Ala	Thr	Lys	
				430					435					440		

PF59083SeqList PF59083.txt

att gta gat gat cca acg act ttc aat ttc aac tac aac aac tcg ttg	1457
Ile Val Asp Asp Pro Thr Thr Phe Asn Phe Asn Tyr Asn Asn Ser Leu	
445 450 455	
tct tca cag cat cac aag gac aga tca gga ttt atc aat act gac aaa	1505
Ser Ser Gln His His Lys Asp Arg Ser Gly Phe Ile Asn Thr Asp Lys	
460 465 470	
tat aag aga ctg aag aag ttc cta caa ttg act act gag gtg att ata	1553
Tyr Lys Arg Leu Lys Lys Phe Leu Gln Leu Thr Thr Glu Val Ile Ile	
475 480 485	
gga aca cat cgt ctg act tca gat acg aat acg gga gcg ggc gag aat	1601
Gly Thr His Arg Leu Thr Thr Ser Asp Thr Asn Thr Gly Ala Gly Glu Asn	
490 495 500	
gcc cag atc gac tta tcg aga aga tca tct tct ctg ata tcg aat cca	1649
Ala Gln Ile Asp Leu Ser Arg Arg Ser Ser Ser Leu Ile Ser Asn Pro	
510 515 520	
aac aat tct cca cct aat atc aat aac aat agc aat agg cag gct tcg	1697
Asn Asn Ser Pro Pro Asn Ile Asn Asn Asn Ser Asn Arg Gln Ala Ser	
525 530 535	
tat att aat gcc att ccg gag gct gtg gaa atg aac aat ttc cag tca	1745
Tyr Ile Asn Ala Ile Pro Glu Ala Val Glu Met Asn Phe Gln Ser	
540 545 550	
cct cca tac ttt gag aat ttg aac cag agt caa ggt cac agc caa acc	1793
Pro Pro Tyr Phe Glu Asn Leu Asn Gln Ser Gln Gly His Ser Gln Thr	
555 560 565	
aga cag ttt acc cct ttg cct acg aac ttc agt tca ata ccc aat tat	1841
Arg Gln Phe Thr Pro Leu Pro Thr Asn Phe Ser Ser Ile Pro Asn Tyr	
570 575 580	
tca gaa ttg agt gga tcc ggt tcg aat gct atg gga ggg tcg att tct	1889
Ser Glu Leu Ser Gly Ser Gly Ser Asn Ala Met Gly Gly Ser Ile Ser	
590 595 600	
gag aag gaa cgc tta aga ctc ctt gaa tcg agt ttg ttg cct tca gct	1937
Glu Lys Glu Arg Leu Arg Leu Leu Glu Ser Ser Leu Leu Pro Ser Ala	
605 610 615	
ccg cct atg gaa caa gaa gac gat aac acc aat aat aat agt aat aat	1985
Pro Pro Met Glu Gln Glu Asp Asn Thr Asn Asn Asn Ser Asn Asn	
620 625 630	
agc cag tac cag ttc ttt acg tac caa aac tct tcc acc gcg acc tca	2033
Ser Gln Tyr Gln Phe Phe Thr Tyr Gln Asn Ser Ser Thr Ala Thr Ser	
635 640 645	
cag atg gca gag aac aac gac gaa cag tat gat gca att gac ttt gtg	2081
Gln Met Ala Glu Asn Asn Asp Glu Gln Tyr Asp Ala Ile Asp Phe Val	
650 655 660	
ccc aac tac aat tct gcc agt aac gac aga ctc ctc gct gaa gga aga	2129
Pro Asn Tyr Asn Ser Ala Ser Asn Asp Arg Leu Leu Ala Glu Gly Arg	
670 675 680	
caa gcc ggc act ggt gct gct tct act ttg acg aga gaa tct ggt agt	2177
Gln Ala Gly Thr Gly Ala Ala Ser Thr Leu Thr Arg Glu Ser Gly Ser	
685 690 695	
gat tct gct tca cat gcg taatgcagca taagatagga ctatatagct	2225
Asp Ser Ala Ser His Ala	
700	
agaaagtata gatgccatga attcaag	2252

<210> 9912
 <211> 703
 <212> PRT
 <213> Pichia stipitis

<400> 9912
 Met Arg Arg Ala Val Leu Lys Ile Ile Pro Thr Pro Lys Phe Leu Ser
 1 5 10 15
 Gly Ser Thr Glu Pro Leu His Ser Ser Asn Phe Arg Ile Asp Phe Asn
 20 25 30
 Ser Val Ala Asp Phe Tyr Ile Gln Leu Asp Lys Pro His Lys Thr Trp
 35 40 45
 Leu Pro Gly Asp Glu Val Pro Gly Lys Ile Ile Leu Ile Ser Lys Lys
 50 55 60

PF59083SeqList PF59083.txt

Asn 65	Leu	Ala	Asn	Ile	Val 70	Ile	Thr	Leu	Ser	Leu 75	Ile	Gly	Tyr	Val	Lys 80
Ile	Asn	Ala	Leu	Ser 85	His	Ser	Lys	Leu	Arg 90	Pro	Ile	Lys	His	Ser 95	Leu
Phe	Asp	His	Thr 100	Ile	Lys	Ile	Tyr	Gly 105	Asp	Gly	Leu	Leu	Pro 110	Glu	Ala
Leu	Gly	Ser 115	Val	Ser	Glu	Ala	Asp 120	Phe	Thr	Asn	Gly	Leu	Tyr 125	Lys	Gly
Glu	His 130	Val	Phe	Pro	Phe	Ile 135	Val	Lys	Leu	Pro	Asn 140	Lys	Arg	Val	Phe
Thr 145	Ser	Ile	Asp	Phe	Gly 150	Lys	Gly	Ser	Ile	Ser 155	Tyr	Ile	Leu	Arg	Ala 160
Ser	Leu	Gly	Asn 165	Ser	Ser	Ser	Tyr	Thr	Thr 170	Thr	Gly	Ala	Ser	Thr 175	Thr
Ser	Ile	Ser	Thr 180	Ser	Ser	Asn	Ser	Ile 185	Gln	Pro	Thr	Ser	Ser 190	Ile	Phe
Ala	Lys	Thr 195	Lys	Ser	Leu	Lys	Ile 200	Leu	Gln	Asn	Pro	Ser 205	Tyr	Thr	Ser
Glu	Lys 210	Leu	Ile	His	Leu	Val 215	Asn	Pro	Ile	Asp	Val 220	Thr	Thr	Leu	Thr
Pro 225	Pro	Lys	Pro	Lys	Arg 230	Leu	Ile	Leu	Lys	Asp 235	Pro	Arg	Thr	Gln	His 240
Ser	Lys	Lys	Leu	Ser 245	Arg	Thr	Gln	Ser	Ser 250	Thr	Ser	Thr	Ile	Asn 255	Thr
Ile	Asn	Thr 260	Ile	Asn	Thr	Tyr	Ser	Thr 265	Val	Ser	Ser	Asn	Asn 270	Ser	Asp
Thr	Tyr	Glu 275	Ala	Pro	Asn	Ala	Thr 280	Gly	Thr	Asn	Thr	Asn 285	Gly	Ser	Asn
Asn	Pro 290	Ser	Pro	Lys	Pro	Asn 295	Val	Val	Leu	Pro	Gly 300	Leu	Asp	Lys	Ser
Ser 305	Ile	Lys	Pro	Glu	Thr 310	Ile	Lys	Val	Cys	Leu 315	Glu	Ile	Pro	Gln	Arg 320
Gly	Tyr	Leu	Arg	Gly 325	Glu	Leu	Ile	Pro	Ile 330	Lys	Leu	Ser	Ile	Ser 335	His
Leu	Lys	Lys	Ile 340	Gln	Asp	Leu	His	Gly 345	Ile	Ile	Ile	Thr	Leu 350	Val	Arg
Val	Cys	Arg 355	Leu	Asp	Asn	Gly	Thr 360	Glu	Ser	Phe	Phe	Glu	Ser 365	Phe	Arg
Lys	Asp 370	Leu	Gln	Gln	Leu	Val 375	Leu	Pro	Ile	Phe	Val 380	Asp	Pro	Val	Thr
Phe 385	Gln	Ser	Glu	Ile	Asn 390	Thr	Ser	Val	Arg	Val 395	Pro	Ala	Asp	Ala	Phe 400
Pro	Thr	Ile	Leu	Gly 405	Cys	Pro	Leu	Val	Ser 410	Phe	Gln	Tyr	Phe	Ile 415	Glu
Val	Leu	Val	Asn 420	Leu	Ser	Gly	Lys	Ser 425	Leu	Val	Leu	Asp	Asn 430	Asp	Ala
Pro	Thr	Asp 435	His	His	Ser	Ala	Thr 440	Lys	Ile	Val	Asp	Asp 445	Pro	Thr	Thr
Phe	Asn 450	Phe	Asn	Tyr	Asn 455	Ser	Ser	Leu	Ser	Ser	Gln	His	His	Lys	Asp
Arg 465	Ser	Gly	Phe	Ile	Asn 470	Thr	Asp	Lys	Tyr	Lys 475	Arg	Leu	Lys	Lys	Phe 480
Leu	Gln	Leu	Thr 485	Thr	Glu	Val	Ile	Ile	Gly 490	Thr	His	Arg	Leu	Thr 495	Ser
Asp	Thr	Asn	Thr 500	Gly	Ala	Gly	Glu	Asn 505	Ala	Gln	Ile	Asp	Leu 510	Ser	Arg
Arg	Ser	Ser 515	Ser	Leu	Ile	Ser	Asn 520	Pro	Asn	Asn	Ser	Pro 525	Pro	Asn	Ile
Asn	Asn 530	Asn	Ser	Asn	Arg	Gln 535	Ala	Ser	Tyr	Ile	Asn 540	Ala	Ile	Pro	Glu
Ala 545	Val	Glu	Met	Asn	Asn 550	Phe	Gln	Ser	Pro	Pro	Tyr	Phe	Glu	Asn	Leu 560
Asn	Gln	Ser	Gln	Gly 565	His	Ser	Gln	Thr	Arg 570	Gln	Phe	Thr	Pro	Leu 575	Pro
Thr	Asn	Phe	Ser 580	Ser	Ile	Pro	Asn	Tyr 585	Ser	Glu	Leu	Ser	Gly 590	Ser	Gly
Ser	Asn	Ala 595	Met	Gly	Gly	Ser	Ile 600	Ser	Glu	Lys	Glu	Arg 605	Leu	Arg	Leu
Leu	Glu	Ser	Ser	Leu	Leu	Pro	Ser	Ala	Pro	Pro	Met	Glu	Gln	Glu	Asp

PF59083SeqList PF59083.txt

610 615 620
 Asp Asn Thr Asn Asn Asn Ser Asn Asn Ser Gln Tyr Gln Phe Phe Thr
 625 630 635 640
 Tyr Gln Asn Ser Ser Thr Ala Thr Ser Gln Met Ala Glu Asn Asn Asp
 645 650 655
 Glu Gln Tyr Asp Ala Ile Asp Phe Val Pro Asn Tyr Asn Ser Ala Ser
 660 665 670
 Asn Asp Arg Leu Leu Ala Glu Gly Arg Gln Ala Gly Thr Gly Ala Ala
 675 680 685
 Ser Thr Leu Thr Arg Glu Ser Gly Ser Asp Ser Ala Ser His Ala
 690 695 700

<210> 9913
 <211> 1647
 <212> DNA
 <213> Ashbya gossypii

<220>
 <221> CDS
 <222> (1)..(1647)

<400> 9913
 atg cac atg agg cta ttt tcc aag ttc aag ctt cac ggt tgc tgc gcc 48
 Met His Met Arg Leu Phe Ser Lys Phe Lys Leu His Gly Ser Ser Ala
 1 5 10 15
 gca tct gag gaa gtg ttt ggt gga aag ttc agt tat acg tct gcg gtc 96
 Ala Ser Glu Glu Val Phe Gly Gly Lys Phe Ser Tyr Thr Ser Ala Val
 20 25 30
 gcc gac ttt tac atc gaa cta ggg gat gcg cac aag atc tgg aag ccc 144
 Ala Asp Phe Tyr Ile Glu Leu Gly Asp Ala His Lys Ile Trp Lys Pro
 35 40 45
 cgg gat gtg gtg acc ggt gag gtg gtg ctg acg ctg cgc aag ccg ctg 192
 Arg Asp Val Val Thr Gly Glu Val Val Leu Thr Leu Arg Lys Pro Leu
 50 55 60
 cgt ggg gtg agc ttg cgg atg tcc ctg gag ggc aat ctg cga gta cag 240
 Arg Gly Val Ser Leu Arg Met Ser Leu Glu Gly Asn Leu Arg Val Gln
 65 70 75 80
 acg ggc agc ggt gct acg tcc cgc ctg aag ttc cag cga acg ctg ttc 288
 Thr Gly Ser Gly Ala Thr Ser Arg Leu Lys Phe Gln Arg Thr Leu Phe
 85 90 95
 agc aaa agc tgc atg atc tac ggc gtc gag cag cca gaa gac gct gag 336
 Ser Lys Ser Ser Met Ile Tyr Gly Val Glu Gln Pro Glu Asp Ala Glu
 100 105 110
 caa gag gga cac ggg ctg aca cgc ggc gat cac cgt ttc ccg ttc cga 384
 Gln Glu Gly His Gly Leu Thr Arg Gly Asp His Arg Phe Pro Phe Arg
 115 120 125
 atg cgg gtg ccc tct aaa aac ata tac aca tgc att gcc ttc gag aag 432
 Met Arg Val Pro Ser Lys Asn Ile Tyr Thr Ser Ile Ala Phe Glu Lys
 130 135 140
 ggg tcc atc tca tat gct gtg ggg tgc gtg tta gag acg cgc agc ggg 480
 Gly Ser Ile Ser Tyr Ala Val Gly Cys Val Leu Glu Thr Arg Ser Gly
 145 150 155 160
 gcg cag agg ctg tct tcc tgt tgc cgc cag ata tct gtt cta gtc cct 528
 Ala Gln Arg Leu Ser Cys Ser Arg Gln Ile Ser Val Leu Val Pro
 165 170 175
 gtg gac gtt agc ctg ctg ccg aag cta cgg ccg aag act gtg gtc cta 576
 Val Asp Val Ser Leu Leu Pro Lys Leu Arg Pro Lys Thr Val Val Leu
 180 185 190
 cag tcc ccg caa ctc cta cgc agc gcg aaa gcg aat tac cca gaa cat 624
 Gln Ser Pro Gln Leu Leu Arg Ser Ala Lys Ala Asn Tyr Pro Glu His
 195 200 205
 gat aca gcg tct tct ctc acg aag cgc acc act gcc tgc gct aac tcc 672
 Asp Thr Ala Ser Ser Leu Thr Lys Arg Thr Thr Ala Ser Ala Asn Ser
 210 215 220
 aat tcc tcc gtg aca acc gtg tgc tct tgc aag act gtg act ata tct 720
 Asn Ser Ser Val Thr Thr Val Cys Ser Ser Lys Thr Val Thr Ile Ser
 225 230 235 240
 gtc gat ctg ccg gaa tcc gga tac gtt att ggg gac acc att agg atc 768
 Val Asp Leu Pro Glu Ser Gly Tyr Val Ile Gly Asp Thr Ile Arg Ile

PF59083SeqList PF59083.txt

aaa gtc cat atc cag cac tac aaa gag tat agg aat tct gcg ggg ctt	245	250	255	816
Lys Val His Ile Gln His Tyr Lys Glu Tyr Arg Asn Ser Ala Gly Leu				
att gca acg ctt gtc cgc att tgc cgt gtt cac agc acc ggc acc gat	260	265	270	864
Ile Ala Thr Leu Val Arg Ile Cys Arg Val His Ser Thr Gly Thr Asp				
gac ccg atg gag act ttc cgc aag gac atc tgc caa tgt gtt gcg cct	275	280	285	912
Asp Pro Met Glu Thr Phe Arg Lys Asp Ile Cys Gln Cys Val Ala Pro				
ctc tac gtc gag ccc gag aca cat acc tgc tcc gtc ggg atg aac ctc	290	295	300	960
Leu Tyr Val Glu Pro Glu Thr His Thr Cys Ser Val Gly Met Asn Leu				
aat gtc ccg ctg gat gcg ttt cca acg cta gtt gtc ccc aac caa ggc	305	310	315	1008
Asn Val Pro Leu Asp Ala Phe Pro Thr Leu Val Val Pro Asn Gln Gly				
ttc acc ttc caa tat tac att gaa gtt ctc gca aat ctg tcg tcg aag	325	330	335	1056
Phe Thr Phe Gln Tyr Tyr Ile Glu Val Leu Ala Asn Leu Ser Ser Lys				
aac att gtt tac aca gag tcc aac cgg gtc ata ggt ggc agc ggc atg	340	345	350	1104
Asn Ile Val Tyr Thr Glu Ser Asn Arg Val Ile Gly Ser Gly Met				
gcc gac att ccc atg cct ggc tcc aag ctg cat cct gtg aag aag atc	355	360	365	1152
Ala Asp Ile Pro Met Pro Gly Ser Lys Leu His Pro Val Lys Lys Ile				
agc atg ctc cct ctc aag ctg caa ggc cct ctg ggc aag cag gac aca	370	375	380	1200
Ser Met Leu Pro Leu Lys Leu Gln Gly Pro Leu Gly Lys Gln Asp Thr				
aac atc gat gag tca ctg atc ttc ttc caa gac atg gtg aat gtc gat	385	390	395	1248
Asn Ile Asp Glu Ser Leu Ile Phe Phe Gln Asp Met Val Asn Val Asp				
aaa ctc aaa cgt ctg cgc aat gta aca ggc act tcg ata gaa gtt gtc	405	410	415	1296
Lys Leu Lys Arg Leu Arg Asn Val Thr Gly Thr Ser Ile Glu Val Val				
att gga aca cat cgg aac aac tcc gtc cag caa gcg cgg cag tcc tgc	420	425	430	1344
Ile Gly Thr His Arg Asn Asn Ser Val Gln Gln Ala Arg Gln Ser Cys				
ccg ggc agt ccc gta ggc ggc tct gac tcc acg atg atg tca gag caa	435	440	445	1392
Pro Gly Ser Pro Val Gly Gly Ser Asp Ser Thr Met Met Ser Glu Gln				
tct gct gcc gga aca tct cta ccc tcc tca gta ctg gac atc tac gac	450	455	460	1440
Ser Ala Ala Gly Thr Ser Leu Pro Ser Ser Val Leu Asp Ile Tyr Asp				
caa cta gct aat agg ctg tcg agt agc gtt gga gat cag ctt ctc cgt	465	470	475	1488
Gln Leu Ala Asn Arg Leu Ser Ser Ser Val Gly Asp Gln Leu Leu Arg				
tac ggc atg tct cca gat tct ggc ccc cat tca gcg aac gat gag ctg	485	490	495	1536
Tyr Gly Met Ser Pro Asp Ser Gly Pro His Ser Ala Asn Asp Glu Leu				
ccg agg tat acg ccc aac gtc gat tac atg gta act gaa gat aaa cgt	500	505	510	1584
Pro Arg Tyr Thr Pro Asn Val Asp Tyr Met Val Thr Glu Asp Lys Arg				
gaa ctt gaa caa agg aag tta aaa gag cta gag agc gaa cca tcc gtg	515	520	525	1632
Glu Leu Glu Gln Arg Lys Leu Lys Glu Leu Glu Ser Glu Pro Ser Val				
gaa gaa gaa cag tga	530	535	540	1647
Glu Glu Glu Gln				

<210> 9914
 <211> 548
 <212> PRT
 <213> Ashbya gossypii

<400> 9914
 Met His Met Arg Leu Phe Ser Lys Phe Lys Leu His Gly Ser Ser Ala
 1 5 10 15
 Ala Ser Glu Glu Val Phe Gly Gly Lys Phe Ser Tyr Thr Ser Ala Val
 20 25 30

PF59083SeqList PF59083.txt

Ala Asp Phe Tyr Ile Glu Leu Gly Asp Ala His Lys Ile Trp Lys Pro
 35 40 45
 Arg Asp Val Val Thr Gly Glu Val Val Leu Thr Leu Arg Lys Pro Leu
 50 55 60
 Arg Gly Val Ser Leu Arg Met Ser Leu Glu Gly Asn Leu Arg Val Gln
 65 70 75 80
 Thr Gly Ser Gly Ala Thr Ser Arg Leu Lys Phe Gln Arg Thr Leu Phe
 85 90 95
 Ser Lys Ser Ser Met Ile Tyr Gly Val Glu Gln Pro Glu Asp Ala Glu
 100 105 110
 Gln Glu Gly His Gly Leu Thr Arg Gly Asp His Arg Phe Pro Phe Arg
 115 120 125
 Met Arg Val Pro Ser Lys Asn Ile Tyr Thr Ser Ile Ala Phe Glu Lys
 130 135 140
 Gly Ser Ile Ser Tyr Ala Val Gly Cys Val Leu Glu Thr Arg Ser Gly
 145 150 155 160
 Ala Gln Arg Leu Ser Ser Cys Ser Arg Gln Ile Ser Val Leu Val Pro
 165 170 175
 Val Asp Val Ser Leu Leu Pro Lys Leu Arg Pro Lys Thr Val Val Leu
 180 185 190
 Gln Ser Pro Gln Leu Leu Arg Ser Ala Lys Ala Asn Tyr Pro Glu His
 195 200 205
 Asp Thr Ala Ser Ser Leu Thr Lys Arg Thr Thr Ala Ser Ala Asn Ser
 210 215 220
 Asn Ser Ser Val Thr Thr Val Cys Ser Ser Lys Thr Val Thr Ile Ser
 225 230 235 240
 Val Asp Leu Pro Glu Ser Gly Tyr Val Ile Gly Asp Thr Ile Arg Ile
 245 250 255
 Lys Val His Ile Gln His Tyr Lys Glu Tyr Arg Asn Ser Ala Gly Leu
 260 265 270
 Ile Ala Thr Leu Val Arg Ile Cys Arg Val His Ser Thr Gly Thr Asp
 275 280 285
 Asp Pro Met Glu Thr Phe Arg Lys Asp Ile Cys Gln Cys Val Ala Pro
 290 295 300
 Leu Tyr Val Glu Pro Glu Thr His Thr Cys Ser Val Gly Met Asn Leu
 305 310 315 320
 Asn Val Pro Leu Asp Ala Phe Pro Thr Leu Val Val Pro Asn Gln Gly
 325 330 335
 Phe Thr Phe Gln Tyr Tyr Ile Glu Val Leu Ala Asn Leu Ser Ser Lys
 340 345 350
 Asn Ile Val Tyr Thr Glu Ser Asn Arg Val Ile Gly Gly Ser Gly Met
 355 360 365
 Ala Asp Ile Pro Met Pro Gly Ser Lys Leu His Pro Val Lys Lys Ile
 370 375 380
 Ser Met Leu Pro Leu Lys Leu Gln Gly Pro Leu Gly Lys Gln Asp Thr
 385 390 395 400
 Asn Ile Asp Glu Ser Leu Ile Phe Phe Gln Asp Met Val Asn Val Asp
 405 410 415
 Lys Leu Lys Arg Leu Arg Asn Val Thr Gly Thr Ser Ile Glu Val Val
 420 425 430
 Ile Gly Thr His Arg Asn Asn Ser Val Gln Gln Ala Arg Gln Ser Cys
 435 440 445
 Pro Gly Ser Pro Val Gly Gly Ser Asp Ser Thr Met Met Ser Glu Gln
 450 455 460
 Ser Ala Ala Gly Thr Ser Leu Pro Ser Ser Val Leu Asp Ile Tyr Asp
 465 470 475 480
 Gln Leu Ala Asn Arg Leu Ser Ser Ser Val Gly Asp Gln Leu Leu Arg
 485 490 495
 Tyr Gly Met Ser Pro Asp Ser Gly Pro His Ser Ala Asn Asp Glu Leu
 500 505 510
 Pro Arg Tyr Thr Pro Asn Val Asp Tyr Met Val Thr Glu Asp Lys Arg
 515 520 525
 Glu Leu Glu Gln Arg Lys Leu Lys Glu Leu Glu Ser Glu Pro Ser Val
 530 535 540
 Glu Glu Glu Gln
 545

<210> 9915

<211> 2349

PF59083SeqList PF59083.txt

<212> DNA

<213> Debaryomyces hansenii

<220>

<221> CDS

<222> (1)..(2349)

<400> 9915

atg aga aga gct gta tca aaa ata atc cca aac gga cct cct agg ttc	48
Met Arg Arg Ala Val Ser Lys Ile Ile Pro Asn Gly Pro Pro Arg Phe	
1 5 10 15	
cta cag agt ggg tca ttg cta tcg gga gat aca aac ttc aag tat aga	96
Leu Gln Ser Gly Ser Leu Leu Ser Gly Asp Thr Asn Phe Lys Tyr Arg	
20 25 30	
ata gat ttc aat tcc gtg gac gag ttt tat atc ctg ctc gca gat ccc	144
Ile Asp Phe Asn Ser Val Asp Glu Phe Tyr Ile Leu Leu Ala Asp Pro	
35 40 45	
cat aga tcc tgg ctt ccc gga gac gaa ata tca gga caa ata ata ttt	192
His Arg Ser Trp Leu Pro Gly Asp Glu Ile Ser Gly Gln Ile Ile Phe	
50 55 60	
ata tct aaa aaa gat ctt gca aac ata gta ata acg ttg tcg ttg ata	240
Ile Ser Lys Lys Asp Leu Ala Asn Ile Val Ile Thr Leu Ser Leu Ile	
65 70 75 80	
ggg agt gtg aag ata aat gca tca tca cac tct aaa tta cga cca gtt	288
Gly Ser Val Lys Ile Asn Ala Ser Ser His Ser Lys Leu Arg Pro Val	
85 90 95	
aaa gag cta tta ttt cat cat aca ata aaa att tat gga gac gaa aat	336
Lys Glu Leu Leu Phe His His Thr Ile Lys Ile Tyr Gly Asp Glu Asn	
100 105 110	
agt ggc aat aat aac gaa aac gga gaa gag ttc agt aat gga ttg ttt	384
Ser Gly Asn Asn Asn Glu Asn Gly Glu Glu Phe Ser Asn Gly Leu Phe	
115 120 125	
aaa ggt gaa cat agg ttt cca ttt att gtt aag ttg cct aac aaa cga	432
Lys Gly Glu His Arg Phe Pro Phe Ile Val Lys Leu Pro Asn Lys Arg	
130 135 140	
gtg ttc act agt att gat ttc ggg aag ggc tca att aaa tat tcg ttg	480
Val Phe Thr Ser Ile Asp Phe Gly Lys Gly Ser Ile Lys Tyr Ser Leu	
145 150 155 160	
aag gca gcc gtg ggg aat gca tca tca ttc gct aat gat agt ccg gca	528
Lys Ala Ala Val Gly Asn Ala Ser Ser Phe Ala Asn Asp Ser Pro Ala	
165 170 175	
gcc tcg ccg tta tcg gac tct aat aat aat aat aat aat aca acg aag	576
Ala Ser Pro Leu Ser Asp Ser Asn Asn Asn Asn Asn Asn Thr Thr Lys	
180 185 190	
aac aat ttt att ctg aag act aaa aac ttg aac ttt cat aat tcg gtc	624
Asn Asn Phe Ile Leu Lys Thr Lys Asn Leu Asn Phe His Asn Ser Val	
195 200 205	
tac aca tcg gaa aag atc att act ttg ata aac ccg ata gat gtt tca	672
Tyr Thr Ser Glu Lys Ile Ile Thr Leu Ile Asn Pro Ile Asp Val Ser	
210 215 220	
aaa ttg cct aga tcc aaa cca aaa aga ctc att atc aaa gat ccc cgt	720
Lys Leu Pro Arg Ser Lys Pro Lys Arg Leu Ile Ile Lys Asp Pro Arg	
225 230 235 240	
cta agt aaa aag tta tcc cga acc caa tcc tcg aca tca aca ttg aat	768
Leu Ser Lys Lys Leu Ser Arg Thr Gln Ser Ser Thr Ser Thr Leu Asn	
245 250 255	
aca gta aat aca ttc aac aca tta tcc tca aat aat tca gat act aca	816
Thr Val Asn Thr Phe Asn Thr Leu Ser Ser Asn Asn Ser Asp Thr Thr	
260 265 270	
aca aac ggt gaa ttt cat tcg aat ggt aat aca cca ggt aat agt gca	864
Thr Asn Gly Glu Phe His Ser Asn Gly Asn Thr Pro Gly Asn Ser Ala	
275 280 285	
tct cag tct aat tcc aat tca cca ttg aat ggg cta gat aat gct aga	912
Ser Gln Ser Asn Ser Asn Ser Pro Leu Asn Gly Leu Asp Asn Ala Arg	
290 295 300	
ccg cag gtt att aaa gtt gcg ctc gag ata cct gaa aga ggt ttt ctt	960
Pro Gln Val Ile Lys Val Ala Leu Glu Ile Pro Glu Arg Gly Phe Leu	
305 310 315 320	
aga ggt gaa ttg att ccg aca aaa ctt aat att aat cat tca aga aaa	1008

PF59083SeqList PF59083.txt

Arg	Gly	Glu	Leu	Ile	Pro	Thr	Lys	Leu	Asn	Ile	Asn	His	Ser	Arg	Lys	
att	caa	gat	tta	aat	ggt	att	atc	gtc	acg	tta	gtt	agg	gta	tgt	aga	1056
Ile	Gln	Asp	Leu	Asn	Gly	Ile	Ile	Val	Thr	Leu	Val	Arg	Val	Cys	Arg	
ctc	agc	aat	ggc	cat	gaa	aac	atg	ggt	gag	tca	ttc	aga	aag	gat	tta	1104
Leu	Ser	Asn	Gly	His	Glu	Asn	Met	Val	Glu	Ser	Phe	Arg	Lys	Asp	Leu	
caa	caa	ctg	gta	ctt	cca	tta	tat	gtt	gat	cca	aac	aca	ttt	caa	tct	1152
Gln	Gln	Leu	Val	Leu	Pro	Leu	Tyr	Val	Asp	Pro	Asn	Thr	Phe	Gln	Ser	
gaa	att	aac	acg	aat	tta	aga	ggt	cca	gca	gat	gca	ttc	cct	acg	ata	1200
Glu	Ile	Asn	Thr	Asn	Leu	Arg	Val	Pro	Ala	Asp	Ala	Phe	Pro	Thr	Ile	
tct	ggg	tgt	cca	cta	gta	tca	ttt	caa	tat	ttc	att	gaa	gta	ttg	atc	1248
Ser	Gly	Cys	Pro	Leu	Val	Ser	Phe	Gln	Tyr	Phe	Ile	Glu	Val	Leu	Ile	
aat	tta	tct	ggg	aaa	tcc	cta	ata	cta	gat	agc	agt	aat	cac	cac	aaa	1296
Asn	Leu	Ser	Gly	Lys	Ser	Leu	Ile	Leu	Asp	Ser	Ser	Asn	His	His	Lys	
ccc	agt	ata	tcg	aca	gat	gaa	gca	aac	cat	tca	tta	ttg	gaa	aat	cct	1344
Pro	Ser	Ile	Ser	Thr	Asp	Glu	Ala	Asn	His	Ser	Leu	Leu	Glu	Asn	Pro	
tca	aat	gat	ttg	aaa	tat	aag	ttt	aat	ttc	aat	tca	aat	gca	tct	atg	1392
Ser	Asn	Asp	Leu	Lys	Tyr	Lys	Phe	Asn	Phe	Asn	Ser	Asn	Ala	Ser	Met	
aat	caa	aat	gaa	cga	tcg	gga	ttt	att	aat	acc	gat	aag	tat	aaa	aga	1440
Asn	Gln	Asn	Glu	Arg	Ser	Gly	Phe	Ile	Asn	Thr	Asp	Lys	Tyr	Lys	Arg	
atg	aag	aaa	ttt	cta	ctt	tta	aca	act	gag	gta	atc	att	gga	act	aat	1488
Met	Lys	Lys	Phe	Leu	Leu	Leu	Thr	Thr	Glu	Val	Ile	Ile	Gly	Thr	Asn	
cgt	ctg	aat	gaa	cgt	ctg	gcc	tac	act	tct	aac	gaa	cga	tct	aat	gaa	1536
Arg	Leu	Asn	Glu	Arg	Leu	Ala	Tyr	Thr	Ser	Asn	Glu	Arg	Ser	Asn	Glu	
cta	tta	cat	gat	aat	ctc	aac	tct	att	tct	ccg	act	tca	aga	aag	tca	1584
Leu	Leu	His	Asp	Asn	Leu	Asn	Ser	Ile	Ser	Pro	Thr	Ser	Arg	Lys	Ser	
tca	tct	ggt	tct	gga	tcc	aat	gat	tcc	cca	tta	tta	ttc	aat	caa	act	1632
Ser	Ser	Val	Ser	Gly	Ser	Asn	Asp	Ser	Pro	Leu	Leu	Phe	Asn	Gln	Thr	
ggg	tca	aca	cca	cct	tcc	cag	caa	ggt	cat	caa	caa	cca	atg	agc	ctt	1680
Gly	Ser	Thr	Pro	Pro	Ser	Gln	Gln	Gly	His	Gln	Gln	Pro	Met	Ser	Leu	
aat	cca	ctc	tca	gaa	gcg	ata	cct	gct	aat	aat	ttt	tct	aca	cct	cct	1728
Asn	Pro	Leu	Ser	Glu	Ala	Ile	Pro	Ala	Asn	Asn	Phe	Ser	Thr	Pro	Pro	
tat	ttt	gag	aac	cag	caa	gat	tca	cca	tta	aat	att	gct	gat	aca	cct	1776
Tyr	Phe	Glu	Asn	Gln	Gln	Asp	Ser	Pro	Leu	Asn	Ile	Ala	Asp	Thr	Pro	
att	cct	ggc	tat	gaa	gaa	gtt	tca	aat	aat	tat	cat	gca	aat	tca	agt	1824
Ile	Pro	Gly	Tyr	Glu	Glu	Val	Ser	Asn	Asn	Tyr	His	Ala	Asn	Ser	Ser	
ttg	gca	cct	gtt	caa	atg	ccg	aca	cat	caa	cat	tta	tcc	gag	aaa	gaa	1872
Leu	Ala	Pro	Val	Gln	Met	Pro	Thr	His	Gln	His	Leu	Ser	Glu	Lys	Glu	
caa	ata	cga	gca	cac	gag	gcg	agc	tta	cta	ccg	tcc	gca	cca	cct	tta	1920
Gln	Ile	Arg	Ala	His	Glu	Ala	Ser	Leu	Leu	Pro	Ser	Ala	Pro	Pro	Leu	
gat	gat	gca	gaa	gaa	aca	gaa	aca	atc	agt	cca	att	gat	aaa	aat	aat	1968
Asp	Asp	Ala	Glu	Glu	Thr	Glu	Thr	Ile	Ser	Pro	Ile	Asp	Lys	Asn	Asn	
gaa	ata	tta	gaa	aat	ata	gag	gaa	ctg	ggg	gaa	gag	gta	aat	caa	tta	2016
Glu	Ile	Leu	Glu	Asn	Ile	Glu	Glu	Leu	Gly	Glu	Glu	Val	Asn	Gln	Leu	
aat	aac	gaa	tca	aac	gat	agt	gca	tca	tcg	agg	cat	tca	cag	tca	ttc	2064
Asn	Asn	Glu	Ser	Asn	Asp	Ser	Ala	Ser	Ser	Arg	His	Ser	Gln	Ser	Phe	
gga	ttt	ttc	act	tac	caa	aat	tcc	aca	tcc	aca	act	ccc	aca	aat		2112

PF59083SeqList PF59083.txt

Gly	Phe	Phe	Thr	Tyr	Gln	Asn	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Thr	Asn	
690						695					700					
cac	gaa	agt	tta	gag	gaa	gag	gag	gaa	gag	gag	gag	gat	aat	tta	tac	2160
His	Glu	Ser	Leu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu	Tyr	
705					710					715					720	
cat	agt	aat	aat	ctt	ctg	aac	tca	cat	gcc	gaa	ata	gat	agc	gaa	tca	2208
His	Ser	Asn	Asn	Leu	Leu	Asn	Ser	His	Ala	Glu	Ile	Asp	Ser	Glu	Ser	
				725					730					735		
act	gat	tgg	gtt	ccc	aat	tat	gaa	act	gct	aat	cac	gat	ata	ttg	ctt	2256
Thr	Asp	Trp	Val	Pro	Asn	Tyr	Glu	Thr	Ala	Asn	His	Asp	Ile	Leu	Leu	
			740					745					750			
gaa	aat	gat	cat	gtc	agt	acc	ggg	act	aat	atg	cat	cca	ggg	aga	aat	2304
Glu	Asn	Asp	His	Val	Ser	Thr	Gly	Thr	Asn	Met	His	Pro	Gly	Arg	Asn	
		755					760					765				
gct	aat	tcg	agt	gca	cgt	ggg	ccg	cag	caa	gat	aat	tca	tct	taa		2349
Ala	Asn	Ser	Ser	Ala	Arg	Gly	Pro	Gln	Gln	Asp	Asn	Ser	Ser			
770						775					780					

<210> 9916

<211> 782

<212> PRT

<213> Debaryomyces hansenii

<400> 9916

Met	Arg	Arg	Ala	Val	Ser	Lys	Ile	Ile	Pro	Asn	Gly	Pro	Pro	Arg	Phe	
1				5					10					15		
Leu	Gln	Ser	Gly	Ser	Leu	Leu	Ser	Gly	Asp	Thr	Asn	Phe	Lys	Tyr	Arg	
			20					25					30			
Ile	Asp	Phe	Asn	Ser	Val	Asp	Glu	Phe	Tyr	Ile	Leu	Leu	Ala	Asp	Pro	
		35					40					45				
His	Arg	Ser	Trp	Leu	Pro	Gly	Asp	Glu	Ile	Ser	Gly	Gln	Ile	Ile	Phe	
	50					55					60					
Ile	Ser	Lys	Lys	Asp	Leu	Ala	Asn	Ile	Val	Ile	Thr	Leu	Ser	Leu	Ile	
65					70					75					80	
Gly	Ser	Val	Lys	Ile	Asn	Ala	Ser	Ser	His	Ser	Lys	Leu	Arg	Pro	Val	
			85						90					95		
Lys	Glu	Leu	Leu	Phe	His	His	Thr	Ile	Lys	Ile	Tyr	Gly	Asp	Glu	Asn	
			100					105					110			
Ser	Gly	Asn	Asn	Asn	Glu	Asn	Gly	Glu	Glu	Phe	Ser	Asn	Gly	Leu	Phe	
		115					120					125				
Lys	Gly	Glu	His	Arg	Phe	Pro	Phe	Ile	Val	Lys	Leu	Pro	Asn	Lys	Arg	
	130					135					140					
Val	Phe	Thr	Ser	Ile	Asp	Phe	Gly	Lys	Gly	Ser	Ile	Lys	Tyr	Ser	Leu	
145					150					155					160	
Lys	Ala	Ala	Val	Gly	Asn	Ala	Ser	Ser	Phe	Ala	Asn	Asp	Ser	Pro	Ala	
			165						170					175		
Ala	Ser	Pro	Leu	Ser	Asp	Ser	Asn	Asn	Asn	Asn	Asn	Asn	Thr	Thr	Lys	
			180					185					190			
Asn	Asn	Phe	Ile	Leu	Lys	Thr	Lys	Asn	Leu	Asn	Phe	His	Asn	Ser	Val	
		195					200					205				
Tyr	Thr	Ser	Glu	Lys	Ile	Ile	Thr	Leu	Ile	Asn	Pro	Ile	Asp	Val	Ser	
	210				215						220					
Lys	Leu	Pro	Arg	Ser	Lys	Pro	Lys	Arg	Leu	Ile	Ile	Lys	Asp	Pro	Arg	
225					230					235					240	
Leu	Ser	Lys	Lys	Leu	Ser	Arg	Thr	Gln	Ser	Ser	Thr	Ser	Thr	Leu	Asn	
			245					250						255		
Thr	Val	Asn	Thr	Phe	Asn	Thr	Leu	Ser	Ser	Asn	Asn	Ser	Asp	Thr	Thr	
			260					265					270			
Thr	Asn	Gly	Glu	Phe	His	Ser	Asn	Gly	Asn	Thr	Pro	Gly	Asn	Ser	Ala	
		275					280					285				
Ser	Gln	Ser	Asn	Ser	Asn	Ser	Pro	Leu	Asn	Gly	Leu	Asp	Asn	Ala	Arg	
	290					295					300					
Pro	Gln	Val	Ile	Lys	Val	Ala	Leu	Glu	Ile	Pro	Glu	Arg	Gly	Phe	Leu	
305					310					315					320	
Arg	Gly	Glu	Leu	Ile	Pro	Thr	Lys	Leu	Asn	Ile	Asn	His	Ser	Arg	Lys	
			325						330					335		
Ile	Gln	Asp	Leu	Asn	Gly	Ile	Ile	Val	Thr	Leu	Val	Arg	Val	Cys	Arg	
		340						345					350			
Leu	Ser	Asn	Gly	His	Glu	Asn	Met	Val	Glu	Ser	Phe	Arg	Lys	Asp	Leu	

PF59083SeqList PF59083.txt

```

      355      360      365
Gln Gln Leu Val Leu Pro Leu Tyr Val Asp Pro Asn Thr Phe Gln Ser
      370      375      380
Glu Ile Asn Thr Asn Leu Arg Val Pro Ala Asp Ala Phe Pro Thr Ile
385      390      395
Ser Gly Cys Pro Leu Val Ser Phe Gln Tyr Phe Ile Glu Val Leu Ile
      405      410      415
Asn Leu Ser Gly Lys Ser Leu Ile Leu Asp Ser Ser Asn His His Lys
      420      425      430
Pro Ser Ile Ser Thr Asp Glu Ala Asn His Ser Leu Leu Glu Asn Pro
      435      440      445
Ser Asn Asp Leu Lys Tyr Lys Phe Asn Phe Asn Ser Asn Ala Ser Met
      450      455      460
Asn Gln Asn Glu Arg Ser Gly Phe Ile Asn Thr Asp Lys Tyr Lys Arg
465      470      475
Met Lys Lys Phe Leu Leu Thr Thr Glu Val Ile Ile Gly Thr Asn
      485      490      495
Arg Leu Asn Glu Arg Leu Ala Tyr Thr Ser Asn Glu Arg Ser Asn Glu
      500      505      510
Leu Leu His Asp Asn Leu Asn Ser Ile Ser Pro Thr Ser Arg Lys Ser
      515      520      525
Ser Ser Val Ser Gly Ser Asn Asp Ser Pro Leu Leu Phe Asn Gln Thr
      530      535      540
Gly Ser Thr Pro Pro Ser Gln Gln Gly His Gln Gln Pro Met Ser Leu
545      550      555
Asn Pro Leu Ser Glu Ala Ile Pro Ala Asn Asn Phe Ser Thr Pro Pro
      565      570      575
Tyr Phe Glu Asn Gln Gln Asp Ser Pro Leu Asn Ile Ala Asp Thr Pro
      580      585      590
Ile Pro Gly Tyr Glu Glu Val Ser Asn Asn Tyr His Ala Asn Ser Ser
      595      600      605
Leu Ala Pro Val Gln Met Pro Thr His Gln His Leu Ser Glu Lys Glu
      610      615      620
Gln Ile Arg Ala His Glu Ala Ser Leu Leu Pro Ser Ala Pro Pro Leu
625      630      635
Asp Asp Ala Glu Glu Thr Glu Thr Ile Ser Pro Ile Asp Lys Asn Asn
      645      650      655
Glu Ile Leu Glu Asn Ile Glu Glu Leu Gly Glu Glu Val Asn Gln Leu
      660      665      670
Asn Asn Glu Ser Asn Asp Ser Ala Ser Ser Arg His Ser Gln Ser Phe
      675      680      685
Gly Phe Phe Thr Tyr Gln Asn Ser Thr Ser Thr Thr Thr Pro Thr Asn
      690      695      700
His Glu Ser Leu Glu Glu Glu Glu Glu Glu Asp Asn Leu Tyr
705      710      715
His Ser Asn Asn Leu Leu Asn Ser His Ala Glu Ile Asp Ser Glu Ser
      725      730      735
Thr Asp Trp Val Pro Asn Tyr Glu Thr Ala Asn His Asp Ile Leu Leu
      740      745      750
Glu Asn Asp His Val Ser Thr Gly Thr Asn Met His Pro Gly Arg Asn
      755      760      765
Ala Asn Ser Ser Ala Arg Gly Pro Gln Gln Asp Asn Ser Ser
      770      775      780

```

<210> 9917

<211> 2328

<212> DNA

<213> Emericella nidulans

<220>

<221> CDS

<222> (1)..(2328)

<400> 9917

```

atg gtt agg gcg acg tgt tca tgt gtc atg tcc gtc aat cct ctc tcc
Met Val Arg Ala Thr Cys Ser Cys Val Met Ser Val Asn Pro Leu Ser
      1      5      10      15
gcc caa acc tct gct tcg ccg ctc agt cgg aat cgg tcc tct ctt ctg
Ala Gln Thr Ser Ala Ser Pro Leu Ser Arg Asn Arg Ser Ser Leu Leu

```

48

96

PF59083SeqList PF59083.txt

	20	25	30	
tcc Ser	aaa Lys	ttc Phe	cgg Arg	144
ttc Phe	tat Tyr	att Ile	gag Glu	192
gtt Val	ata Ile	aaa Lys	ggg Gly	240
aca Thr	cat His	ttg Leu	gtt Val	288
aat Asn	gtt Val	cca Pro	gct Ala	336
ggg Gly	cgc Arg	ggg Gly	cgc Arg	384
ttg Leu	ttt Phe	gaa Glu	gat Asp	432
ggg Gly	att Ile	tac Tyr	aag Lys	480
cct Pro	agc Ser	agc Ser	atc Ile	528
tcc Ser	acc Thr	ttg Leu	acc Lys	576
aga Arg	cgc Arg	ata Ile	aac Asn	624
ccc Pro	aag Lys	cct Pro	cga Arg	672
ccg Pro	aaa Lys	gga Gly	aag Lys	720
tca Ser	tta Leu	gag Glu	cca Pro	768
cct Pro	ccg Pro	ctc Leu	agt Ser	816
agc Ser	aac Asn	agc Ser	cag Gln	864
gct Ala	agt Ser	agc Ser	ggt Gly	912
gtg Val	acc Thr	gat Asp	gga Gly	960
gtg Val	cta Leu	ccc Pro	ggt Gly	1008
aaa Lys	caa Gln	gtg Val	cgc Arg	1056
ggc Gly	cgt Arg	atc Ile	gac Asp	1104
gga Gly	aag Lys	aag Lys	cca Pro	1152
ctg Leu	ggg Gly	ggt Gly	ctt Leu	1200

PF59083SeqList PF59083.txt

385	aaa	gat	ctg	tca	cag	acc	ttt	gcg	cct	ctc	att	gtg	gat	ccg	acg	act	1248
	Lys	Asp	Leu	Ser	Gln	Thr	Phe	Ala	Pro	Leu	Ile	Val	Asp	Pro	Thr	Thr	
				405						410					415		
	ttg	aca	gct	gat	atc	aag	act	tca	atc	cgc	ata	cct	gaa	gat	gct	ttc	1296
	Leu	Thr	Ala	Asp	Ile	Lys	Thr	Ser	Ile	Arg	Ile	Pro	Glu	Asp	Ala	Phe	
				420						425					430		
	ccg	aca	att	acc	cgc	aca	cca	ggg	agc	atg	atc	aac	ttc	cgt	tat	tat	1344
	Pro	Thr	Ile	Thr	Arg	Thr	Pro	Gly	Ser	Met	Ile	Asn	Phe	Arg	Tyr	Tyr	
			435					440					445				
	gtt	gaa	gtg	gtt	gtc	gat	ctg	ggc	aag	ctg	act	tct	ccg	gag	cgt		1392
	Val	Glu	Val	Val	Val	Asp	Leu	Arg	Gly	Lys	Leu	Thr	Ser	Pro	Glu	Arg	
		450					455				460						
	ttt	ctt	ccg	cgg	ttt	aac	cta	gtt	tct	tca	ggg	cgc	aac	ttc	tcc	tca	1440
	Phe	Leu	Pro	Arg	Phe	Asn	Leu	Val	Ser	Ser	Gly	Arg	Asn	Phe	Ser	Ser	
	465					470					475					480	
	aat	ggg	aag	att	gtg	cac	cct	gcc	gat	acg	aat	gga	agc	gcg	atc	aca	1488
	Asn	Gly	Lys	Ile	Val	His	Pro	Ala	Asp	Thr	Asn	Gly	Ser	Ala	Ile	Thr	
				485						490					495		
	gcc	aac	tgg	ggg	gac	aac	att	cta	gac	acg	gat	caa	ata	cgt	cgt	gaa	1536
	Ala	Asn	Trp	Gly	Asp	Asn	Ile	Leu	Asp	Thr	Asp	Gln	Ile	Arg	Arg	Glu	
				500					505					510			
	aag	gga	gtt	gtt	gct	gtg	att	ttc	gag	gtg	gtc	att	ggg	acc	caa	gat	1584
	Lys	Gly	Val	Val	Ala	Val	Ile	Phe	Glu	Val	Val	Ile	Gly	Thr	Gln	Asp	
		515						520					525				
	aca	cag	agg	cgc	aag	agt	gaa	gcc	cgg	cgc	atg	tca	tct	acg	gcg	gag	1632
	Thr	Gln	Arg	Arg	Lys	Ser	Glu	Ala	Arg	Arg	Met	Ser	Ser	Thr	Ala	Glu	
		530					535					540					
	gaa	gca	gag	ttc	cag	cag	ccc	gta	gaa	aac	tcc	gtt	gat	gga	gat	tac	1680
	Glu	Ala	Glu	Phe	Gln	Gln	Pro	Val	Glu	Asn	Ser	Val	Asp	Gly	Asp	Tyr	
	545					550					555					560	
	gct	ggc	cac	gac	tac	cag	ggc	agc	atg	gcg	ggc	cca	gag	ccc	ggc	tat	1728
	Ala	Gly	His	Asp	Tyr	Gln	Gly	Ser	Met	Ala	Gly	Pro	Glu	Pro	Gly	Tyr	
				565						570					575		
	gct	ccg	cta	gag	aac	act	gca	tat	gga	cct	gat	caa	att	cgt	tgg	cca	1776
	Ala	Pro	Leu	Glu	Asn	Thr	Ala	Tyr	Gly	Pro	Asp	Gln	Ile	Arg	Trp	Pro	
				580					585					590			
	gat	tat	cca	gag	cag	tcg	gag	cat	gag	cat	tat	cct	ttc	cag	ccg	ggg	1824
	Asp	Tyr	Pro	Glu	Gln	Ser	Glu	His	Glu	His	Tyr	Pro	Phe	Gln	Pro	Gly	
			595					600					605				
	acg	ctt	ccc	agt	cct	cag	ccg	gat	gag	cct	atg	gac	gaa	aag	gca	cga	1872
	Thr	Leu	Pro	Ser	Pro	Gln	Pro	Asp	Glu	Pro	Met	Asp	Glu	Lys	Ala	Arg	
		610					615					620					
	tta	cgg	cgt	gct	gaa	cag	acg	ctc	ttg	cct	agt	caa	cct	ccg	tgc	gac	1920
	Leu	Arg	Arg	Ala	Glu	Gln	Thr	Leu	Leu	Pro	Ser	Gln	Pro	Pro	Cys	Asp	
	625					630					635					640	
	ccg	gag	gcc	ggg	ccc	tca	tca	gcg	gtg	gaa	gct	gca	atg	cct	acc	gct	1968
	Pro	Glu	Ala	Gly	Pro	Ser	Ser	Ala	Val	Glu	Ala	Ala	Met	Pro	Thr	Ala	
				645						650					655		
	cct	gtg	ctc	cct	gaa	gat	gac	cac	ttg	aac	gat	tat	cac	cac	ctt	ccg	2016
	Pro	Val	Leu	Pro	Glu	Asp	Asp	His	Leu	Asn	Asp	Tyr	His	His	Leu	Pro	
				660					665					670			
	tca	aca	act	gtg	aat	ggg	atg	act	gga	atg	gcg	cca	gca	ctc	atg	tca	2064
	Ser	Thr	Thr	Val	Asn	Gly	Met	Thr	Gly	Met	Ala	Pro	Ala	Leu	Met	Ser	
				675				680						685			
	gcg	gag	tct	gtg	caa	aca	gtc	att	gca	gga	agc	agt	tcc	gca	cct	ctc	2112
	Ala	Glu	Ser	Val	Gln	Thr	Val	Ile	Ala	Gly	Ser	Ser	Ser	Ala	Pro	Leu	
		690					695					700					
	act	agt	ccc	tca	aga	ccc	agt	gaa	gag	gat	aaa	cag	gag	ttg	gag	cgc	2160
	Thr	Ser	Pro	Ser	Arg	Pro	Ser	Glu	Glu	Asp	Lys	Gln	Glu	Leu	Glu	Arg	
	705					710					715					720	
	cag	cgg	tta	atg	atg	gaa	gcc	agt	gcg	cca	ggg	gac	ccg	gat	gca	cgt	2208
	Gln	Arg	Leu	Met	Met	Glu	Ala	Ser	Ala	Pro	Gly	Asp	Pro	Asp	Ala	Arg	
				725						730					735		
	cat	aac	gac	cgc	gcg	gat	gat	ggg	cct	agt	gcg	ccc	att	ttc	cat	gac	2256
	His	Asn	Asp	Arg	Ala	Asp	Asp	Gly	Pro	Ser	Ala	Pro	Ile	Phe	His	Asp	
				740				745						750			
	gat	gac	gat	gat	cag	cag	cta	gtt	gga	ggg	gct	gca	aat	ggg	gac	gag	2304
	Asp	Asp	Asp	Asp	Gln	Gln	Leu	Val	Gly	Gly	Ala	Ala	Asn	Gly	Asp	Glu	

755
 cta tta ccg cgg tat caa cgt tga
 Leu Leu Pro Arg Tyr Gln Arg
 770 775

2328

<210> 9918
 <211> 775
 <212> PRT
 <213> Emericella nidulans

<400> 9918
 Met Val Arg Ala Thr Cys Ser Cys Val Met Ser Val Asn Pro Leu Ser
 1 5 10 15
 Ala Gln Thr Ser Ala Ser Pro Leu Ser Arg Asn Arg Ser Ser Leu Leu
 20 25 30
 Ser Lys Phe Arg Thr Gln Leu Gly Gln Arg Asn Arg Ala Ile Thr Asp
 35 40 45
 Phe Tyr Ile Glu Pro Asp Asp Pro Trp Arg Ser Tyr Phe Pro Gly Asp
 50 55 60
 Val Ile Lys Gly Thr Val Ser Leu Thr Val Val Arg Pro Val Arg Ile
 65 70 75 80
 Thr His Leu Val Ile Ser Leu His Gly Ile Val Lys Val Phe Lys Asn
 85 90 95
 Asn Val Pro Ala Gly Glu Thr Pro Pro Asp Val Gly Ser Leu Gly Pro
 100 105 110
 Gly Arg Gly Arg Arg Gly Ala Glu Tyr Leu Gly Asn Gly Val Ala Thr
 115 120 125
 Leu Phe Glu Asp Glu Val Val Leu Cys Gly Glu Gly Arg Leu Lys Glu
 130 135 140
 Gly Ile Tyr Lys Phe Arg Phe Glu Met Ser Phe Pro Pro Tyr Pro Leu
 145 150 155 160
 Pro Ser Ser Ile Ser Phe Glu Arg Gly Thr Ile Ser Tyr Met Leu Thr
 165 170 175
 Ser Thr Leu Thr Lys Pro Thr Thr Met Asn Pro Thr Leu Ser Cys Arg
 180 185 190
 Arg Arg Ile Asn Leu Leu Glu Asn Ile Asp Ile Ala Ala Phe Pro Ala
 195 200 205
 Pro Lys Pro Arg Val Val Thr Leu Glu Pro Ile Ser Lys Arg Ser Lys
 210 215 220
 Pro Lys Gly Lys Thr Lys Ala Ala Gly Phe Asp Ala Pro Asp Thr Ala
 225 230 235 240
 Ser Leu Glu Pro Ser Ala Ser Gly Gly Ile Thr Val Pro Glu His Arg
 245 250 255
 Pro Pro Leu Ser Pro Ala Pro Ser Asn Val Ser Ser Ser Ser Arg Leu
 260 265 270
 Ser Asn Ser Ser Gln Ser Phe Gln Ile Val Thr Asp Pro Gly Ser Thr
 275 280 285
 Ala Ser Ser Gly Val Arg Asn Ser Glu Ala Arg Ser Asn Thr Pro Ser
 290 295 300
 Val Thr Asp Gly Ile Ile Thr Ala Lys Ala Glu Val Leu Arg Ala Gly
 305 310 315 320
 Val Leu Pro Gly Asp Thr Leu Pro Ile Lys Ile Thr Ile Asn His Thr
 325 330 335
 Lys Gln Val Arg Ser Ala His Gly Ile Ile Thr Leu Tyr Arg Ser
 340 345 350
 Gly Arg Ile Asp Leu His Pro Ala Ile Pro Met Gly Ser Thr Ala Asn
 355 360 365
 Gly Lys Lys Pro Ile Tyr Glu Asp Tyr Tyr Pro Arg Ser Arg Thr Gly
 370 375 380
 Leu Gly Gly Leu Thr Leu Gly Thr Ser Arg Ala Ser Ser Val Phe Arg
 385 390 395 400
 Lys Asp Leu Ser Gln Thr Phe Ala Pro Leu Ile Val Asp Pro Thr Thr
 405 410 415
 Leu Thr Ala Asp Ile Lys Thr Ser Ile Arg Ile Pro Glu Asp Ala Phe
 420 425 430
 Pro Thr Ile Thr Arg Thr Pro Gly Ser Met Ile Asn Phe Arg Tyr Tyr
 435 440 445
 Val Glu Val Val Val Asp Leu Arg Gly Lys Leu Thr Ser Pro Glu Arg
 450 455 460

PF59083SeqList PF59083.txt

Phe 465 Leu Pro Arg Phe 470 Asn 470 Leu Val Ser Ser Gly 475 Arg Asn Phe Ser Ser 480
 Asn Gly Lys Ile Val 485 His Pro Ala Asp Thr Asn Gly Ser Ala Ile Thr 495
 Ala Asn Trp Gly 500 Asp Asn Ile Leu Asp Thr Asp Gln Ile Arg Arg Glu 510
 Lys Gly Val Val Ala Val Ile Phe 520 Glu Val Val Ile Gly Thr Gln Asp 525
 Thr Gln 530 Arg Arg Lys Ser Glu 535 Ala Arg Arg Met Ser 540 Ser Thr Ala Glu 545
 Glu 545 Ala Glu Phe Gln Gln 550 Pro Val Glu Asn Ser 555 Val Asp Gly Asp Tyr 560
 Ala Gly His Asp Tyr 565 Gln Gly Ser Met Ala Gly Pro Glu Pro Gly Tyr 575
 Ala Pro Leu Glu 580 Asn Thr Ala Tyr Gly 585 Pro Asp Gln Ile Arg Arg Trp Pro 590
 Asp Tyr Pro 595 Glu Gln Ser Glu His Glu His Tyr Pro Phe 605 Gln Pro Gly 610
 Thr Leu 610 Pro Ser Pro Gln Pro 615 Asp Glu Pro Met Asp 620 Glu Lys Ala Arg 625
 Leu 625 Arg Arg Ala Glu Gln 630 Thr Leu Leu Pro Ser 635 Gln Pro Pro Cys Asp 640
 Pro Glu Ala Gly Pro 645 Ser Ser Ala Val Glu Ala Ala Met Pro Thr Ala 655
 Pro Val Leu Pro 660 Glu Asp Asp His Leu 665 Asn Asp Tyr His His 670 Leu Pro 675
 Ser Thr Thr Val Asn Gly Met Thr 680 Gly Met Ala Pro Ala Leu Met Ser 685
 Ala Glu Ser Val Gln Thr Val 695 Ile Ala Gly Ser Ser 700 Ser Ala Pro Leu 705
 Thr 705 Ser Pro Ser Arg Pro 710 Ser Glu Glu Asp Lys 715 Gln Glu Leu Glu Arg 720
 Gln Arg Leu Met Met 725 Glu Ala Ser Ala Pro Gly Asp Pro Asp Ala Arg 735
 His Asn Asp Arg 740 Ala Asp Asp Gly Pro 745 Ser Ala Pro Ile Phe His Asp 750
 Asp Asp Asp 755 Gln Gln Leu Val 760 Gly Gly Ala Ala Asn Gly Asp Glu 765
 Leu Leu 770 Pro Arg Tyr Gln Arg 775

<210> 9919

<211> 1719

<212> DNA

<213> Kluyveromyces lactis

<220>

<221> CDS

<222> (1)..(1719)

<400> 9919

atg gga tta ttt gat aaa ctt ctg cgg tcg aac gaa cga gct gag cga	48
Met Gly Leu Phe Asp 5 Lys Leu Leu Arg Ser 10 Asn Glu Arg Ala Glu Arg 15	
ggt tct cct agt gca ttt gtg gtg agt agc ttc gat tca gtg agc aat	96
Gly Ser Pro Ser Ala Phe Val Val Ser Ser Phe Asp Ser Val Ser Asn 20	
gct ggc aag agc tcc att ttc aag cac tcc ggt atg aaa tcg tac att	144
Ala Gly Lys 35 Ser Ser Ile Phe Lys 40 His Ser Gly Met Lys 45 Ser Tyr Ile 50	
ttg gag ttt gaa att gta ctt gat gat gtg cac aga gtg tgg aaa ccg	192
Leu Glu Phe Glu Ile Val Leu Asp Asp Val His Arg Val Trp Lys Pro 55	
aac gag act atc agt ggg act gtg aag ctt cga ttg aga aaa gat gtg	240
Asn Glu Thr Ile Ser 70 Thr Val Lys Leu Arg 75 Leu Arg Lys Asp Val 80	
cct aat gtt tgg att aaa ctt gct cat ata gga gag ttt caa ctc cat	288
Pro Asn Val Trp Ile 85 Lys Leu Ala His Ile 90 Gly Glu Phe Gln Leu His 95	

PF59083SeqList PF59083.txt

tcc	aat	aac	ccg	atg	acc	gca	ggg	tct	cta	aaa	tcg	aaa	tac	tct	gat	336
Ser	Asn	Asn	Pro	Met	Thr	Ala	Gly	Ser	Leu	Lys	Ser	Lys	Tyr	Ser	Asp	
			100					105					110			
aca	gtg	ttt	tgc	agg	tcc	acg	agt	att	tat	ggg	agt	gag	gag	aat	cca	384
Thr	Val	Phe	Cys	Arg	Ser	Thr	Ser	Ile	Tyr	Gly	Ser	Glu	Glu	Asn	Pro	
		115					120					125				
tta	cac	ttg	act	ggc	ggg	gaa	cac	aag	ttt	cca	ttc	tct	tgt	aaa	att	432
Leu	His	Leu	Thr	Gly	Gly	Glu	His	Lys	Phe	Pro	Phe	Ser	Cys	Lys	Ile	
	130					135					140					
aat	ggg	aag	aac	ttg	gtg	agc	tcg	ata	gat	ttt	aag	aag	ggg	tcc	ata	480
Asn	Gly	Lys	Asn	Leu	Val	Ser	Ser	Ile	Asp	Phe	Lys	Lys	Gly	Ser	Ile	
145					150					155					160	
aga	tat	tgg	gtt	caa	gca	gag	ctt	cat	gcc	caa	aag	acg	cct	cct	atc	528
Arg	Tyr	Trp	Val	Gln	Ala	Glu	Leu	His	Ala	Gln	Lys	Thr	Pro	Pro	Ile	
			165						170							
ttt	tgc	aag	cag	cat	tac	cag	ttg	att	gtg	cca	ata	gac	gtc	ggc	caa	576
Phe	Cys	Lys	Gln	His	Tyr	Gln	Leu	Ile	Val	Pro	Ile	Asp	Val	Gly	Gln	
			180					185					190			
tta	cca	aag	cca	aat	atc	aag	acg	gtg	gtc	tta	caa	tca	ccc	aac	tca	624
Leu	Pro	Lys	Pro	Asn	Ile	Lys	Thr	Val	Val	Leu	Gln	Ser	Pro	Asn	Ser	
		195					200					205				
agc	aat	aat	gga	atc	cat	gtt	aga	aga	ctt	atg	gca	gca	ggg	tct	gca	672
Ser	Asn	Asn	Gly	Ile	His	Val	Arg	Arg	Leu	Met	Ala	Ala	Gly	Ser	Ala	
	210					215					220					
gac	cca	caa	gac	ggg	gct	tcg	tct	ctg	act	agg	aaa	aca	ggc	gga	tcc	720
Asp	Pro	Gln	Asp	Gly	Ala	Ser	Ser	Leu	Thr	Arg	Lys	Thr	Gly	Gly	Ser	
225					230					235					240	
tct	act	atc	act	aat	ggg	tca	tca	agc	tca	aat	aat	tca	ggg	aat	tcc	768
Ser	Thr	Ile	Thr	Asn	Gly	Ser	Ser	Ser	Ser	Asn	Asn	Ser	Gly	Asn	Ser	
				245				250						255		
aac	gct	tcc	atg	ctc	gct	gat	aac	aag	act	gtc	aag	atc	tcg	gta	gag	816
Asn	Ala	Ser	Met	Leu	Ala	Asp	Asn	Lys	Thr	Val	Lys	Ile	Ser	Val	Glu	
			260					265					270			
att	ccc	tgt	cta	gga	tac	acc	atc	gga	gaa	gaa	att	ccg	ggt	aaa	gtc	864
Ile	Pro	Cys	Leu	Gly	Tyr	Thr	Ile	Gly	Glu	Glu	Ile	Pro	Val	Lys	Val	
		275					280					285				
cac	gtc	act	cat	tac	aaa	caa	tac	ttc	cac	cct	gcg	ggg	ttg	att	gca	912
His	Val	Thr	His	Tyr	Lys	Gln	Tyr	Phe	His	Pro	Ala	Gly	Leu	Ile	Ala	
	290					295					300					
acg	ttg	gtc	aga	atc	tct	cgg	gtt	tca	aac	cct	aga	aat	aca	gaa	cag	960
Thr	Leu	Val	Arg	Ile	Ser	Arg	Val	Ser	Asn	Pro	Arg	Asn	Thr	Glu	Gln	
305					310					315					320	
atc	gaa	aca	ttt	aga	aaa	gat	atc	tgt	caa	ggg	gtt	gcc	cca	tta	tat	1008
Ile	Glu	Thr	Phe	Arg	Lys	Asp	Ile	Cys	Gln	Gly	Val	Ala	Pro	Leu	Tyr	
			325						330					335		
aca	gac	ccc	gaa	acg	cat	gaa	gct	gtt	ata	atg	ttg	aaa	cta	aag	gtt	1056
Thr	Asp	Pro	Glu	Thr	His	Glu	Ala	Val	Ile	Met	Leu	Lys	Leu	Lys	Val	
			340				345						350			
cca	tta	gac	acc	ttc	ccg	agt	ttg	gat	tta	aag	aat	aag	ttc	ttc	act	1104
Pro	Leu	Asp	Thr	Phe	Pro	Ser	Leu	Asp	Leu	Lys	Asn	Lys	Phe	Phe	Thr	
		355					360					365				
ttc	cag	tat	tac	gtg	gag	atc	cta	gca	aat	ttg	tca	agg	aag	aat	ttg	1152
Phe	Gln	Tyr	Tyr	Val	Glu	Ile	Leu	Ala	Asn	Leu	Ser	Arg	Lys	Asn	Leu	
	370				375						380					
gta	tac	aca	gag	tcc	aat	aga	ctt	gtg	ggg	gga	cag	aga	act	agt	agt	1200
Val	Tyr	Thr	Glu	Ser	Asn	Arg	Leu	Val	Gly	Gly	Gln	Arg	Thr	Ser	Ser	
385					390				395						400	
ata	ccg	atg	ccg	tcg	aac	aag	ttt	tcg	atg	ttc	caa	gac	ctc	tca	aac	1248
Ile	Pro	Met	Pro	Ser	Asn	Lys	Phe	Ser	Met	Phe	Gln	Asp	Leu	Ser	Asn	
			405						410				415			
cag	ggg	gag	gtt	act	gct	ggc	gaa	gat	gat	tca	gta	acg	ttt	ttc	caa	1296
Gln	Gly	Glu	Val	Thr	Ala	Gly	Glu	Asp	Asp	Ser	Val	Thr	Phe	Phe	Gln	
			420				425						430			
gat	ttg	att	aat	gta	gac	aga	ctc	aaa	cgt	cta	aga	aac	gtt	aca	ggg	1344
Asp	Leu	Ile	Asn	Val	Asp	Arg	Leu	Lys	Arg	Leu	Arg	Asn	Val	Thr	Gly	
		435				440						445				
atg	tca	atc	gaa	gtt	gtg	atc	gga	aca	cac	aga	gaa	gaa	cat	gag	cct	1392
Met	Ser	Ile	Glu	Val	Val	Ile	Gly	Thr	His	Arg	Glu	Glu	His	Glu	Pro	
	450					455					460					

PF59083SeqList PF59083.txt

gaa	tcg	ccc	aca	gtg	gac	cgt	ctg	gat	tcc	cat	tct	atc	aac	caa	tta	1440
Glu	Ser	Pro	Thr	Val	Asp	Arg	Leu	Asp	Ser	His	Ser	Ile	Asn	Gln	Leu	
465					470				475						480	
cct	gat	gat	gtg	gat	gca	gtt	tac	aac	caa	tgc	tct	agc	gct	gaa	tct	1488
Pro	Asp	Asp	Val	Asp	Ala	Val	Tyr	Asn	Gln	Cys	Ser	Ser	Ala	Glu	Ser	
				485					490					495		
cca	ata	gac	gaa	gct	tac	gac	tat	ttg	tta	cat	aga	cat	aac	ggg	cca	1536
Pro	Ile	Asp	Glu	Ala	Tyr	Asp	Tyr	Leu	Leu	His	Arg	His	Asn	Gly	Pro	
			500					505					510			
tca	cct	tcc	tct	cgt	atc	ttc	acg	gat	acg	gat	atg	act	ttg	tgc	tat	1584
Ser	Pro		Ser	Arg	Ile	Phe	Thr	Asp	Thr	Asp	Met	Thr	Leu	Cys	Tyr	
		515					520					525				
ccg	gct	gac	cct	gtt	cca	ctg	tat	agt	cgt	gga	tta	gat	gac	ttc	act	1632
Pro	Ala	Asp	Pro	Val	Pro	Leu	Tyr	Ser	Arg	Gly	Leu	Asp	Asp	Phe	Thr	
	530					535					540					
ggg	tgt	tca	atg	tca	ggt	gtt	aca	gat	gat	aaa	caa	gaa	cta	gag	caa	1680
Gly	Cys	Ser	Met	Ser	Gly	Val	Thr	Asp	Asp	Lys	Gln	Glu	Leu	Glu	Gln	
545					550					555					560	
atg	cgg	ttg	aaa	gaa	ttg	gaa	agc	gaa	ccg	ccc	ata	taa				1719
Met	Arg	Leu	Lys	Glu	Leu	Glu	Ser	Glu	Pro	Pro	Ile					
				565					570							

<210> 9920

<211> 572

<212> PRT

<213> Kluyveromyces fragilis

<400> 9920

Met	Gly	Leu	Phe	Asp	Lys	Leu	Leu	Arg	Ser	Asn	Glu	Arg	Ala	Glu	Arg	
1				5					10					15		
Gly	Ser	Pro	Ser	Ala	Phe	Val	Val	Ser	Ser	Phe	Asp	Ser	Val	Ser	Asn	
			20					25					30			
Ala	Gly	Lys	Ser	Ser	Ile	Phe	Lys	His	Ser	Gly	Met	Lys	Ser	Tyr	Ile	
		35					40				45					
Leu	Glu	Phe	Glu	Ile	Val	Leu	Asp	Asp	Val	His	Arg	Val	Trp	Lys	Pro	
	50					55					60					
Asn	Glu	Thr	Ile	Ser	Gly	Thr	Val	Lys	Leu	Arg	Leu	Arg	Lys	Asp	Val	
65					70					75					80	
Pro	Asn	Val	Trp	Ile	Lys	Leu	Ala	His	Ile	Gly	Glu	Phe	Gln	Leu	His	
			85						90					95		
Ser	Asn	Asn	Pro	Met	Thr	Ala	Gly	Ser	Leu	Lys	Ser	Lys	Tyr	Ser	Asp	
			100					105					110			
Thr	Val	Phe	Cys	Arg	Ser	Thr	Ser	Ile	Tyr	Gly	Ser	Glu	Glu	Asn	Pro	
		115					120					125				
Leu	His	Leu	Thr	Gly	Gly	Glu	His	Lys	Phe	Pro	Phe	Ser	Cys	Lys	Ile	
	130					135					140					
Asn	Gly	Lys	Asn	Leu	Val	Ser	Ser	Ile	Asp	Phe	Lys	Lys	Gly	Ser	Ile	
145					150					155					160	
Arg	Tyr	Trp	Val	Gln	Ala	Glu	Leu	His	Ala	Gln	Lys	Thr	Pro	Pro	Ile	
			165						170					175		
Phe	Cys	Lys	Gln	His	Tyr	Gln	Leu	Ile	Val	Pro	Ile	Asp	Val	Gly	Gln	
			180					185					190			
Leu	Pro	Lys	Pro	Asn	Ile	Lys	Thr	Val	Val	Leu	Gln	Ser	Pro	Asn	Ser	
		195					200					205				
Ser	Asn	Asn	Gly	Ile	His	Val	Arg	Arg	Leu	Met	Ala	Ala	Gly	Ser	Ala	
	210					215					220					
Asp	Pro	Gln	Asp	Gly	Ala	Ser	Ser	Leu	Thr	Arg	Lys	Thr	Gly	Gly	Ser	
225					230					235					240	
Ser	Thr	Ile	Thr	Asn	Gly	Ser	Ser	Ser	Ser	Asn	Asn	Ser	Gly	Asn	Ser	
				245						250				255		
Asn	Ala	Ser	Met	Leu	Ala	Asp	Asn	Lys	Thr	Val	Lys	Ile	Ser	Val	Glu	
			260					265						270		
Ile	Pro	Cys	Leu	Gly	Tyr	Thr	Ile	Gly	Glu	Glu	Ile	Pro	Val	Lys	Val	
		275					280					285				
His	Val	Thr	His	Tyr	Lys	Gln	Tyr	Phe	His	Pro	Ala	Gly	Leu	Ile	Ala	
	290					295					300					
Thr	Leu	Val	Arg	Ile	Ser	Arg	Val	Ser	Asn	Pro	Arg	Asn	Thr	Glu	Gln	
305					310					315					320	
Ile	Glu	Thr	Phe	Arg	Lys	Asp	Ile	Cys	Gln	Gly	Val	Ala	Pro	Leu	Tyr	

PF59083SeqList PF59083.txt

```

          325          330          335
Thr Asp Pro Glu Thr His Glu Ala Val Ile Met Leu Lys Leu Lys Val
          340          345          350
Pro Leu Asp Thr Phe Pro Ser Leu Asp Leu Lys Asn Lys Phe Phe Thr
          355          360          365
Phe Gln Tyr Tyr Val Glu Ile Leu Ala Asn Leu Ser Arg Lys Asn Leu
          370          375          380
Val Tyr Thr Glu Ser Asn Arg Leu Val Gly Gly Gln Arg Thr Ser Ser
          385          390          400
Ile Pro Met Pro Ser Asn Lys Phe Ser Met Phe Gln Asp Leu Ser Asn
          405          410          415
Gln Gly Glu Val Thr Ala Gly Glu Asp Asp Ser Val Thr Phe Phe Gln
          420          425          430
Asp Leu Ile Asn Val Asp Arg Leu Lys Arg Leu Arg Asn Val Thr Gly
          435          440          445
Met Ser Ile Glu Val Val Ile Gly Thr His Arg Glu Glu His Glu Pro
          450          455          460
Glu Ser Pro Thr Val Asp Arg Leu Asp Ser His Ser Ile Asn Gln Leu
          465          470          475
Pro Asp Asp Val Asp Ala Val Tyr Asn Gln Cys Ser Ser Ala Glu Ser
          485          490          495
Pro Ile Asp Glu Ala Tyr Asp Tyr Leu Leu His Arg His Asn Gly Pro
          500          505          510
Ser Pro Ser Ser Arg Ile Phe Thr Asp Thr Asp Met Thr Leu Cys Tyr
          515          520          525
Pro Ala Asp Pro Val Pro Leu Tyr Ser Arg Gly Leu Asp Asp Phe Thr
          530          535          540
Gly Cys Ser Met Ser Gly Val Thr Asp Asp Lys Gln Glu Leu Glu Gln
          545          550          555
Met Arg Leu Lys Glu Leu Glu Ser Glu Pro Pro Ile
          565          570

```

<210> 9921
 <211> 2313
 <212> DNA
 <213> Magnaporthe grisea

<220>
 <221> CDS
 <222> (1)..(2313)

```

<400> 9921
atg ggc ggc tcc tcg gcc tcc agg aac caa tct tcg ctg ctt gaa gac      48
Met Gly Gly Ser Ser Ala Ser Arg Asn Gln Ser Ser Leu Leu Glu Asp
1      5      10      15
acg cac acg agc cga tcg cta atc tct cgc ctc ttt tcg cgt tca aag      96
Thr His Thr Ser Arg Ser Leu Ile Ser Arg Leu Phe Ser Arg Ser Lys
20      25      30
acg cga cac att acc gat ttc cac atc cgc ccc gtc gat ccg cac cgc      144
Thr Arg His Ile Thr Asp Phe Ile Arg Pro Val Asp Pro His Arg
35      40      45
aag tac gcc aaa ggc gac cat gtc acc ggc gcc gtt gtt ttg act gtc      192
Lys Tyr Ala Lys Gly Asp His Val Thr Gly Ala Val Val Leu Thr Val
50      55      60
ctc agg cca att cgc atc aca cac cta act gtt gct ctc cac ggc ttc      240
Leu Arg Pro Ile Arg Ile Thr His Leu Thr Val Ala Leu His Gly Phe
65      70      75
gtc aag gtc ttc aag agt ccc aac gca gcc cac gaa gcc acg atc aat      288
Val Lys Val Phe Lys Ser Pro Asn Ala Ala His Glu Ala Thr Ile Asn
85      90      95
acc gcg cag att gcc tct ggc gtt acc aac cgg aca cga tac ctt ggc      336
Thr Ala Gln Ile Ala Ser Gly Val Thr Asn Arg Thr Arg Tyr Leu Gly
100      105      110
aat ggc ctc gcg tca ctc ttc caa gat gag cag gtt ctt agc gcc gac      384
Asn Gly Leu Ala Ser Leu Phe Gln Asp Glu Gln Val Leu Ser Ala Asp
115      120      125
gga aag ctg gag gcg ggg cgt tac gag ttc aat ttt gat ctc gtg ttt      432
Gly Lys Leu Glu Ala Gly Arg Tyr Glu Phe Asn Phe Asp Leu Val Phe
130      135      140

```

PF59083SeqList PF59083.txt																
cca	tcc	aag	gtt	aac	ctt	cca	acg	agc	atc	gat	gaa	aat	tta	ctt	ggt	480
Pro	Ser	Lys	Val	Asn	Leu	Pro	Thr	Ser	Ile	Asp	Glu	Asn	Leu	Leu	Gly	
145				150						155					160	
gga	gaa	agt	aga	cat	agg	atc	cat	ccc	agc	acc	gcg	gcc	gcg	aac	gat	528
Gly	Glu	Ser	Arg	His	Arg	Ile	His	Pro	Ser	Thr	Ala	Ala	Ala	Asn	Asp	
				165				170						175		
atc	tct	cga	gcc	aat	atc	cag	gag	gac	acg	gag	gag	gag	gac	gga	ccg	576
Ile	Ser	Arg	Ala	Asn	Ile	Gln	Glu	Asp	Thr	Glu	Glu	Glu	Asp	Gly	Pro	
			180					185					190			
acc	aag	gca	cct	gag	agt	gtt	gct	gca	gaa	tcc	aac	atc	gca	aac	gat	624
Thr	Lys	Ala	Pro	Glu	Ser	Val	Ala	Ala	Glu	Ser	Asn	Ile	Ala	Asn	Asp	
			195				200					205				
gcc	gcc	ttc	gag	ggc	cag	caa	gcc	ccg	caa	agt	ccc	aca	cgt	acc	gag	672
Ala	Ala	Phe	Glu	Gly	Gln	Gln	Ala	Pro	Gln	Ser	Pro	Thr	Arg	Thr	Glu	
			210			215					220					
atg	ccc	gat	gtc	atg	agc	gag	gtc	agc	aca	gag	agc	gcc	atc	acg	agt	720
Met	Pro	Asp	Val	Met	Ser	Glu	Val	Ser	Thr	Glu	Ser	Ala	Ile	Thr	Ser	
225				230						235					240	
agc	agt	gcg	ggc	gca	agc	gtt	gga	tac	aag	gtc	agt	gag	gca	acg	gga	768
Ser	Ser	Ala	Gly	Ala	Ser	Val	Gly	Tyr	Lys	Val	Ser	Glu	Ala	Thr	Gly	
			245					250						255		
agt	tct	tcg	ggc	tca	caa	ttt	ggg	gcc	aga	aca	cct	acg	gtt	gag	gaa	816
Ser	Ser	Ser	Gly	Ser	Gln	Phe	Gly	Ala	Arg	Thr	Pro	Thr	Val	Glu	Glu	
			260					265					270			
aag	acc	atc	acc	gcc	agc	gtc	gaa	atg	ctc	aag	ggg	ggc	tgc	cta	ccg	864
Lys	Thr	Ile	Thr	Ala	Ser	Val	Glu	Met	Leu	Lys	Gly	Gly	Cys	Leu	Pro	
			275				280					285				
gga	gac	ttt	gtc	ccc	gtc	aag	atc	tca	gtg	cac	cac	atc	aag	agg	ata	912
Gly	Asp	Phe	Val	Pro	Val	Lys	Ile	Ser	Val	His	His	Ile	Lys	Arg	Ile	
			290			295					300					
aaa	agc	gtt	cat	gga	gtc	att	gtc	act	ctg	tac	agg	caa	gga	aga	ata	960
Lys	Ser	Val	His	Gly	Val	Ile	Val	Thr	Leu	Tyr	Arg	Gln	Gly	Arg	Ile	
305				310						315					320	
gac	tcg	gca	ccg	ccc	ata	tcg	tct	ttc	cag	ggc	ctg	tcc	aag	gaa	gac	1008
Asp	Ser	Ala	Pro	Pro	Ile	Ser	Ser	Phe	Gln	Gly	Leu	Ser	Lys	Glu	Asp	
				325				330						335		
gtg	cgt	cgc	ctg	gaa	aag	gaa	gaa	tat	ttc	cca	cgg	tcg	aaa	aca	ggg	1056
Val	Arg	Arg	Leu	Glu	Lys	Glu	Glu	Tyr	Phe	Pro	Arg	Ser	Lys	Thr	Gly	
			340					345					350			
ctg	agc	ggc	ttg	tct	ttg	tca	tca	gct	ggg	tcc	tgc	agc	gtc	ttc	cgc	1104
Leu	Ser	Gly	Leu	Ser	Leu	Ser	Ser	Ala	Gly	Ser	Cys	Ser	Val	Phe	Arg	
			355				360					365				
aag	gat	ctc	tcg	cag	gcc	ttt	ggg	cct	ctg	atc	atc	gac	ccc	atc	aca	1152
Lys	Asp	Leu	Ser	Gln	Ala	Phe	Gly	Pro	Leu	Ile	Ile	Asp	Pro	Ile	Thr	
						375					380					
ctg	gac	gca	agc	gtg	acg	att	tcg	gtt	cga	gta	cca	gag	gat	gtc	ttt	1200
Leu	Asp	Ala	Ser	Val	Thr	Ile	Ser	Val	Arg	Val	Pro	Glu	Asp	Val	Phe	
385				390						395					400	
cct	acc	atc	aag	ggc	gtg	ccc	ggg	gag	ctg	att	agc	ttc	aag	tat	caa	1248
Pro	Thr	Ile	Lys	Gly	Val	Pro	Gly	Glu	Leu	Ile	Ser	Phe	Lys	Tyr	Gln	
				405				410						415		
atg	gag	gta	ata	gtg	gac	ttg	gga	ggc	aag	ctg	gcc	agc	caa	atc	tcg	1296
Met	Glu	Val	Ile	Val	Asp	Leu	Gly	Gly	Lys	Leu	Ala	Ser	Gln	Ile	Ser	
			420					425					430			
tcg	gta	caa	tcc	aaa	gcc	ggc	ggc	ata	tct	gcc	ggg	ggc	gca	atg	ccc	1344
Ser	Val	Gln	Ser	Lys	Ala	Gly	Gly	Ile	Ser	Ala	Gly	Gly	Ala	Met	Pro	
			435				440					445				
tct	gcc	aga	aac	cca	tac	gaa	agc	gga	ggc	tcg	tct	atc	atg	gga	agc	1392
Ser	Ala	Arg	Asn	Pro	Tyr	Glu	Ser	Gly	Gly	Ser	Ser	Ile	Met	Gly	Ser	
						455						460				
tgg	ggc	aac	agc	atc	ata	gat	acg	gac	cag	ctg	cgt	cgc	cac	aag	ggg	1440
Trp	Gly	Asn	Ser	Ile	Ile	Asp	Thr	Asp	Gln	Leu	Arg	Arg	His	Lys	Gly	
465				470						475					480	
gtc	atc	tcg	gtt	gtg	ttc	gaa	gtt	cct	gta	ggg	agc	gtg	gac	tca	agt	1488
Val	Ile	Ser	Val	Val	Phe	Glu	Val	Pro	Val	Gly	Ser	Val	Asp	Ser	Ser	
				485				490						495		
cga	caa	agg	aca	agg	ggc	ggg	tct	ctt	cgt	ccg	aat	ccc	caa	gcg	cgc	1536
Arg	Gln	Arg	Thr	Arg	Gly	Gly	Ser	Leu	Arg	Pro	Asn	Pro	Gln	Ala	Arg	
			500					505					510			

PF59083SeqList PF59083.txt

cag	ccg	tcg	caa	gcg	acc	gaa	tcg	tcg	caa	ata	ccg	aca	gta	ggc	tat	1584
Gln	Pro	Ser	Gln	Ala	Thr	Glu	Ser	Ser	Gln	Ile	Pro	Thr	Val	Gly	Tyr	
		515					520					525				
gga	ccg	gaa	gac	aaa	cag	cgg	gct	cag	tca	gag	cca	gct	ggg	caa	gag	1632
Gly	Pro	Glu	Asp	Lys	Gln	Arg	Ala	Gln	Ser	Glu	Pro	Ala	Gly	Gln	Glu	
		530				535					540					
gac	tat	gtt	cac	agt	cat	gga	agt	cag	ggc	aac	gga	cct	atg	gga	cca	1680
Asp	Tyr	Val	His	Ser	His	Gly	Ser	Gln	Gly	Asn	Gly	Pro	Met	Gly	Pro	
545					550				555						560	
agt	act	gaa	tat	gta	ccc	agc	ccg	tac	tac	act	cca	cac	gat	cct	cgt	1728
Ser	Thr	Glu	Tyr	Val	Pro	Ser	Pro	Tyr	Tyr	Thr	Pro	His	Asp	Pro	Arg	
				565				570						575		
caa	cag	cat	gcg	ccg	atc	tac	ata	cca	ccc	cca	gat	gtg	ccg	aac	gat	1776
Gln	Gln	His	Ala	Pro	Ile	Tyr	Ile	Pro	Pro	Pro	Asp	Val	Pro	Asn	Asp	
			580					585					590			
atg	ggc	ctg	tca	gaa	aag	gaa	cga	gcg	cgc	cga	gcg	gag	cag	aga	ctg	1824
Met	Gly	Leu	Ser	Glu	Lys	Glu	Arg	Ala	Arg	Arg	Ala	Glu	Gln	Arg	Leu	
		595					600					605				
ctg	cca	agt	cag	cct	cca	gca	gcc	cca	ttt	gca	agc	acg	tta	tcc	gag	1872
Leu	Pro	Ser	Gln	Pro	Pro	Ala	Ala	Pro	Phe	Ala	Ser	Thr	Leu	Ser	Glu	
		610				615						620				
act	acc	ctt	gag	gat	ata	tac	aac	gtc	gag	gac	gac	gca	gca	gca	ggg	1920
Thr	Thr	Leu	Glu	Asp	Ile	Tyr	Asn	Val	Glu	Asp	Asp	Ala	Ala	Ala	Gly	
625					630				635						640	
ccg	tcg	tcg	gct	ccc	atc	gta	gga	aac	tct	aac	ggg	gtt	gca	acg	gca	1968
Pro	Ser	Ser	Ala	Pro	Ile	Val	Gly	Asn	Ser	Asn	Gly	Val	Ala	Thr	Ala	
				645				650						655		
ccg	act	ctg	gac	gag	gtt	gaa	tct	ggc	gaa	gca	gcg	gtt	ggc	aac	agt	2016
Pro	Thr	Leu	Asp	Glu	Val	Glu	Ser	Gly	Glu	Ala	Ala	Val	Gly	Asn	Ser	
			660					665					670			
gag	gac	aag	ctg	gag	aga	gag	cgt	cac	cgt	ctg	ctg	caa	gag	gca	agc	2064
Glu	Asp	Lys	Leu	Glu	Arg	Glu	Arg	His	Arg	Leu	Leu	Gln	Glu	Ala	Ser	
		675					680					685				
gcc	ccg	cct	gat	ttc	ccc	gaa	gac	tat	gac	acg	ggg	gac	cca	ggg	cct	2112
Ala	Pro	Pro	Asp	Phe	Pro	Glu	Asp	Tyr	Asp	Thr	Gly	Asp	Pro	Gly	Pro	
		690				695					700					
agt	aat	caa	ggg	cct	gtc	acg	agt	gcg	acg	gcg	ccg	gca	tta	agc	ttt	2160
Ser	Asn	Gln	Gly	Pro	Val	Thr	Ser	Ala	Thr	Ala	Pro	Ala	Leu	Ser	Phe	
705					710				715						720	
cag	ccc	tcg	gca	cct	ata	ctc	tcc	gag	gac	gag	gag	gac	cct	ggc	agc	2208
Gln	Pro	Ser	Ala	Pro	Ile	Leu	Ser	Glu	Asp	Asp	Glu	Asp	Pro	Gly	Ser	
				725				730						735		
tcg	tat	ttc	aat	cag	cac	acg	agc	aca	ggg	gat	tac	atg	ggg	gct	ggg	2256
Ser	Tyr	Phe	Asn	Gln	His	Thr	Ser	Thr	Gly	Asp	Tyr	Met	Gly	Ala	Gly	
			740					745					750			
gcc	ctg	ggg	cgt	cca	att	acg	gca	cct	cac	gag	cca	ctt	cct	cga	tat	2304
Ala	Leu	Gly	Arg	Pro	Ile	Thr	Ala	Pro	His	Glu	Pro	Leu	Pro	Arg	Tyr	
		755					760					765				
cag	agg	tag														2313
Gln	Arg															
		770														

<210> 9922

<211> 770

<212> PRT

<213> Magnaporthe grisea

<400> 9922

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

PF59083SeqList PF59083.txt

				85				90					95		
Thr	Ala	Gln	Ile	Ala	Ser	Gly	Val	Thr	Asn	Arg	Thr	Arg	Tyr	Leu	Gly
			100					105					110		
Asn	Gly	Leu	Ala	Ser	Leu	Phe	Gln	Asp	Glu	Gln	Val	Leu	Ser	Ala	Asp
		115					120					125			
Gly	Lys	Leu	Glu	Ala	Gly	Arg	Tyr	Glu	Phe	Asn	Phe	Asp	Leu	Val	Phe
	130					135					140				
Pro	Ser	Lys	Val	Asn	Leu	Pro	Thr	Ser	Ile	Asp	Glu	Asn	Leu	Leu	Gly
145					150					155					160
Gly	Glu	Ser	Arg	His	Arg	Ile	His	Pro	Ser	Thr	Ala	Ala	Ala	Asn	Asp
				165					170					175	
Ile	Ser	Arg	Ala	Asn	Ile	Gln	Glu	Asp	Thr	Glu	Glu	Glu	Asp	Gly	Pro
			180					185					190		
Thr	Lys	Ala	Pro	Glu	Ser	Val	Ala	Ala	Glu	Ser	Asn	Ile	Ala	Asn	Asp
		195					200					205			
Ala	Ala	Phe	Glu	Gly	Gln	Gln	Ala	Pro	Gln	Ser	Pro	Thr	Arg	Thr	Glu
	210					215					220				
Met	Pro	Asp	Val	Met	Ser	Glu	Val	Ser	Thr	Glu	Ser	Ala	Ile	Thr	Ser
225					230					235					240
Ser	Ser	Ala	Gly	Ala	Ser	Val	Gly	Tyr	Lys	Val	Ser	Glu	Ala	Thr	Gly
				245					250					255	
Ser	Ser	Ser	Gly	Ser	Gln	Phe	Gly	Ala	Arg	Thr	Pro	Thr	Val	Glu	Glu
			260					265					270		
Lys	Thr	Ile	Thr	Ala	Ser	Val	Glu	Met	Leu	Lys	Gly	Gly	Cys	Leu	Pro
		275					280					285			
Gly	Asp	Phe	Val	Pro	Val	Lys	Ile	Ser	Val	His	His	Ile	Lys	Arg	Ile
	290					295					300				
Lys	Ser	Val	His	Gly	Val	Ile	Val	Thr	Leu	Tyr	Arg	Gln	Gly	Arg	Ile
305					310					315					320
Asp	Ser	Ala	Pro	Pro	Ile	Ser	Ser	Phe	Gln	Gly	Leu	Ser	Lys	Glu	Asp
				325					330					335	
Val	Arg	Arg	Leu	Glu	Lys	Glu	Glu	Tyr	Phe	Pro	Arg	Ser	Lys	Thr	Gly
			340					345					350		
Leu	Ser	Gly	Leu	Ser	Leu	Ser	Ser	Ala	Gly	Ser	Cys	Ser	Val	Phe	Arg
		355					360					365			
Lys	Asp	Leu	Ser	Gln	Ala	Phe	Gly	Pro	Leu	Ile	Ile	Asp	Pro	Ile	Thr
	370					375					380				
Leu	Asp	Ala	Ser	Val	Thr	Ile	Ser	Val	Arg	Val	Pro	Glu	Asp	Val	Phe
385					390					395					400
Pro	Thr	Ile	Lys	Gly	Val	Pro	Gly	Glu	Leu	Ile	Ser	Phe	Lys	Tyr	Gln
			405						410					415	
Met	Glu	Val	Ile	Val	Asp	Leu	Gly	Gly	Lys	Leu	Ala	Ser	Gln	Ile	Ser
			420					425					430		
Ser	Val	Gln	Ser	Lys	Ala	Gly	Gly	Ile	Ser	Ala	Gly	Gly	Ala	Met	Pro
		435					440					445			
Ser	Ala	Arg	Asn	Pro	Tyr	Glu	Ser	Gly	Gly	Ser	Ser	Ile	Met	Gly	Ser
	450					455					460				
Trp	Gly	Asn	Ser	Ile	Ile	Asp	Thr	Asp	Gln	Leu	Arg	Arg	His	Lys	Gly
465					470					475					480
Val	Ile	Ser	Val	Val	Phe	Glu	Val	Pro	Val	Gly	Ser	Val	Asp	Ser	Ser
			485						490					495	
Arg	Gln	Arg	Thr	Arg	Gly	Gly	Ser	Leu	Arg	Pro	Asn	Pro	Gln	Ala	Arg
			500					505					510		
Gln	Pro	Ser	Gln	Ala	Thr	Glu	Ser	Gln	Ile	Pro	Thr	Val	Gly	Tyr	
		515					520					525			
Gly	Pro	Glu	Asp	Lys	Gln	Arg	Ala	Gln	Ser	Glu	Pro	Ala	Gly	Gln	Glu
	530					535					540				
Asp	Tyr	Val	His	Ser	His	Gly	Ser	Gln	Gly	Asn	Gly	Pro	Met	Gly	Pro
545					550					555					560
Ser	Thr	Glu	Tyr	Val	Pro	Ser	Pro	Tyr	Tyr	Thr	Pro	His	Asp	Pro	Arg
				565					570					575	
Gln	Gln	His	Ala	Pro	Ile	Tyr	Ile	Pro	Pro	Pro	Asp	Val	Pro	Asn	Asp
			580					585					590		
Met	Gly	Leu	Ser	Glu	Lys	Glu	Arg	Ala	Arg	Arg	Ala	Glu	Gln	Arg	Leu
		595					600					605			
Leu	Pro	Ser	Gln	Pro	Pro	Ala	Ala	Pro	Phe	Ala	Ser	Thr	Leu	Ser	Glu
	610					615					620				
Thr	Thr	Leu	Glu	Asp	Ile	Tyr	Asn	Val	Glu	Asp	Asp	Ala	Ala	Ala	Gly
625					630					635					640

PF59083SeqList PF59083.txt

Pro Ser Ser Ala Pro Ile Val Gly Asn Ser Asn Gly Val Ala Thr Ala
645 650 655
Pro Thr Leu Asp Glu Val Glu Ser Gly Glu Ala Ala Val Gly Asn Ser
660 665 670
Glu Asp Lys Leu Glu Arg Glu Arg His Arg Leu Leu Gln Glu Ala Ser
675 680 685
Ala Pro Pro Asp Phe Pro Glu Asp Tyr Asp Thr Gly Asp Pro Gly Pro
690 695 700
Ser Asn Gln Gly Pro Val Thr Ser Ala Thr Ala Pro Ala Leu Ser Phe
705 710 715 720
Gln Pro Ser Ala Pro Ile Leu Ser Glu Asp Glu Asp Pro Gly Ser
725 730 735
Ser Tyr Phe Asn Gln His Thr Ser Thr Gly Asp Tyr Met Gly Ala Gly
740 745 750
Ala Leu Gly Arg Pro Ile Thr Ala Pro His Glu Pro Leu Pro Arg Tyr
755 760 765
Gln Arg
770

<210> 9923

<211> 1629

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(1629)

<400> 9923

atg tcg tta ctg aga ctg tgg aac aaa gaa tca agg gca cca tca aaa	48
Met Ser Leu Leu Arg 5 Leu Trp Asn Lys Glu 10 Ser Arg Ala Pro Ser 15 Lys	
ata aag agt cat ggt att gtt ggc agt tac ggc aac agc atg ctg gcc	96
Ile Lys Ser His 20 Gly Ile Val Gly Ser 25 Tyr Gly Asn Ser Met 30 Leu Ala	
cat aac aac gtg aag caa ttt cgt ata gac ata gac gaa ccg cat aga	144
His Asn Asn Val 35 Lys Gln Phe Arg 40 Ile Asp Ile Asp Glu Pro His Arg	
gta tgg aaa ccg aat gaa agc ata acc gga gaa gcg gtc att gac ata	192
Val Trp Lys Pro Asn Glu Ser 55 Ile Thr Gly Glu 60 Val Ile Asp Ile	
aag aga gac ata act aac gta gcg atc aaa tta tcg cta gta tgt gag	240
Lys Arg Asp Ile Thr Asn 70 Val Ala Ile Lys Leu 75 Ser Leu Val Cys 80 Glu	
gtt cgc gtg aaa acg ggg aac agt cca acc tcc aag aat aag aga att	288
Val Arg Val 85 Lys Thr Gly Asn Ser Pro Thr 90 Ser Lys Asn Lys Arg 95 Ile	
gag aaa acc tta gag aag tcg acg ttt ctt tat gga cag gac tac gta	336
Glu Lys Thr 100 Leu Glu Lys Ser Thr 105 Phe Leu Tyr Gly Gln Asp Tyr Val	
aag aca gct ttt tcg gct aag gaa aag aaa ccg cat gtt gac aaa acc	384
Lys Thr Ala Phe Ser Ala Lys Glu Lys Lys Pro His Val 125 Asp Lys Thr	
acc att ctc aat ggt tta agc aag ggg gaa cac agg ttt ccc ttt agg	432
Thr Ile 130 Leu Asn Gly Leu Ser 135 Lys Gly Glu His Arg Phe Pro Phe Arg	
ata cga ata cca cga ggc aga gga atg ttg agc tct ata aag ttc gaa	480
Ile Arg Ile Pro Arg Gly Arg Gly Met Leu Ser 155 Ser Ile Lys Phe Glu	
agg ggc tcg ata aca tac ttc ctc tct tgc act tta gaa tcc ctc aac	528
Arg Gly Ser Ile Thr Tyr Phe Leu Ser Cys Thr Leu Glu Ser Leu Asn	
165 170 175	
aac atc aac gga tta aaa aaa ccg gaa gca aga tgc gaa cgt gag ttt	576
Asn Ile Asn 180 Leu Lys Lys Pro Glu Ala Arg Cys Glu Arg Glu Phe	
185 190 195	
gca gtc ata gtt ccg ctg gac gtc tcg agg ctg ccc aag ccg aaa act	624
Ala Val Ile Val Pro Leu Asp Val Ser Arg Leu Pro Lys Pro Lys Thr	
200 205	
aag aca gtg gtt tta caa tca gca tct atg gtc caa aac aaa aag aac	672

PF59083SeqList PF59083.txt

Lys	Thr	Val	Val	Leu	Gln	Ser	Ala	Ser	Met	Val	Gln	Asn	Lys	Lys	Asn	
210						215					220					
aaa	tct	aca	gag	gac	gaa	tcc	tca	tcg	tat	aca	caa	tta	act	caa	aag	720
Lys	Ser	Thr	Glu	Asp	Glu	Ser	Ser	Ser	Tyr	Thr	Gln	Leu	Thr	Gln	Lys	
225					230					235					240	
tct	act	act	tct	aat	tct	tct	agc	agt	tca	gta	aac	tcc	aag	acg	tcc	768
Ser	Thr	Thr	Ser	Asn	Ser	Ser	Ser	Ser	Ser	Val	Asn	Ser	Lys	Thr	Ser	
				245					250					255		
ccc	tta	cca	aat	aaa	acg	gtg	act	ata	tcc	gta	gac	ata	ccg	cag	gct	816
Pro	Leu	Pro	Asn	Lys	Thr	Val	Thr	Ile	Ser	Val	Asp	Ile	Pro	Gln	Ala	
				260				265					270			
gga	ttc	atg	att	ggg	gaa	att	atc	cct	ata	gac	gtt	aag	att	gac	cac	864
Gly	Phe	Met	Ile	Gly	Glu	Ile	Ile	Pro	Ile	Asp	Val	Lys	Ile	Asp	His	
				275			280					285				
tat	aag	cct	ttc	tat	gcc	cct	gcg	ggg	ctc	acc	acc	act	ttg	gtg	agg	912
Tyr	Lys	Pro	Phe	Tyr	Ala	Pro	Ala	Gly	Leu	Thr	Thr	Thr	Leu	Val	Arg	
				290		295					300					
ata	tgt	agg	gtg	ggc	ggg	gca	ggc	aaa	gat	gat	cct	atg	gag	act	ttc	960
Ile	Cys	Arg	Val	Gly	Gly	Ala	Gly	Lys	Asp	Asp	Pro	Met	Glu	Thr	Phe	
305				310						315					320	
aga	aaa	gat	ata	tgt	cag	agt	atc	tct	cct	ata	tat	att	aac	cct	gaa	1008
Arg	Lys	Asp	Ile	Cys	Gln	Ser	Ile	Ser	Pro	Ile	Tyr	Ile	Asn	Pro	Glu	
				325					330					335		
acg	ttg	cag	ttt	caa	tct	aga	gtt	tat	ctg	aaa	gtg	ccc	ctt	gat	gca	1056
Thr	Leu	Gln	Phe	Gln	Ser	Arg	Val	Tyr	Leu	Lys	Val	Pro	Leu	Asp	Ala	
				340				345					350			
ttt	tcg	acc	ctt	act	act	gtg	gga	aaa	ttt	ttc	tcc	ttc	caa	tac	tat	1104
Phe	Ser	Thr	Leu	Thr	Thr	Val	Gly	Lys	Phe	Phe	Ser	Phe	Gln	Tyr	Tyr	
				355		360						365				
atc	gag	ggt	atg	gtt	aac	tta	tca	aaa	aaa	aac	gtg	gtt	tac	aca	gaa	1152
Ile	Glu	Val	Met	Val	Asn	Leu	Ser	Lys	Lys	Asn	Val	Val	Tyr	Thr	Glu	
				370		375					380					
tct	aat	aga	ata	ata	gga	act	cct	att	gga	gaa	caa	aat	ggc	ttg	ggc	1200
Ser	Asn	Arg	Ile	Ile	Gly	Thr	Pro	Ile	Gly	Glu	Gln	Asn	Gly	Leu	Gly	
385					390					395				400		
gta	gag	aat	aat	atc	aac	cgt	atc	caa	agg	aaa	atg	cta	cgt	atg	gtc	1248
Val	Glu	Asn	Asn	Ile	Asn	Arg	Ile	Gln	Arg	Lys	Met	Leu	Arg	Met	Val	
				405				410						415		
aat	cca	gaa	acg	ttg	gag	aac	gat	tct	gag	ggg	tat	gaa	tcc	agt	ata	1296
Asn	Pro	Glu	Thr	Leu	Glu	Asn	Asp	Ser	Glu	Gly	Tyr	Glu	Ser	Ser	Ile	
				420				425					430			
ttt	ttc	aaa	gat	atg	gta	aat	gtg	gaa	aag	cta	aag	aga	ctg	agg	aat	1344
Phe	Phe	Lys	Asp	Met	Val	Asn	Val	Glu	Lys	Leu	Lys	Arg	Leu	Arg	Asn	
				435		440						445				
gta	act	ggg	atg	tcc	ata	gaa	acc	gtc	ata	gga	acg	acg	aga	tcc	gaa	1392
Val	Thr	Gly	Met	Ser	Ile	Glu	Thr	Val	Ile	Gly	Thr	Thr	Arg	Ser	Glu	
				450		455					460					
cag	cag	caa	tct	gat	gca	agc	atc	cca	tcc	caa	tcc	tca	atc	acg	gct	1440
Gln	Gln	Gln	Ser	Asp	Ala	Ser	Ile	Pro	Ser	Gln	Ser	Ser	Ile	Thr	Ala	
465					470					475					480	
cct	caa	aat	tct	cca	tcg	aat	tta	aga	gat	tg	ttg	gcc	cca	tta	aat	1488
Pro	Gln	Asn	Ser	Pro	Ser	Asn	Leu	Arg	Asp	Trp	Leu	Ala	Pro	Leu	Asn	
				485				490						495		
gca	tat	gat	agt	gac	gat	gtt	cca	gtt	cca	aag	tat	tcg	cca	aat	gat	1536
Ala	Tyr	Asp	Ser	Asp	Asp	Val	Pro	Val	Pro	Lys	Tyr	Ser	Pro	Asn	Asp	
				500				505					510			
aaa	gtc	agt	gta	ccg	tcg	gaa	gac	aaa	caa	gaa	ctt	gaa	caa	aaa	aga	1584
Lys	Val	Ser	Val	Pro	Ser	Glu	Asp	Lys	Gln	Glu	Leu	Glu	Gln	Lys	Arg	
				515			520					525				
cta	caa	cag	tta	gaa	agc	gat	cct	ccc	cct	tgt	gat	gac	tat	taa		1629
Leu	Gln	Gln	Leu	Glu	Ser	Asp	Pro	Pro	Pro	Cys	Asp	Asp	Tyr			
				530		535					540					

<210> 9924

<211> 542

<212> PRT

<213> Saccharomyces cerevisiae

<400> 9924

PF59083SeqList PF59083.txt

```

Met Ser Leu Leu Arg Leu Trp Asn Lys Glu Ser Arg Ala Pro Ser Lys
1   5   10   15
Ile Lys Ser His Gly Ile Val Gly Ser Tyr Gly Asn Ser Met Leu Ala
20  25  30
His Asn Asn Val Lys Gln Phe Arg Ile Asp Ile Asp Glu Pro His Arg
35  40  45
Val Trp Lys Pro Asn Glu Ser Ile Thr Gly Glu Ala Val Ile Asp Ile
50  55  60
Lys Arg Asp Ile Thr Asn Val Ala Ile Lys Leu Ser Leu Val Cys Glu
65  70  75  80
Val Arg Val Lys Thr Gly Asn Ser Pro Thr Ser Lys Asn Lys Arg Ile
85  90  95
Glu Lys Thr Leu Glu Lys Ser Thr Phe Leu Tyr Gly Gln Asp Tyr Val
100 105 110
Lys Thr Ala Phe Ser Ala Lys Glu Lys Lys Pro His Val Asp Lys Thr
115 120 125
Thr Ile Leu Asn Gly Leu Ser Lys Gly Glu His Arg Phe Pro Phe Arg
130 135 140
Ile Arg Ile Pro Arg Gly Arg Gly Met Leu Ser Ser Ile Lys Phe Glu
145 150 155 160
Arg Gly Ser Ile Thr Tyr Phe Leu Ser Cys Thr Leu Glu Ser Leu Asn
165 170 175
Asn Ile Asn Gly Leu Lys Lys Pro Glu Ala Arg Cys Glu Arg Glu Phe
180 185 190
Ala Val Ile Val Pro Leu Asp Val Ser Arg Leu Pro Lys Pro Lys Thr
195 200 205
Lys Thr Val Val Leu Gln Ser Ala Ser Met Val Gln Asn Lys Lys Asn
210 215 220
Lys Ser Thr Glu Asp Glu Ser Ser Ser Tyr Thr Gln Leu Thr Gln Lys
225 230 235 240
Ser Thr Thr Ser Asn Ser Ser Ser Ser Val Asn Ser Lys Thr Ser
245 250 255
Pro Leu Pro Asn Lys Thr Val Thr Ile Ser Val Asp Ile Pro Gln Ala
260 265 270
Gly Phe Met Ile Gly Glu Ile Ile Pro Ile Asp Val Lys Ile Asp His
275 280 285
Tyr Lys Pro Phe Tyr Ala Pro Ala Gly Leu Thr Thr Thr Leu Val Arg
290 295 300
Ile Cys Arg Val Gly Gly Ala Gly Lys Asp Asp Pro Met Glu Thr Phe
305 310 315 320
Arg Lys Asp Ile Cys Gln Ser Ile Ser Pro Ile Tyr Ile Asn Pro Glu
325 330 335
Thr Leu Gln Phe Gln Ser Arg Val Tyr Leu Lys Val Pro Leu Asp Ala
340 345 350
Phe Ser Thr Leu Thr Thr Val Gly Lys Phe Phe Ser Phe Gln Tyr Tyr
355 360 365
Ile Glu Val Met Val Asn Leu Ser Lys Lys Asn Val Val Tyr Thr Glu
370 375 380
Ser Asn Arg Ile Ile Gly Thr Pro Ile Gly Glu Gln Asn Gly Leu Gly
385 390 395 400
Val Glu Asn Asn Ile Asn Arg Ile Gln Arg Lys Met Leu Arg Met Val
405 410 415
Asn Pro Glu Thr Leu Glu Asn Asp Ser Glu Gly Tyr Glu Ser Ser Ile
420 425 430
Phe Phe Lys Asp Met Val Asn Val Glu Lys Leu Lys Arg Leu Arg Asn
435 440 445
Val Thr Gly Met Ser Ile Glu Thr Val Ile Gly Thr Thr Arg Ser Glu
450 455 460
Gln Gln Gln Ser Asp Ala Ser Ile Pro Ser Gln Ser Ser Ile Thr Ala
465 470 475 480
Pro Gln Asn Ser Pro Ser Asn Leu Arg Asp Trp Leu Ala Pro Leu Asn
485 490 495
Ala Tyr Asp Ser Asp Asp Val Pro Val Pro Lys Tyr Ser Pro Asn Asp
500 505 510
Lys Val Ser Val Pro Ser Glu Asp Lys Gln Glu Leu Glu Gln Lys Arg
515 520 525
Leu Gln Gln Leu Glu Ser Asp Pro Pro Pro Cys Asp Asp Tyr
530 535 540

```

<210> 9925
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 9925
 atggatccta tggagacttt cagaa 25

<210> 9926
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 9926
 ttaatagtca tcacaagggg gagg 24

<210> 9927
 <211> 675
 <212> PRT
 <213> Artificial sequence

<220>
 <223> consensus sequence

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is any amino acid

<220>
 <221> Variant
 <222> (4)..(8)
 <223> Xaa in position 4 to 8 is any amino acid

<220>
 <221> Variant
 <222> (10)..(19)
 <223> Xaa in position 10 to 19 is any amino acid

<220>
 <221> Variant
 <222> (21)..(38)
 <223> Xaa in position 21 to 38 is any amino acid

<220>
 <221> Variant
 <222> (40)..(68)
 <223> Xaa in position 40 to 68 is any amino acid

<220>
 <221> Variant
 <222> (69)..(74)
 <223> Xaa in position 69 to 74 is any or no amino acid

<220>
 <221> Variant
 <222> (76)..(82)
 <223> Xaa in position 76 to 82 is any amino acid

<220>
 <221> Variant
 <222> (83)..(100)

<223> Xaa in position 83 to 100 is any or no amino acid

<220>

<221> Variant

<222> (102)..(103)

<223> Xaa in position 102 to 103 is any amino acid

<220>

<221> Variant

<222> (105)..(107)

<223> Xaa in position 105 to 107 is any amino acid

<220>

<221> Variant

<222> (109)..(109)

<223> Xaa in position 109 is any amino acid

<220>

<221> Variant

<222> (111)..(114)

<223> Xaa in position 111 to 114 is any amino acid

<220>

<221> Variant

<222> (116)..(121)

<223> Xaa in position 116 to 121 is any amino acid

<220>

<221> Variant

<222> (122)..(122)

<223> Xaa in position 122 is any or no amino acid

<220>

<221> Variant

<222> (125)..(125)

<223> Xaa in position 125 is any amino acid

<220>

<221> Variant

<222> (127)..(127)

<223> Xaa in position 127 is any amino acid

<220>

<221> Variant

<222> (128)..(128)

<223> Xaa in position 128 is any or no amino acid

<220>

<221> Variant

<222> (130)..(132)

<223> Xaa in position 130 to 132 is any amino acid

<220>

<221> Variant

<222> (134)..(230)

<223> Xaa in position 134 to 230 is any amino acid

<220>

<221> Variant

<222> (231)..(297)

<223> Xaa in position 231 to 297 is any or no amino acid

<220>

<221> Variant

<222> (299)..(301)

<223> Xaa in position 299 to 301 is any amino acid

<220>

<221> Variant

<222> (303)..(312)
<223> Xaa in position 303 to 312 is any amino acid

<220>
<221> Variant
<222> (314)..(314)
<223> Xaa in position 314 is any amino acid

<220>
<221> Variant
<222> (316)..(321)
<223> Xaa in position 316 to 321 is any amino acid

<220>
<221> Variant
<222> (323)..(325)
<223> Xaa in position 323 to 325 is any amino acid

<220>
<221> Variant
<222> (328)..(328)
<223> Xaa in position 328 is any amino acid

<220>
<221> Variant
<222> (330)..(331)
<223> Xaa in position 330 to 331 is any amino acid

<220>
<221> Variant
<222> (333)..(338)
<223> Xaa in position 333 to 338 is any amino acid

<220>
<221> Variant
<222> (339)..(380)
<223> Xaa in position 339 to 380 is any or no amino acid

<220>
<221> Variant
<222> (385)..(386)
<223> Xaa in position 385 to 386 is any amino acid

<220>
<221> Variant
<222> (388)..(390)
<223> Xaa in position 388 to 390 is any amino acid

<220>
<221> Variant
<222> (392)..(395)
<223> Xaa in position 392 to 395 is any amino acid

<220>
<221> Variant
<222> (397)..(397)
<223> Xaa in position 397 is any amino acid

<220>
<221> Variant
<222> (399)..(408)
<223> Xaa in position 399 to 408 is any amino acid

<220>
<221> Variant
<222> (411)..(411)
<223> Xaa in position 411 is any amino acid

<220>

```

<221> Variant
<222> (413)..(413)
<223> Xaa in position 413 is any amino acid

<220>
<221> Variant
<222> (415)..(415)
<223> Xaa in position 415 is any amino acid

<220>
<221> Variant
<222> (417)..(424)
<223> Xaa in position 417 to 424 is any amino acid

<220>
<221> Variant
<222> (425)..(426)
<223> Xaa in position 425 to 426 is any or no amino acid

<220>
<221> Variant
<222> (428)..(428)
<223> Xaa in position 428 is any amino acid

<220>
<221> Variant
<222> (430)..(431)
<223> Xaa in position 430 to 431 is any amino acid

<220>
<221> Variant
<222> (434)..(436)
<223> Xaa in position 434 to 436 is any amino acid

<220>
<221> Variant
<222> (438)..(439)
<223> Xaa in position 438 to 439 is any amino acid

<220>
<221> Variant
<222> (441)..(480)
<223> Xaa in position 441 to 480 is any amino acid

<220>
<221> Variant
<222> (481)..(507)
<223> Xaa in position 481 to 507 is any or no amino acid

<220>
<221> Variant
<222> (509)..(511)
<223> Xaa in position 509 to 511 is any amino acid

<220>
<221> Variant
<222> (513)..(517)
<223> Xaa in position 513 to 517 is any amino acid

<220>
<221> Variant
<222> (519)..(520)
<223> Xaa in position 519 to 520 is any amino acid

<220>
<221> Variant
<222> (524)..(566)
<223> Xaa in position 524 to 566 is any amino acid

```


PF59083SeqList PF59083.txt

<220>
 <221> Variant
 <222> (567)..(619)
 <223> Xaa in position 567 to 619 is any or no amino acid

<220>
 <221> Variant
 <222> (621)..(635)
 <223> Xaa in position 621 to 635 is any amino acid

<220>
 <221> Variant
 <222> (636)..(658)
 <223> Xaa in position 636 to 658 is any or no amino acid

<220>
 <221> Variant
 <222> (660)..(669)
 <223> Xaa in position 660 to 669 is any amino acid

<220>
 <221> Variant
 <222> (671)..(671)
 <223> Xaa in position 671 is any amino acid

<220>
 <221> Variant
 <222> (673)..(673)
 <223> Xaa in position 673 is any amino acid

<400> 9927
 Phe Xaa Ile Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 85 90 95
 Xaa Xaa Xaa Xaa Leu Xaa Xaa Gly Xaa Xaa Xaa Phe Xaa Phe Xaa Xaa
 100 105 110
 Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ile Xaa Phe Xaa Xaa
 115 120 125
 Gly Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 130 135 140
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 145 150 155 160
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 165 170 175
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 180 185 190
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 210 215 220
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 225 230 235 240
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 245 250 255
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 260 265 270
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 275 280 285
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Gly Xaa Xaa
 290 295 300

[illegible]

<213> Artificial sequence

<223> protein pattern

<223> Xaa in position 5 is Ile or Leu

<223> Xaa in position 6 is any amino acid

$\langle 220 \rangle$

```

<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is any amino acid

<220>
<221> Variant
<222> (9)..(9)
<223> Xaa in position 9 is Phe, Ile or Val

<220>
<221> Variant
<222> (10)..(10)
<223> Xaa in position 10 is any amino acid

<220>
<221> Variant
<222> (12)..(12)
<223> Xaa in position 12 is Ile or Leu

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is any amino acid

<220>
<221> Variant
<222> (14)..(14)
<223> Xaa in position 14 is Ile or Val

<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is Asp or Asn

<220>
<221> Variant
<222> (17)..(17)
<223> Xaa in position 17 is any amino acid

<220>
<221> Variant
<222> (19)..(19)
<223> Xaa in position 19 is Phe, Leu or Met

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is Asp, Gln or Thr

<220>
<221> Variant
<222> (21)..(21)
<223> Xaa in position 21 is any amino acid

<220>
<221> Variant
<222> (22)..(22)
<223> Xaa in position 22 is Asp, Glu, Gln or Ser

<220>
<221> Variant
<222> (23)..(26)
<223> Xaa in position 23 to 26 is any amino acid

<220>
<221> Variant
<222> (27)..(27)
<223> Xaa in position 27 is Ile, Leu or Val

```

PF59083SeqList PF59083.txt

```

<220>
<221> Variant
<222> (28)..(28)
<223> Xaa in position 28 is Lys or Arg

<220>
<221> Variant
<222> (29)..(29)
<223> Xaa in position 29 is Ile, Leu or Val

<220>
<221> Variant
<222> (31)..(31)
<223> Xaa in position 31 is any amino acid

<220>
<221> Variant
<222> (33)..(33)
<223> Xaa in position 33 is Ala, Ser or Val

<220>
<221> Variant
<222> (35)..(35)
<223> Xaa in position 35 is Pro or Ser

<220>
<221> Variant
<222> (37)..(37)
<223> Xaa in position 37 is Ile or Leu

<400> 9928
Phe Arg Lys Asp Xaa Xaa Gln Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Pro
1      5      10      15
Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Asp
      20      25      30
Xaa Phe Xaa Thr Xaa
      35

<210> 9929
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
<221> Variant
<222> (2)..(4)
<223> Xaa in position 2 to 4 is any or no amino acid

<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is any amino acid

<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is any amino acid

<220>
<221> Variant
<222> (9)..(9)
<223> Xaa in position 9 is Ile, Met or Val

<220>
<221> Variant

```

<222> (12)..(12)
 <223> Xaa in position 12 is Ile, Leu, Met or Val

 <220>
 <221> Variant
 <222> (13)..(13)
 <223> Xaa in position 13 is Ile or Val

 <220>
 <221> Variant
 <222> (14)..(14)
 <223> Xaa in position 14 is Asp or Asn

 <220>
 <221> Variant
 <222> (16)..(17)
 <223> Xaa in position 16 to 17 is any amino acid

 <220>
 <221> Variant
 <222> (18)..(18)
 <223> Xaa in position 18 is Lys or Arg

 <400> 9929
 Ser Xaa Xaa Xaa Phe Xaa Tyr Xaa Xaa Glu Val Xaa Xaa Xaa Leu Xaa
 1 5 10 15
 Xaa Xaa

<210> 9930
 <211> 19
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (3)..(3)
 <223> Xaa in position 3 is any amino acid

<220>
 <221> Variant
 <222> (5)..(5)
 <223> Xaa in position 5 is any amino acid

<220>
 <221> Variant
 <222> (7)..(7)
 <223> Xaa in position 7 is Gln or Arg

<220>
 <221> Variant
 <222> (8)..(8)
 <223> Xaa in position 8 is any amino acid

<220>
 <221> Variant
 <222> (9)..(9)
 <223> Xaa in position 9 is Lys or Arg

<220>
 <221> Variant
 <222> (11)..(12)
 <223> Xaa in position 11 to 12 is any amino acid

<220>

PF59083SeqList PF59083.txt

<221> Variant
 <222> (13)..(13)
 <223> Xaa in position 13 is any or no amino acid

<220>
 <221> Variant
 <222> (15)..(15)
 <223> Xaa in position 15 is any or no amino acid

<220>
 <221> Variant
 <222> (17)..(17)
 <223> Xaa in position 17 is Ala, Asp or Glu

<220>
 <221> Variant
 <222> (19)..(19)
 <223> Xaa in position 19 is Gly, Pro or Ser

<400> 9930
 Asp Lys Xaa Glu Xaa Glu Xaa Xaa Xaa Leu Xaa Xaa Xaa Glu Xaa Ser
 1 5 10 15
 Xaa Pro Xaa

<210> 9931
 <211> 2430
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(2430)

<400> 9931
 atg tct tct gta gaa gaa ttg act cag ctg ttt tca cag gtt ggg ttt 48
 Met Ser Ser Val Glu Glu Leu Thr Gln Leu Phe Ser Gln Val Gly Phe
 1 5 10 15
 gaa gat aaa aag gtg aag gag att gtc aag aat aaa aag gtt tct gat 96
 Glu Asp Lys Lys Val Lys Glu Ile Val Lys Asn Lys Lys Val Ser Asp
 20 25 30
 tca ctt tac aaa ttg att aag gag act cct tcg gac tat caa tgg aac 144
 Ser Leu Tyr Lys Leu Ile Lys Glu Thr Pro Ser Asp Tyr Gln Trp Asn
 35 40 45
 aaa tct act aga gcg cta gta cac aac ctg gca tct ttt gtc aaa ggt 192
 Lys Ser Thr Arg Ala Leu Val His Asn Leu Ala Ser Phe Val Lys Gly
 50 55 60
 aca gat cta ccc aag tct gaa tta att gtt aac ggc atc att aat ggt 240
 Thr Asp Leu Pro Lys Ser Glu Leu Ile Val Asn Gly Ile Ile Asn Gly
 65 70 75 80
 gat ttg aag aca tct ctg caa gtc gat gcc gca ttt aaa tat gta aag 288
 Asp Leu Lys Thr Ser Leu Gln Val Asp Ala Ala Phe Lys Tyr Val Lys
 85 90 95
 gct aat ggc gag gca tcc acc aaa atg ggt atg aat gaa aac tct ggt 336
 Ala Asn Gly Glu Ala Ser Thr Lys Met Gly Met Asn Glu Asn Ser Gly
 100 105 110
 gtt ggt att gag att aca gag gat cag gtt aga aat tac gtc atg cag 384
 Val Gly Ile Glu Ile Thr Glu Asp Gln Val Arg Asn Tyr Val Met Gln
 115 120 125
 tac att caa gaa aac aag gaa aga att tta act gaa cgc tat aaa ctg 432
 Tyr Ile Gln Glu Asn Lys Glu Arg Ile Leu Thr Glu Arg Tyr Lys Leu
 130 135 140
 gtg cca ggt att ttt gcc gat gtt aaa aac tta aag gag ctg aag tgg 480
 Val Pro Gly Ile Phe Ala Asp Val Lys Asn Leu Lys Glu Leu Lys Trp
 145 150 155 160
 gcc gat cca cgt agt ttc aag cca att atc gac caa gaa gtc tta aaa 528
 Ala Asp Pro Arg Ser Phe Lys Pro Ile Ile Asp Gln Glu Val Leu Lys
 165 170 175
 ctt ttg ggt cca aag gat gag aga gac tta atc aag aag aag acc aag 576

PF59083SeqList PF59083.txt

Leu	Leu	Gly	Pro	Lys	Asp	Glu	Arg	Asp	Leu	Ile	Lys	Lys	Lys	Thr	Lys	
180								185						190		
aat	aat	gaa	aag	aag	aaa	acc	aat	tct	gcc	aag	aag	agt	tct	gat	aat	624
Asn	Asn	Glu	Lys	Lys	Lys	Thr	Asn	Ser	Ala	Lys	Lys	Ser	Ser	Asp	Asn	
195							200					205				
tct	gca	tca	tcc	ggg	cca	aag	agg	act	atg	ttc	aat	gaa	ggg	ttc	cta	672
Ser	Ala	Ser	Ser	Gly	Pro	Lys	Arg	Thr	Met	Phe	Asn	Glu	Gly	Phe	Leu	
210						215					220					
ggg	gat	ttg	cat	aaa	gtg	ggg	gaa	aac	cca	caa	gct	tac	cca	gaa	tta	720
Gly	Asp	Leu	His	Lys	Val	Gly	Glu	Asn	Pro	Gln	Ala	Tyr	Pro	Glu	Leu	
225					230					235					240	
atg	aag	gaa	cac	ctt	gag	gtt	act	ggg	ggc	aaa	gtt	cgt	aca	agg	ttc	768
Met	Lys	Glu	His	Leu	Glu	Val	Thr	Gly	Gly	Lys	Val	Arg	Thr	Arg	Phe	
				245				250						255		
cct	ccg	gag	ccc	aat	gga	tat	ttg	cat	att	ggg	cat	tct	aaa	gct	att	816
Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ser	Lys	Ala	Ile	
				260				265					270			
atg	gtt	aat	ttt	ggg	tat	gct	aaa	tat	cac	aat	ggg	acc	tgt	tat	tta	864
Met	Val	Asn	Phe	Gly	Tyr	Ala	Lys	Tyr	His	Asn	Gly	Thr	Cys	Tyr	Leu	
		275					280					285				
aga	ttt	gac	gat	acc	aac	ccc	gaa	aag	gaa	gct	cct	gaa	tat	ttt	gaa	912
Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Lys	Glu	Ala	Pro	Glu	Tyr	Phe	Glu	
290						295					300					
tcc	att	aag	aga	atg	gtt	tct	tgg	tta	ggg	ttt	aaa	cca	tgg	aaa	att	960
Ser	Ile	Lys	Arg	Met	Val	Ser	Trp	Leu	Gly	Phe	Lys	Pro	Trp	Lys	Ile	
305					310					315					320	
act	tac	tca	agt	gat	tat	ttt	gac	gag	ctt	tat	cgc	ctc	gct	gaa	gtg	1008
Thr	Tyr	Ser	Ser	Asp	Tyr	Phe	Asp	Glu	Leu	Tyr	Arg	Leu	Ala	Glu	Val	
				325				330						335		
ttg	atc	aaa	aac	ggc	aaa	gct	tac	gtt	tgt	cat	tgt	acc	gcc	gaa	gaa	1056
Leu	Ile	Lys	Asn	Gly	Lys	Ala	Tyr	Val	Cys	His	Cys	Thr	Ala	Glu	Glu	
				340				345					350			
att	aaa	aga	ggg	cgt	ggg	att	aaa	gaa	gac	ggg	act	cca	ggg	ggg	gag	1104
Ile	Lys	Arg	Gly	Arg	Gly	Ile	Lys	Glu	Asp	Gly	Thr	Pro	Gly	Gly	Glu	
		355					360					365				
aga	tat	gct	tgt	aag	cat	cgt	gat	cag	tcg	ata	gaa	caa	aac	ctg	caa	1152
Arg	Tyr	Ala	Cys	Lys	His	Arg	Asp	Gln	Ser	Ile	Glu	Gln	Asn	Leu	Gln	
		370				375					380					
gaa	ttc	aga	gat	atg	aga	gat	ggc	aag	tac	aaa	cct	ggg	gaa	gct	atc	1200
Glu	Phe	Arg	Asp	Met	Arg	Asp	Gly	Lys	Tyr	Lys	Pro	Gly	Glu	Ala	Ile	
385					390					395					400	
tta	aga	atg	aaa	cag	gat	cta	aat	tca	cca	agc	cca	caa	atg	tgg	gac	1248
Leu	Arg	Met	Lys	Gln	Asp	Leu	Asn	Ser	Pro	Ser	Pro	Gln	Met	Trp	Asp	
				405				410						415		
ttg	att	gcg	tat	aga	gtt	tta	aat	gct	cca	cat	cca	aga	acg	gga	aca	1296
Leu	Ile	Ala	Tyr	Arg	Val	Leu	Asn	Ala	Pro	His	Pro	Arg	Thr	Gly	Thr	
				420				425					430			
aaa	tgg	aga	att	tat	cct	act	tac	gat	ttt	aca	cat	tgt	ttg	gtc	gat	1344
Lys	Trp	Arg	Ile	Tyr	Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys	Leu	Val	Asp	
		435					440					445				
tca	atg	gaa	aat	att	aca	cat	tct	tta	tgt	act	act	gaa	ttc	tac	cta	1392
Ser	Met	Glu	Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Thr	Glu	Phe	Tyr	Leu	
		450				455					460					
tct	aga	gaa	agc	tat	gaa	tgg	tta	tgt	gat	cag	gtt	cat	gtg	ttc	aga	1440
Ser	Arg	Glu	Ser	Tyr	Glu	Trp	Leu	Cys	Asp	Gln	Val	His	Val	Phe	Arg	
465					470					475					480	
ccc	gct	caa	aga	gaa	tat	ggg	cgt	ttg	aat	atc	acc	ggg	aca	gtt	tta	1488
Pro	Ala	Gln	Arg	Glu	Tyr	Gly	Arg	Leu	Asn	Ile	Thr	Gly	Thr	Val	Leu	
				485				490						495		
tcc	aaa	aga	aaa	att	gcg	caa	ttg	gtg	gat	gaa	aaa	ttc	gtt	aga	ggc	1536
Ser	Lys	Arg	Lys	Ile	Ala	Gln	Leu	Val	Asp	Glu	Lys	Phe	Val	Arg	Gly	
				500				505					510			
tgg	gac	gat	cct	aga	cta	ttc	acg	ctt	gaa	gct	ata	cgc	aga	cgt	ggg	1584
Trp	Asp	Asp	Pro	Arg	Leu	Phe	Thr	Leu	Glu	Ala	Ile	Arg	Arg	Arg	Gly	
		515				520						525				
gtt	cct	cct	ggg	gcc	att	tta	tcc	ttt	atc	aac	aca	tta	ggg	gtt	acc	1632
Val	Pro	Pro	Gly	Ala	Ile	Leu	Ser	Phe	Ile	Asn	Thr	Leu	Gly	Val	Thr	
		530				535					540					
aca	agt	acc	aca	aac	att	caa	gtt	gtg	agg	ttt	gag	agc	gct	gtt	aga	1680

PF59083SeqList PF59083.txt

Thr 545	Ser	Thr	Thr	Asn	Ile 550	Gln	Val	Val	Arg	Phe 555	Glu	Ser	Ala	Val	Arg 560	
aag	tac	cta	gaa	gat	acc	aca	ccg	aga	tta	atg	ttt	gtg	ttg	gat	cct	1728
Lys	Tyr	Leu	Glu	Asp 565	Thr	Thr	Pro	Arg	Leu 570	Met	Phe	Val	Leu	Asp 575	Pro	
gtt	gaa	gtt	gtt	gtc	gat	aat	tta	tct	gac	gat	tat	gaa	gaa	ttg	gca	1776
Val	Glu	Val	Val	Val	Asp	Asn	Leu	Ser	Asp	Asp	Tyr	Glu	Glu	Leu	Ala	
			580					585					590			
act	att	cct	tac	aga	cct	ggt	act	cca	gaa	ttt	ggt	gaa	aga	act	gta	1824
Thr	Ile	Pro	Tyr	Arg	Pro	Gly	Thr	Pro	Glu	Phe	Gly	Glu	Arg	Thr	Val	
		595					600					605				
cca	ttt	aca	aac	aaa	ttc	tac	att	gaa	agg	tca	gat	ttc	tca	gaa	aac	1872
Pro	Phe	Thr	Asn	Lys	Phe	Tyr	Ile	Glu	Arg	Ser	Asp	Phe	Ser	Glu	Asn	
	610					615					620					
gtt	gat	gat	aag	gaa	ttt	ttc	aga	tta	aca	cca	aac	caa	cca	gtt	ggt	1920
Val	Asp	Asp	Lys	Glu	Phe	Phe	Arg	Leu	Thr	Pro	Asn	Gln	Pro	Val	Gly	
					630					635					640	
tta	att	aaa	gtc	tca	cac	aca	gtt	tct	ttc	aaa	agt	ttg	gaa	aaa	gat	1968
Leu	Ile	Lys	Val	Ser	His	Thr	Val	Ser	Phe	Lys	Ser	Leu	Glu	Lys	Asp	
				645					650					655		
gaa	gct	ggt	aaa	att	ata	aga	att	cat	gtc	aac	tat	gat	aac	aag	gtt	2016
Glu	Ala	Gly	Lys	Ile	Ile	Arg	Ile	His	Val	Asn	Tyr	Asp	Asn	Lys	Val	
			660				665						670			
gaa	gaa	ggt	tgc	aaa	cca	aag	aaa	cca	aaa	act	tat	att	caa	tgg	gtt	2064
Glu	Glu	Gly	Ser	Lys	Pro	Lys	Lys	Pro	Lys	Thr	Tyr	Ile	Gln	Trp	Val	
		675					680					685				
cct	atc	tct	tca	aaa	tat	aat	tct	cca	ttg	aga	gtt	act	gaa	act	agg	2112
Pro	Ile	Ser	Ser	Lys	Tyr	Asn	Ser	Pro	Leu	Arg	Val	Thr	Glu	Thr	Arg	
	690					695					700					
gtt	tac	aac	caa	ttg	ttc	aaa	tct	gaa	aat	cca	tct	tct	cat	cct	gaa	2160
Val	Tyr	Asn	Gln	Leu	Phe	Lys	Ser	Glu	Asn	Pro	Ser	Ser	His	Pro	Glu	
					710					715					720	
ggc	ttc	ttg	aag	gac	atc	aac	cca	gaa	agt	gaa	gtc	gtt	tat	aaa	gaa	2208
Gly	Phe	Leu	Lys	Asp	Ile	Asn	Pro	Glu	Ser	Glu	Val	Val	Tyr	Lys	Glu	
				725					730					735		
tct	gtc	atg	gaa	cat	aac	ttc	ggg	gac	gtt	gtc	aag	aac	agt	cca	tgg	2256
Ser	Val	Met	Glu	His	Asn	Phe	Gly	Asp	Val	Val	Lys	Asn	Ser	Pro	Trp	
			740				745						750			
gtc	gtt	gat	tct	gtt	aaa	aac	tgc	gaa	ttt	tat	gtt	gaa	gaa	gat	aag	2304
Val	Val	Asp	Ser	Val	Lys	Asn	Ser	Glu	Phe	Tyr	Val	Glu	Glu	Asp	Lys	
		755					760					765				
gat	tcc	aaa	gaa	gtg	tgt	aga	ttc	caa	gct	atg	aga	gta	ggt	tat	ttc	2352
Asp	Ser	Lys	Glu	Val	Cys	Arg	Phe	Gln	Ala	Met	Arg	Val	Gly	Tyr	Phe	
		770				775					780					
act	ctg	gat	aaa	gag	agt	act	tct	aag	gtt	att	ttg	aat	aga	ata		2400
Thr	Leu	Asp	Lys	Glu	Ser	Thr	Ser	Lys	Val	Ile	Leu	Asn	Arg	Ile	800	
					790				795							
gtt	agc	ttg	aag	gac	gca	act	tcc	aag	tga							2430
Val	Ser	Leu	Lys	Asp	Ala	Thr	Ser	Lys								
				805												

<210> 9932

<211> 809

<212> PRT

<213> Saccharomyces cerevisiae

<400> 9932

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

PF59083SeqList PF59083.txt

Ala	Asn	Gly	Glu	Ala	Ser	Thr	Lys	Met	Gly	Met	Asn	Glu	Asn	Ser	Gly
			100					105					110		
Val	Gly	Ile	Glu	Ile	Thr	Glu	Asp	Gln	Val	Arg	Asn	Tyr	Val	Met	Gln
		115					120					125			
Tyr	Ile	Gln	Glu	Asn	Lys	Glu	Arg	Ile	Leu	Thr	Glu	Arg	Tyr	Lys	Leu
	130					135					140				
Val	Pro	Gly	Ile	Phe	Ala	Asp	Val	Lys	Asn	Leu	Lys	Glu	Leu	Lys	Trp
145				150					155						160
Ala	Asp	Pro	Arg	Ser	Phe	Lys	Pro	Ile	Ile	Asp	Gln	Glu	Val	Leu	Lys
				165				170						175	
Leu	Leu	Gly	Pro	Lys	Asp	Glu	Arg	Asp	Leu	Ile	Lys	Lys	Lys	Thr	Lys
			180					185					190		
Asn	Asn	Glu	Lys	Lys	Lys	Thr	Asn	Ser	Ala	Lys	Lys	Ser	Ser	Asp	Asn
		195					200					205			
Ser	Ala	Ser	Ser	Gly	Pro	Lys	Arg	Thr	Met	Phe	Asn	Glu	Gly	Phe	Leu
	210					215					220				
Gly	Asp	Leu	His	Lys	Val	Gly	Glu	Asn	Pro	Gln	Ala	Tyr	Pro	Glu	Leu
225					230					235					240
Met	Lys	Glu	His	Leu	Glu	Val	Thr	Gly	Gly	Lys	Val	Arg	Thr	Arg	Phe
				245				250						255	
Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ser	Lys	Ala	Ile
			260					265					270		
Met	Val	Asn	Phe	Gly	Tyr	Ala	Lys	Tyr	His	Asn	Gly	Thr	Cys	Tyr	Leu
		275					280					285			
Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Lys	Glu	Ala	Pro	Glu	Tyr	Phe	Glu
	290					295					300				
Ser	Ile	Lys	Arg	Met	Val	Ser	Trp	Leu	Gly	Phe	Lys	Pro	Trp	Lys	Ile
305					310					315					320
Thr	Tyr	Ser	Ser	Asp	Tyr	Phe	Asp	Glu	Leu	Tyr	Arg	Leu	Ala	Glu	Val
				325				330						335	
Leu	Ile	Lys	Asn	Gly	Lys	Ala	Tyr	Val	Cys	His	Cys	Thr	Ala	Glu	Glu
			340					345					350		
Ile	Lys	Arg	Gly	Arg	Gly	Ile	Lys	Glu	Asp	Gly	Thr	Pro	Gly	Gly	Glu
		355					360					365			
Arg	Tyr	Ala	Cys	Lys	His	Arg	Asp	Gln	Ser	Ile	Glu	Gln	Asn	Leu	Gln
	370					375					380				
Glu	Phe	Arg	Asp	Met	Arg	Asp	Gly	Lys	Tyr	Lys	Pro	Gly	Glu	Ala	Ile
385					390					395					400
Leu	Arg	Met	Lys	Gln	Asp	Leu	Asn	Ser	Pro	Ser	Pro	Gln	Met	Trp	Asp
				405					410					415	
Leu	Ile	Ala	Tyr	Arg	Val	Leu	Asn	Ala	Pro	His	Pro	Arg	Thr	Gly	Thr
			420					425					430		
Lys	Trp	Arg	Ile	Tyr	Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys	Leu	Val	Asp
		435					440					445			
Ser	Met	Glu	Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Thr	Glu	Phe	Tyr	Leu
	450					455					460				
Ser	Arg	Glu	Ser	Tyr	Glu	Trp	Leu	Cys	Asp	Gln	Val	His	Val	Phe	Arg
465					470					475					480
Pro	Ala	Gln	Arg	Glu	Tyr	Gly	Arg	Leu	Asn	Ile	Thr	Gly	Thr	Val	Leu
				485					490					495	
Ser	Lys	Arg	Lys	Ile	Ala	Gln	Leu	Val	Asp	Glu	Lys	Phe	Val	Arg	Gly
			500					505					510		
Trp	Asp	Asp	Pro	Arg	Leu	Phe	Thr	Leu	Glu	Ala	Ile	Arg	Arg	Arg	Gly
		515					520					525			
Val	Pro	Pro	Gly	Ala	Ile	Leu	Ser	Phe	Ile	Asn	Thr	Leu	Gly	Val	Thr
	530					535					540				
Thr	Ser	Thr	Thr	Asn	Ile	Gln	Val	Val	Arg	Phe	Glu	Ser	Ala	Val	Arg
545					550					555					560
Lys	Tyr	Leu	Glu	Asp	Thr	Thr	Pro	Arg	Leu	Met	Phe	Val	Leu	Asp	Pro
				565					570					575	
Val	Glu	Val	Val	Val	Asp	Asn	Leu	Ser	Asp	Asp	Tyr	Glu	Glu	Leu	Ala
			580					585					590		
Thr	Ile	Pro	Tyr	Arg	Pro	Gly	Thr	Pro	Glu	Phe	Gly	Glu	Arg	Thr	Val
		595				600						605			
Pro	Phe	Thr	Asn	Lys	Phe	Tyr	Ile	Glu	Arg	Ser	Asp	Phe	Ser	Glu	Asn
	610					615					620				
Val	Asp	Asp	Lys	Glu	Phe	Phe	Arg	Leu	Thr	Pro	Asn	Gln	Pro	Val	Gly
625					630					635					640
Leu	Ile	Lys	Val	Ser	His	Thr	Val	Ser	Phe	Lys	Ser	Leu	Glu	Lys	Asp

PF59083SeqList PF59083.txt

645 650 655
 Glu Ala Gly Lys Ile Ile Arg Ile His Val Asn Tyr Asp Asn Lys Val
 660 665 670
 Glu Glu Gly Ser Lys Pro Lys Lys Pro Lys Thr Tyr Ile Gln Trp Val
 675 680 685
 Pro Ile Ser Ser Lys Tyr Asn Ser Pro Leu Arg Val Thr Glu Thr Arg
 690 695 700
 Val Tyr Asn Gln Leu Phe Lys Ser Glu Asn Pro Ser Ser His Pro Glu
 705 710 715
 Gly Phe Leu Lys Asp Ile Asn Pro Glu Ser Glu Val Val Tyr Lys Glu
 725 730 735
 Ser Val Met Glu His Asn Phe Gly Asp Val Val Lys Asn Ser Pro Trp
 740 745 750
 Val Val Asp Ser Val Lys Asn Ser Glu Phe Tyr Val Glu Glu Asp Lys
 755 760 765
 Asp Ser Lys Glu Val Cys Arg Phe Gln Ala Met Arg Val Gly Tyr Phe
 770 775 780
 Thr Leu Asp Lys Glu Ser Thr Thr Ser Lys Val Ile Leu Asn Arg Ile
 785 790 795 800
 Val Ser Leu Lys Asp Ala Thr Ser Lys
 805

<210> 9933

<211> 2577

<212> DNA

<213> Cryptococcus neoformans var. neoformans JEC21

<220>

<221> CDS

<222> (1)..(2577)

<400> 9933

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

PF59083SeqList PF59083.txt															
Ala	Ala	Ala	Ala	Ala	Ala	Ala	Lys	Pro	Lys	Ala	Lys	Ala	Pro	Lys	Ala
gct	gaa	aaa	ccc	ggt	aaa	cct	gct	tcc	acc	act	gct	gcc	ggt	gct	acc
Ala	Glu	Lys	Pro	Val	Lys	Pro	Val	Ser	Thr	Thr	Ala	Ala	Val	Ala	Thr
210	210	195				215					220				
aaa	tct	tct	tcc	gct	acc	cct	gct	atc	cct	aca	aac	att	ttt	gag	gaa
Lys	Ser	Ser	Ser	Ala	Thr	Pro	Ala	Ile	Pro	Thr	Asn	Ile	Phe	Glu	Glu
225					230					235					240
ggc	ttc	ctt	tcc	gaa	ttc	cac	aaa	gtc	ggg	gaa	aac	ccc	cag	agt	gat
Gly	Phe	Leu	Ser	Glu	Phe	His	Lys	Val	Gly	Glu	Asn	Pro	Gln	Ser	Asp
				245					250					255	
ccc	aag	ttg	aag	gag	gag	cat	ttg	gcg	tgg	aca	aag	ggg	cag	gtg	tac
Pro	Lys	Leu	Lys	Glu	Glu	His	Leu	Ala	Trp	Thr	Lys	Gly	Gln	Val	Tyr
			260					265					270		
acc	cga	ttc	cca	cca	gag	cct	aat	gga	tac	cta	cat	att	gga	cac	gtc
Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Val
			275				280					285			
aag	gct	atc	atg	gtc	gac	ttt	ggg	tat	gcc	aaa	tac	cac	ggg	ggg	cga
Lys	Ala	Ile	Met	Val	Asp	Phe	Gly	Tyr	Ala	Lys	Tyr	His	Gly	Gly	Arg
	290					295					300				
aca	tac	ctc	aga	tac	gac	gat	acc	aat	cct	gaa	gct	gaa	gaa	ggc	cga
Thr	Tyr	Leu	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Glu	Gly	Arg
305					310					315					320
tac	ttt	caa	tct	atc	ctc	gag	act	ggt	cga	tgg	ctt	ggg	ttt	gag	cct
Tyr	Phe	Gln	Ser	Ile	Leu	Glu	Thr	Val	Arg	Trp	Leu	Gly	Phe	Glu	Pro
				325					330					335	
tgg	aag	att	act	tac	tcc	agc	gac	aac	ttt	gac	agg	tta	tac	gag	ctc
Trp	Lys	Ile	Thr	Tyr	Ser	Ser	Asp	Asn	Phe	Asp	Arg	Leu	Tyr	Glu	Leu
			340					345					350		
gcg	ggt	gaa	ttg	att	cgg	cga	gga	aag	gga	tac	gtc	tgt	act	tgt	gac
Ala	Val	Glu	Leu	Ile	Arg	Arg	Gly	Lys	Gly	Tyr	Val	Cys	Thr	Cys	Asp
		355					360					365			
gct	gag	aaa	atc	aag	gaa	gac	cga	ggg	atg	ggc	aag	ggg	aac	ccc	atc
Ala	Glu	Lys	Ile	Lys	Glu	Asp	Arg	Gly	Met	Gly	Lys	Gly	Asn	Pro	Ile
	370					375				380					
cct	tgt	gtg	cac	cga	gac	cga	cct	atc	gag	gag	tct	ctt	cat	gag	ttt
Pro	Cys	Val	His	Arg	Asp	Arg	Pro	Ile	Glu	Glu	Ser	Leu	His	Glu	Phe
385					390					395					400
gaa	cga	atg	aag	aat	ggc	gag	tat	aag	gaa	aag	gag	gag	tgc	atg	agg
Glu	Arg	Met	Lys	Asn	Gly	Glu	Tyr	Lys	Glu	Lys	Glu	Ala	Cys	Met	Arg
				405					410					415	
atg	aag	atg	gac	ttg	aat	agc	ggc	aac	cct	tat	atg	tgg	gac	act	gtt
Met	Lys	Met	Asp	Leu	Asn	Ser	Gly	Asn	Pro	Tyr	Met	Trp	Asp	Thr	Val
			420				425						430		
gcc	tac	cga	gtc	aag	aag	gcg	cct	cat	cac	agg	acc	ggg	gac	aag	tgg
Ala	Tyr	Arg	Val	Lys	Lys	Ala	Pro	His	His	Arg	Thr	Gly	Asp	Lys	Trp
			435				440					445			
aag	atc	tac	ccc	act	tat	gac	ttt	aca	cat	tgt	ctt	tgt	gat	agc	att
Lys	Ile	Tyr	Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys	Leu	Cys	Asp	Ser	Ile
	450					455					460				
gag	aac	atc	acg	cac	tct	ctc	tgt	acc	atc	gaa	ttt	atc	ccc	gct	cgt
Glu	Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Ile	Glu	Phe	Ile	Pro	Ala	Arg
465					470					475					480
gaa	tcc	tac	gaa	tgg	ctc	tgt	gac	gcc	ctc	agc	ggt	tac	aag	gct	cgt
Glu	Ser	Tyr	Glu	Trp	Leu	Cys	Asp	Ala	Leu	Ser	Val	Tyr	Lys	Ala	Arg
				485					490					495	
cag	tac	gaa	ttc	gca	cgt	ctc	aac	ctc	cag	ggg	act	ttc	ctc	tcc	aaa
Gln	Tyr	Glu	Phe	Ala	Arg	Leu	Asn	Leu	Gln	Gly	Thr	Phe	Leu	Ser	Lys
			500				505						510		
cga	aag	atc	gcg	aag	ctt	gtc	cag	aac	ggc	cac	gtc	aag	gac	tgg	gat
Arg	Lys	Ile	Ala	Lys	Leu	Val	Gln	Asn	Gly	His	Val	Lys	Asp	Trp	Asp
			515				520					525			
gac	cct	cgt	ctt	tac	act	atc	atc	gcc	ctt	cgt	cga	cgc	ggc	att	cct
Asp	Pro	Arg	Leu	Tyr	Thr	Ile	Ile	Ala	Leu	Arg	Arg	Arg	Gly	Ile	Pro
	530					535					540				
ccc	ggc	gcc	ttg	ctc	tcc	ttt	gtt	tcc	gag	ctt	ggg	gtg	acc	aac	atc
Pro	Gly	Ala	Leu	Leu	Ser	Phe	Val	Ser	Glu	Leu	Gly	Val	Thr	Asn	Ile
545					550					555					560
cct	tcc	acc	act	gaa	att	caa	aag	ttc	gaa	tct	tgc	gtc	cga	ggg	tac

PF59083SeqList PF59083.txt

Pro	Ser	Thr	Thr	Glu 565	Ile	Gln	Lys	Phe	Glu 570	Ser	Cys	Val	Arg	Gly 575	Tyr	
ctt	gag	agc	tcc	gcg	ccc	agg	ttg	atg	atg	gtt	ctc	aac	cct	atc	aaa	1776
Leu	Glu	Ser	Ser	Ala	Pro	Arg	Leu	Met	Met	Val	Leu	Asn	Pro	Ile	Lys	
			580					585					590			
atc	atc	atc	gac	aat	gtg	ccc	gac	gat	tac	cgt	gtc	cag	gtc	gaa	gtg	1824
Ile	Ile	Ile	Asp	Asn	Val	Pro	Asp	Asp	Tyr	Arg	Val	Gln	Val	Glu	Val	
		595					600					605				
cct	ctc	cat	ccc	aaa	atc	cct	gct	atg	ggc	act	gtc	cag	acc	atc	ttc	1872
Pro	Leu	His	Pro	Lys	Ile	Pro	Ala	Met	Gly	Thr	Val	Gln	Thr	Ile	Phe	
		610				615					620					
acc	aag	gaa	gtc	tac	atc	gat	gct	gac	gat	ttc	aga	gag	gtc	gat	tct	1920
Thr	Lys	Glu	Val	Tyr	Ile	Asp	Ala	Asp	Asp	Phe	Arg	Glu	Val	Asp	Ser	
625					630					635					640	
ccc	gac	tac	ttc	cgt	ctg	gcc	ccc	ggc	aag	tct	gtc	ggc	ttg	ttc	aag	1968
Pro	Asp	Tyr	Phe	Arg	Leu	Ala	Pro	Gly	Lys	Ser	Val	Gly	Leu	Phe	Lys	
				645					650					655		
gct	ccc	tac	cct	gtt	act	tgc	aca	tcc	ttc	acc	aag	gac	ccc	gtt	acc	2016
Ala	Pro	Tyr	Pro	Val	Thr	Cys	Thr	Ser	Phe	Thr	Lys	Asp	Pro	Val	Thr	
			660					665					670			
ggg	cgt	gtt	acc	gag	gta	cat	tgt	acg	ctc	gcc	ggc	gaa	ggc	ttc	aag	2064
Gly	Arg	Val	Thr	Glu	Val	His	Cys	Thr	Leu	Ala	Gly	Glu	Gly	Phe	Lys	
		675					680					685				
aag	cca	aag	gct	tac	atc	cag	tgg	gtc	aat	gcg	ccc	gag	gca	gtt	aag	2112
Lys	Pro	Lys	Ala	Tyr	Ile	cag	Trp	Val	Asn	Ala	Pro	Glu	Ala	Val	Lys	
		690				695					700					
atc	gac	gaa	gtg	cga	tac	ttc	aag	aag	ctt	ttc	aag	tct	gat	ccc	cct	2160
Ile	Asp	Glu	Val	Arg	Tyr	Phe	Lys	Lys	Leu	Phe	Lys	Ser	Asp	Pro	Pro	
705					710					715					720	
cct	gcg	gac	tat	gag	gca	gat	gtc	gac	ccc	gat	tct	ctt	gag	gtt	tac	2208
Pro	Ala	Asp	Tyr	Glu	Ala	Asp	Val	Asp	Pro	Asp	Ser	Leu	Glu	Val	Tyr	
				725					730					735		
agc	aat	gct	gtg	att	gag	cct	gcg	ttc	tat	gaa	ctt	gct	aag	aag	cag	2256
Ser	Asn	Ala	Val	Ile	Glu	Pro	Ala	Phe	Tyr	Glu	Leu	Ala	Lys	Lys	Gln	
			740					745					750			
atc	tcc	gat	gcg	agg	aaa	gac	agt	gaa	gaa	cgt	acg	aag	aag	gcc	gtc	2304
Ile	Ser	Asp	Ala	Arg	Lys	Asp	Ser	Glu	Glu	Arg	Thr	Lys	Lys	Ala	Val	
		755				760						765				
gag	cag	gct	gct	aag	cct	gat	aca	tct	tct	gct	cct	gtg	gaa	ggc	agt	2352
Glu	Gln	Ala	Ala	Lys	Pro	Asp	Thr	Ser	Ser	Ala	Pro	Val	Glu	Gly	Ser	
		770				775					780					
gcg	gcg	gct	cag	cac	aag	gat	gag	gag	ccc	gta	gct	act	gct	gag	cag	2400
Ala	Ala	Ala	Gln	His	Lys	Asp	Glu	Glu	Pro	Val	Ala	Thr	Ala	Glu	Gln	
785					790					795					800	
ttg	gtg	ggg	aac	gag	aac	atc	aga	ttc	cag	ggg	atg	agg	ttg	gcg	tac	2448
Leu	Val	Gly	Asn	Glu	Asn	Ile	Arg	Phe	Gln	Gly	Met	Arg	Leu	Ala	Tyr	
			805						810					815		
ttt	act	ttg	gac	agg	gaa	agc	aag	ttg	ggc	tgc	ttg	gag	aag	gag	gat	2496
Phe	Thr	Leu	Asp	Arg	Glu	Ser	Lys	Leu	Gly	Cys	Leu	Glu	Lys	Glu	Asp	
			820					825					830			
gtc	aag	ggc	agg	agc	gag	ggg	gac	aag	att	ata	cta	aac	agg	att	gtc	2544
Val	Lys	Gly	Arg	Ser	Glu	Gly	Asp	Lys	Ile	Ile	Leu	Asn	Arg	Ile	Val	
		835				840						845				
tcg	ctc	aag	gag	gat	gcg	ggc	aag	agt	gct	tag						2577
Ser	Leu	Lys	Glu	Asp	Ala	Gly	Lys	Ser	Ala							
		850				855										

<210> 9934

<211> 858

<212> PRT

<213> Cryptococcus neoformans var. neoformans JEC21

<400> 9934

Met	Pro	Pro	Lys	Phe	Asp	Pro	Asn	Ser	Pro	Glu	Asn	Ala	Pro	Leu	Ile	
1				5					10					15		
Gln	Leu	Phe	Gln	Ser	Leu	Gly	Leu	Ala	Ser	Asn	Ser	Ala	Thr	Glu	Leu	
			20					25				30				
Val	Arg	Gln	Pro	Lys	Ser	Gly	Lys	Ala	Phe	Lys	Ser	Leu	Ile	Asp	Glu	
		35					40					45				

PF59083SeqList PF59083.txt

Tyr	Gly	Leu	Thr	Asn	Asn	Lys	Tyr	Asp	Glu	Lys	Gln	Ala	Gly	Ala	Leu
Val	Lys	Leu	Ser	Ser	Val	Ser	Ala	Lys	Leu	Gly	Ser	Glu	Gln	Lys	Asp
65					70					75					80
Phe	Leu	Val	Gln	Lys	Ile	Val	Lys	Gly	Asp	Val	Lys	Thr	Pro	Asp	Gln
				85					90					95	
Val	Thr	Ala	Ala	Val	Lys	Phe	Ala	Glu	Lys	Asn	Pro	Asp	Leu	Lys	Ala
			100					105					110		
Asn	Glu	Glu	Ala	Phe	Asp	Lys	Glu	Cys	Gly	Val	Gly	Ile	Asn	Ile	Thr
		115					120					125			
Leu	Ala	Asp	Leu	Pro	Glu	Leu	Lys	Ser	Tyr	Ile	Thr	Ser	Leu	Pro	
	130					135				140					
Ser	Pro	Pro	Glu	Gly	Trp	Asn	Ser	Leu	Gly	Pro	Ile	Leu	Gly	Gly	Ile
145					150					155					160
Lys	Gly	Gly	Ala	Ser	Asp	Leu	Arg	Trp	Ala	Asn	Ala	Thr	Glu	Val	Lys
				165					170					175	
Ser	Thr	Leu	Glu	Ser	Ile	Phe	Val	Ser	Leu	Phe	Gly	Thr	Lys	Glu	Ala
			180					185					190		
Ala	Ala	Ala	Ala	Ala	Ala	Ala	Lys	Pro	Lys	Ala	Lys	Ala	Pro	Lys	Ala
		195					200					205			
Ala	Glu	Lys	Pro	Val	Lys	Pro	Val	Ser	Thr	Thr	Ala	Ala	Val	Ala	Thr
	210					215					220				
Lys	Ser	Ser	Ser	Ala	Thr	Pro	Ala	Ile	Pro	Thr	Asn	Ile	Phe	Glu	Glu
225					230					235					240
Gly	Phe	Leu	Ser	Glu	Phe	His	Lys	Val	Gly	Glu	Asn	Pro	Gln	Ser	Asp
				245					250					255	
Pro	Lys	Leu	Lys	Glu	Glu	His	Leu	Ala	Trp	Thr	Lys	Gly	Gln	Val	Tyr
			260					265					270		
Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Val
		275					280					285			
Lys	Ala	Ile	Met	Val	Asp	Phe	Gly	Tyr	Ala	Lys	Tyr	His	Gly	Gly	Arg
	290					295					300				
Thr	Tyr	Leu	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Glu	Gly	Arg
305					310					315					320
Tyr	Phe	Gln	Ser	Ile	Leu	Glu	Thr	Val	Arg	Trp	Leu	Gly	Phe	Glu	Pro
				325					330					335	
Trp	Lys	Ile	Thr	Tyr	Ser	Ser	Asp	Asn	Phe	Asp	Arg	Leu	Tyr	Glu	Leu
			340					345					350		
Ala	Val	Glu	Leu	Ile	Arg	Arg	Gly	Lys	Gly	Tyr	Val	Cys	Thr	Cys	Asp
		355					360					365			
Ala	Glu	Lys	Ile	Lys	Glu	Asp	Arg	Gly	Met	Gly	Lys	Gly	Asn	Pro	Ile
	370					375					380				
Pro	Cys	Val	His	Arg	Asp	Arg	Pro	Ile	Glu	Glu	Ser	Leu	His	Glu	Phe
385					390					395					400
Glu	Arg	Met	Lys	Asn	Gly	Glu	Tyr	Lys	Glu	Lys	Glu	Ala	Cys	Met	Arg
				405					410					415	
Met	Lys	Met	Asp	Leu	Asn	Ser	Gly	Asn	Pro	Tyr	Met	Trp	Asp	Thr	Val
			420					425					430		
Ala	Tyr	Arg	Val	Lys	Lys	Ala	Pro	His	His	Arg	Thr	Gly	Asp	Lys	Trp
		435					440					445			
Lys	Ile	Tyr	Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys	Leu	Cys	Asp	Ser	Ile
	450					455					460				
Glu	Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Ile	Glu	Phe	Ile	Pro	Ala	Arg
465					470					475					480
Glu	Ser	Tyr	Glu	Trp	Leu	Cys	Asp	Ala	Leu	Ser	Val	Tyr	Lys	Ala	Arg
			485						490					495	
Gln	Tyr	Glu	Phe	Ala	Arg	Leu	Asn	Leu	Gln	Gly	Thr	Phe	Leu	Ser	Lys
			500					505					510		
Arg	Lys	Ile	Ala	Lys	Leu	Val	Gln	Asn	Gly	His	Val	Lys	Asp	Trp	Asp
		515					520					525			
Asp	Pro	Arg	Leu	Tyr	Thr	Ile	Ile	Ala	Leu	Arg	Arg	Arg	Gly	Ile	Pro
	530					535					540				
Pro	Gly	Ala	Leu	Leu	Ser	Phe	Val	Ser	Glu	Leu	Gly	Val	Thr	Asn	Ile
545					550					555					560
Pro	Ser	Thr	Thr	Glu	Ile	Gln	Lys	Phe	Glu	Ser	Cys	Val	Arg	Gly	Tyr
			565						570					575	
Leu	Glu	Ser	Ser	Ala	Pro	Arg	Leu	Met	Met	Val	Leu	Asn	Pro	Ile	Lys
			580					585					590		
Ile	Ile	Ile	Asp	Asn	Val	Pro	Asp	Asp	Tyr	Arg	Val	Gln	Val	Glu	Val

PF59083SeqList PF59083.txt

595
 Pro Leu His Pro Lys Ile Pro 600
 610
 Thr Lys Glu Val Tyr Ile 615
 625
 Pro Asp Tyr Phe Arg 630
 645
 Ala Pro Tyr Pro Val Thr Cys Thr Ser Phe Thr Lys Asp Pro Val Thr
 660
 Gly Arg Val Thr Glu Val His Cys Thr Leu Ala Gly Glu Gly Phe Lys
 675
 Lys Pro Lys Ala Tyr Ile Gln Trp Val Asn Ala Pro Glu Ala Val Lys
 690
 Ile Asp Glu Val Arg Tyr 710
 705
 Pro Ala Asp Tyr Glu 725
 710
 Ser Asn Ala Val Ile Glu Pro Ala Phe Tyr Glu Leu Ala Lys Lys Gln
 740
 Ile Ser Asp Ala Arg Lys Asp Ser Glu Glu Arg Thr Lys Lys Ala Val
 755
 Glu Gln Ala Ala Lys Pro Asp Thr Ser Ser Ala Pro Val Glu Gly Ser
 770
 Ala Ala Ala Gln His Lys 790
 785
 Leu Val Gly Asn Glu Asn Ile Arg Phe Gln 810
 805
 Phe Thr Leu Asp Arg Glu Ser Lys Leu Gly Cys Leu Glu Lys Glu Asp
 820
 Val Lys Gly Arg Ser Glu Gly Asp Lys Ile Ile Leu Asn Arg Ile Val
 835
 Ser Leu Lys Glu Asp Ala Gly Lys Ser Ala
 850
 855

<210> 9935
 <211> 2361
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(2361)

<400> 9935
 atg gtt ctc aaa gac gat aac tcc gag aaa tct att gag ctc ttc att 48
 Met Val Leu Lys Asp Asp Asn Ser Glu Lys Ser Ile Glu Leu Phe Ile
 1 5 10 15
 agt att ggt ttg gac gag aaa aca gct cgt aat acc atc aat aat aac 96
 Ser Ile Gly Leu Asp Glu Lys Thr Ala Arg Asn Thr Ile Asn Asn Asn
 20 25 30
 aag gtc acc gcc aat ctc acc gcc gtt atc cac gag gct gct gtt act 144
 Lys Val Thr Ala Asn Leu Thr Ala Val Ile His Glu Ala Ala Val Thr
 35 40 45
 gat ggg tgc gat cga aat act ggc aat ctg tta tac tcg gtc gct act 192
 Asp Gly Cys Asp Arg Asn Thr Gly Asn Leu Leu Tyr Ser Val Ala Thr
 50 55 60
 aag ttc cct aca aat gct ctt gtg cat cgc cct aca ttg ctc aag tac 240
 Lys Phe Pro Thr Asn Ala Leu Val His Arg Pro Thr Leu Leu Lys Tyr
 65 70 75 80
 att gtt aac tct aag att aaa act cca gcc caa ttg gaa gct gca ttt 288
 Ile Val Asn Ser Lys Ile Lys Thr Pro Ala Gln Leu Glu Ala Ala Phe
 85 90 95
 gcc ttt ttt gcc agt acc ggt cct gag gac ttt aag ctg aat gag ttt 336
 Ala Phe Phe Ala Ser Thr Gly Pro Glu Asp Phe Lys Leu Asn Glu Phe
 100 105 110
 gaa gag gca tgt ggt gtt ggg att gaa gtt tcc cca gaa gat att gag 384
 Glu Glu Ala Cys Gly Val Gly Ile Glu Val Ser Pro Glu Asp Ile Glu
 115 120 125
 aaa gca gtt aaa gga atc ttt gaa gag aat aag aaa ata ttg gag 432

PF59083SeqList PF59083.txt

Lys	Ala	Val	Lys	Gly	Ile	Phe	Glu	Glu	Asn	Lys	Lys	Thr	Ile	Leu	Glu	
130	130					135					140					
cag	cgc	tat	cga	act	aat	gtg	ggg	gaa	tta	ttt	gga	cat	gtc	cgg	aaa	480
Gln	Arg	Tyr	Arg	Thr	Asn	Val	Gly	Glu	Leu	Phe	Gly	His	Val	Arg	Lys	
145					150					155					160	
agt	ttg	cca	tgg	gcc	gat	cct	aag	att	gta	aag	aaa	ctc	ata	gat	gag	528
Ser	Leu	Pro	Trp	Ala	Asp	Pro	Lys	Ile	Val	Lys	Lys	Leu	Ile	Asp	Glu	
				165					170					175		
aaa	atg	tat	gag	ctg	ctt	ggg	gag	aaa	acc	gct	gct	gat	aat	gaa	aaa	576
Lys	Met	Tyr	Glu	Leu	Leu	Gly	Glu	Lys	Thr	Ala	Ala	Asp	Asn	Glu	Lys	
			180						185				190			
cct	aca	aaa	aag	aag	gag	aag	aag	gag	aag	cct	gcc	aaa	gtc	gag	gaa	624
Pro	Thr	Lys	Lys	Lys	Glu	Lys	Lys	Glu	Lys	Pro	Ala	Lys	Val	Glu	Glu	
		195				200					205					
aag	aaa	gct	gtg	gtg	gaa	act	acc	gca	gag	cca	tct	gaa	gag	gag	ctt	672
Lys	Lys	Ala	Val	Val	Glu	Thr	Thr	Ala	Glu	Pro	Ser	Glu	Glu	Glu	Leu	
	210					215					220					
aat	cca	tat	act	ata	ttc	cct	cag	cca	gaa	caa	aat	ttt	atg	gtt	cac	720
Asn	Pro	Tyr	Thr	Ile	Phe	Pro	Gln	Pro	Glu	Gln	Asn	Phe	Met	Val	His	
225					230					235					240	
aca	gaa	gtg	ttt	ttc	agt	gat	ggc	tct	att	ctc	aga	tgt	agc	aat	aca	768
Thr	Glu	Val	Phe	Phe	Ser	Asp	Gly	Ser	Ile	Leu	Arg	Cys	Ser	Asn	Thr	
			245						250					255		
aag	gaa	gta	ctt	gac	aaa	cat	ctc	aag	gtg	act	gga	ggg	aaa	gtt	tat	816
Lys	Glu	Val	Leu	Asp	Lys	His	Leu	Lys	Val	Thr	Gly	Gly	Lys	Val	Tyr	
			260						265				270			
act	cgg	ttc	ccc	cct	gaa	cca	aat	ggg	tat	ctt	cat	att	gga	cat	gcc	864
Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ala	
		275					280					285				
aag	gct	atg	ttt	gtt	gat	ttt	ggg	ctt	gca	aag	gag	cga	ggg	ggg	tgc	912
Lys	Ala	Met	Phe	Val	Asp	Phe	Gly	Leu	Ala	Lys	Glu	Arg	Gly	Gly	Cys	
	290					295					300					
tgt	tat	cta	agg	tat	gat	gat	aca	aat	cca	gag	gca	gaa	aag	gaa	gag	960
Cys	Tyr	Leu	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys	Glu	Glu	
305					310					315					320	
tat	att	aat	cat	att	gaa	gaa	att	gtt	aag	tgg	atg	ggg	tgg	gaa	ccc	1008
Tyr	Ile	Asn	His	Ile	Glu	Glu	Ile	Val	Lys	Trp	Met	Gly	Trp	Glu	Pro	
			325						330					335		
ttc	aag	gaa	ctg	tat	gat	ttg	gca	gtg	gag	ttg	att	cgg	aga	ggg	cat	1056
Phe	Lys	Glu	Leu	Tyr	Asp	Leu	Ala	Val	Glu	Leu	Ile	Arg	Arg	Gly	His	
			340						345				350			
gct	tat	gtt	gat	cat	cag	act	gct	gat	gag	ata	aaa	gag	tac	aga	gag	1104
Ala	Tyr	Val	Asp	His	Gln	Thr	Ala	Asp	Glu	Ile	Lys	Glu	Tyr	Arg	Glu	
		355				360						365				
aag	aaa	atg	aac	agc	ccc	tgg	agg	gac	aga	cct	att	gaa	gaa	tct	cta	1152
Lys	Lys	Met	Asn	Ser	Pro	Trp	Arg	Asp	Arg	Pro	Ile	Glu	Glu	Ser	Leu	
		370				375					380					
aaa	ctt	ttt	gat	gaa	atg	aga	cga	ggc	atc	att	gag	gaa	ggg	aag	gca	1200
Lys	Leu	Phe	Asp	Glu	Met	Arg	Arg	Gly	Ile	Ile	Glu	Glu	Gly	Lys	Ala	
385					390					395					400	
acc	cta	aga	atg	aag	caa	gat	atg	cag	agt	gac	aat	ttt	aat	atg	tat	1248
Thr	Leu	Arg	Met	Lys	Gln	Asp	Met	Gln	Ser	Asp	Asn	Phe	Asn	Met	Tyr	
			405						410					415		
gat	ctt	att	gcc	tat	cga	ata	aag	ttc	gca	cct	cat	cct	aag	gct	ggg	1296
Asp	Leu	Ile	Ala	Tyr	Arg	Ile	Lys	Phe	Ala	Pro	His	Pro	Lys	Ala	Gly	
			420					425					430			
gac	aag	tgg	tgt	atc	tat	ccg	agt	tat	gat	tat	gcc	cac	tgc	act	gtt	1344
Asp	Lys	Trp	Cys	Ile	Tyr	Pro	Ser	Tyr	Asp	Tyr	Ala	His	Cys	Thr	Val	
		435				440						445				
gat	tct	ctt	gag	aat	ata	acg	cat	tcg	ctc	tgt	act	ctt	gaa	ttt	gaa	1392
Asp	Ser	Leu	Glu	Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Leu	Glu	Phe	Glu	
		450				455					460					
acc	cgg	cgt	gct	tca	tac	tat	tgg	ctg	tta	cat	tcc	ctg	agt	ctc	tac	1440
Thr	Arg	Arg	Ala	Ser	Tyr	Tyr	Trp	Leu	Leu	His	Ser	Leu	Ser	Leu	Tyr	
465					470					475					480	
atg	cca	tat	gtg	tgg	gaa	tat	tca	cgg	ttg	aat	gtg	aca	aac	act	gta	1488
Met	Pro	Tyr	Val	Trp	Glu	Tyr	Ser	Arg	Leu	Asn	Val	Thr	Asn	Thr	Val	
			485						490					495		
atg	tcc	aag	cgt	aag	ttg	aat	tac	ata	gtg	aca	aac	aag	tat	gtt	gat	1536

PF59083SeqList PF59083.txt

Met	Ser	Lys	Arg	Lys	Leu	Asn	Tyr	Ile	Val	Thr	Asn	Lys	Tyr	Val	Asp	
			500					505					510			
ggg	tgg	gat	gat	cca	cgt	ctt	ttg	aca	ctt	tct	ggg	ttg	aga	cgg	agg	1584
Gly	Trp	Asp	Asp	Pro	Arg	Leu	Leu	Thr	Leu	Ser	Gly	Leu	Arg	Arg	Arg	
		515					520					525				
ggg	gtg	act	tca	act	gcg	att	aat	gca	ttt	gta	cga	ggc	att	ggg	att	1632
Gly	Val	Thr	Ser	Thr	Ala	Ile	Asn	Ala	Phe	Val	Arg	Gly	Ile	Gly	Ile	
	530					535					540					
act	aga	agt	gat	ggg	agc	atg	ata	cac	gta	agt	cgt	ctt	gag	cat	cat	1680
Thr	Arg	Ser	Asp	Gly	Ser	Met	Ile	His	Val	Ser	Arg	Leu	Glu	His	His	
545					550					555					560	
att	aga	gag	gaa	ttg	aat	aaa	aca	gcc	cct	cgc	acc	atg	gtg	gtg	ctt	1728
Ile	Arg	Glu	Glu	Leu	Asn	Lys	Thr	Ala	Pro	Arg	Thr	Met	Val	Val	Leu	
			565					570						575		
aat	cct	ctt	aaa	gtg	gtc	atc	acc	aat	ttg	gaa	tca	gac	aag	ctt	ata	1776
Asn	Pro	Leu	Lys	Val	Val	Ile	Thr	Asn	Leu	Glu	Ser	Asp	Lys	Leu	Ile	
			580					585						590		
gag	ctt	gat	gcc	aaa	agg	tgg	cct	gat	gct	cag	aac	gat	gat	ccc	tca	1824
Glu	Leu	Asp	Ala	Lys	Arg	Trp	Pro	Asp	Ala	Gln	Asn	Asp	Asp	Pro	Ser	
		595					600					605				
gca	ttc	tac	aag	gta	ccg	ttc	tct	aga	gtt	gta	tac	att	gac	caa	tct	1872
Ala	Phe	Tyr	Lys	Val	Pro	Phe	Ser	Arg	Val	Val	Tyr	Ile	Asp	Gln	Ser	
	610					615					620					
gac	ttc	cga	atg	aag	gat	tca	aaa	gat	tat	tat	ggg	ctc	gcc	cct	ggg	1920
Asp	Phe	Arg	Met	Lys	Asp	Ser	Lys	Asp	Tyr	Tyr	Gly	Leu	Ala	Pro	Gly	
625					630				635						640	
aaa	tct	gtt	ttg	cta	aga	tat	gct	ttc	cca	atc	aag	tgc	acc	aat	gtt	1968
Lys	Ser	Val	Leu	Leu	Arg	Tyr	Ala	Phe	Pro	Ile	Lys	Cys	Thr	Asn	Val	
			645					650						655		
gtc	ttt	gct	gat	gac	aat	gaa	acc	gtt	cgt	gag	att	cat	gcg	gaa	tat	2016
Val	Phe	Ala	Asp	Asp	Asn	Glu	Thr	Val	Arg	Glu	Ile	His	Ala	Glu	Tyr	
			660					665					670			
gac	ccc	gag	aaa	aag	tca	aag	cca	aag	ggg	gtt	cta	cac	tgg	gtc	gct	2064
Asp	Pro	Glu	Lys	Lys	Ser	Lys	Pro	Lys	Gly	Val	Leu	His	Trp	Val	Ala	
		675					680					685				
gaa	tct	tcc	cca	gga	gaa	gag	ccc	ata	aag	gtg	gaa	gtc	cga	tta	ttt	2112
Glu	Ser	Ser	Pro	Gly	Glu	Glu	Pro	Ile	Lys	Val	Glu	Val	Arg	Leu	Phe	
	690					695					700					
gag	aaa	ctc	ttt	aac	tcc	gag	aac	ccg	gct	gaa	ctc	aat	gat	gct	tgg	2160
Glu	Lys	Leu	Phe	Asn	Ser	Glu	Asn	Pro	Ala	Glu	Leu	Asn	Asp	Ala	Trp	
705					710				715						720	
ctc	act	gac	att	aac	cca	aac	tct	aaa	atg	gta	att	tct	ggg	gcc	tat	2208
Leu	Thr	Asp	Ile	Asn	Pro	Asn	Ser	Lys	Met	Val	Ile	Ser	Gly	Ala	Tyr	
			725					730						735		
gct	gta	tca	acc	ctt	aaa	gat	gct	gca	gtt	ggg	gac	aga	ttc	caa	ttc	2256
Ala	Val	Ser	Thr	Leu	Lys	Asp	Ala	Ala	Val	Gly	Asp	Arg	Phe	Gln	Phe	
			740					745					750			
gag	agg	cta	ggg	tat	tac	gcg	gtg	gac	aag	gac	tct	gag	cca	gga	aag	2304
Glu	Arg	Leu	Gly	Tyr	Tyr	Ala	Val	Asp	Lys	Asp	Ser	Glu	Pro	Gly	Lys	
		755					760					765				
ctt	gtg	ttc	aac	cgg	acg	gtc	aca	ctc	aga	gac	agc	tac	ggg	aaa	ggg	2352
Leu	Val	Phe	Asn	Arg	Thr	Val	Thr	Leu	Arg	Asp	Ser	Tyr	Gly	Lys	Gly	
	770					775					780					
gga	aag	taa														2361
Gly	Lys															
785																

<210> 9936

<211> 786

<212> PRT

<213> Arabidopsis thaliana

<400> 9936

Met	Val	Leu	Lys	Asp	Asp	Asn	Ser	Glu	Lys	Ser	Ile	Glu	Leu	Phe	Ile
1				5					10					15	
Ser	Ile	Gly	Leu	Asp	Glu	Lys	Thr	Ala	Arg	Asn	Thr	Ile	Asn	Asn	Asn
			20					25					30		
Lys	Val	Thr	Ala	Asn	Leu	Thr	Ala	Val	Ile	His	Glu	Ala	Ala	Val	Thr
		35					40					45			

PF59083SeqList PF59083.txt

Asp	Gly	Cys	Asp	Arg	Asn	Thr	Gly	Asn	Leu	Leu	Tyr	Ser	Val	Ala	Thr
	50					55					60				
Lys	Phe	Pro	Thr	Asn	Ala	Leu	Val	His	Arg	Pro	Thr	Leu	Leu	Lys	Tyr
65					70					75					80
Ile	Val	Asn	Ser	Lys	Ile	Lys	Thr	Pro	Ala	Gln	Leu	Glu	Ala	Ala	Phe
				85					90					95	
Ala	Phe	Phe	Ala	Ser	Thr	Gly	Pro	Glu	Asp	Phe	Lys	Leu	Asn	Glu	Phe
			100					105					110		
Glu	Glu	Ala	Cys	Gly	Val	Gly	Ile	Glu	Val	Ser	Pro	Glu	Asp	Ile	Glu
		115					120					125			
Lys	Ala	Val	Lys	Gly	Ile	Phe	Glu	Glu	Asn	Lys	Lys	Thr	Ile	Leu	Glu
	130					135					140				
Gln	Arg	Tyr	Arg	Thr	Asn	Val	Gly	Glu	Leu	Phe	Gly	His	Val	Arg	Lys
145					150					155					160
Ser	Leu	Pro	Trp	Ala	Asp	Pro	Lys	Ile	Val	Lys	Lys	Leu	Ile	Asp	Glu
				165					170					175	
Lys	Met	Tyr	Glu	Leu	Leu	Gly	Glu	Lys	Thr	Ala	Ala	Asp	Asn	Glu	Lys
			180					185					190		
Pro	Thr	Lys	Lys	Lys	Glu	Lys	Lys	Glu	Lys	Pro	Ala	Lys	Val	Glu	Glu
		195					200					205			
Lys	Lys	Ala	Val	Val	Glu	Thr	Thr	Ala	Glu	Pro	Ser	Glu	Glu	Glu	Leu
	210					215					220				
Asn	Pro	Tyr	Thr	Ile	Phe	Pro	Gln	Pro	Glu	Gln	Asn	Phe	Met	Val	His
225					230					235					240
Thr	Glu	Val	Phe	Phe	Ser	Asp	Gly	Ser	Ile	Leu	Arg	Cys	Ser	Asn	Thr
				245					250					255	
Lys	Glu	Val	Leu	Asp	Lys	His	Leu	Lys	Val	Thr	Gly	Gly	Lys	Val	Tyr
			260					265					270		
Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ala
		275					280					285			
Lys	Ala	Met	Phe	Val	Asp	Phe	Gly	Leu	Ala	Lys	Glu	Arg	Gly	Gly	Cys
	290					295					300				
Cys	Tyr	Leu	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys	Glu	Glu
305					310					315					320
Tyr	Ile	Asn	His	Ile	Glu	Glu	Ile	Val	Lys	Trp	Met	Gly	Trp	Glu	Pro
				325					330					335	
Phe	Lys	Glu	Leu	Tyr	Asp	Leu	Ala	Val	Glu	Leu	Ile	Arg	Arg	Gly	His
			340					345					350		
Ala	Tyr	Val	Asp	His	Gln	Thr	Ala	Asp	Glu	Ile	Lys	Glu	Tyr	Arg	Glu
		355					360					365			
Lys	Lys	Met	Asn	Ser	Pro	Trp	Arg	Asp	Arg	Pro	Ile	Glu	Glu	Ser	Leu
	370					375					380				
Lys	Leu	Phe	Asp	Glu	Met	Arg	Arg	Gly	Ile	Ile	Glu	Glu	Gly	Lys	Ala
385					390					395					400
Thr	Leu	Arg	Met	Lys	Gln	Asp	Met	Gln	Ser	Asp	Asn	Phe	Asn	Met	Tyr
				405					410					415	
Asp	Leu	Ile	Ala	Tyr	Arg	Ile	Lys	Phe	Ala	Pro	His	Pro	Lys	Ala	Gly
			420					425					430		
Asp	Lys	Trp	Cys	Ile	Tyr	Pro	Ser	Tyr	Asp	Tyr	Ala	His	Cys	Thr	Val
		435					440					445			
Asp	Ser	Leu	Glu	Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Leu	Glu	Phe	Glu
	450					455					460				
Thr	Arg	Arg	Ala	Ser	Tyr	Tyr	Trp	Leu	Leu	His	Ser	Leu	Ser	Leu	Tyr
465					470					475					480
Met	Pro	Tyr	Val	Trp	Glu	Tyr	Ser	Arg	Leu	Asn	Val	Thr	Asn	Thr	Val
				485					490					495	
Met	Ser	Lys	Arg	Lys	Leu	Asn	Tyr	Ile	Val	Thr	Asn	Lys	Tyr	Val	Asp
			500					505					510		
Gly	Trp	Asp	Pro	Arg	Leu	Leu	Thr	Leu	Ser	Gly	Leu	Arg	Arg	Arg	
		515				520					525				
Gly	Val	Thr	Ser	Thr	Ala	Ile	Asn	Ala	Phe	Val	Arg	Gly	Ile	Gly	Ile
	530					535					540				
Thr	Arg	Ser	Asp	Gly	Ser	Met	Ile	His	Val	Ser	Arg	Leu	Glu	His	His
545					550					555					560
Ile	Arg	Glu	Glu	Leu	Asn	Lys	Thr	Ala	Pro	Arg	Thr	Met	Val	Val	Leu
				565					570					575	
Asn	Pro	Leu	Lys	Val	Val	Ile	Thr	Asn	Leu	Glu	Ser	Asp	Lys	Leu	Ile
			580					585					590		
Glu	Leu	Asp	Ala	Lys	Arg	Trp	Pro	Asp	Ala	Gln	Asn	Asp	Asp	Pro	Ser

PF59083SeqList PF59083.txt

595
 Ala Phe Tyr Lys Val Pro Phe 600 Ser Arg Val Val Tyr 605 Ile Asp Gln Ser
 610 Phe Arg Met Lys Asp 615 Ser Lys Asp Tyr Tyr 620 Gly Leu Ala Pro Gly
 625 Lys Ser Val Leu Leu 630 Arg Tyr Ala Phe Pro 635 Ile Lys Cys Thr Asn Val
 645 Val Phe Ala Asp Asp Asn Glu Thr Val Arg Glu Ile His Ala Glu Tyr
 660 Asp Pro Glu Lys Lys Ser Lys Pro 665 Lys Gly Val Leu His Trp Val Ala
 675 Glu Ser Ser Pro Gly Glu Glu Pro 680 Ile Lys Val Glu Val Arg Leu Phe
 690 Glu Lys Leu Phe Asn Ser 695 Glu Asn Pro Ala Glu Leu Asn Asp Ala Trp
 705 Leu Thr Asp Ile Asn 710 Pro Asn Ser Lys Met 715 Val Ile Ser Gly Ala Tyr
 725 Ala Val Ser Thr Leu Lys Asp Ala Ala Val Gly Asp Arg Phe Gln Phe
 740 Glu Arg Leu Gly Tyr Tyr Ala Val 745 Asp Lys Asp Ser Glu Pro Gly Lys
 755 Leu Val Phe Asn Arg Thr Val 760 Thr Leu Arg Asp Ser Tyr Gly Lys Gly
 770 Gly Lys 775 780 785

<210> 9937

<211> 2388

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2388)

<400> 9937

atg gtt ctc aaa gac gat aac tcc gag aaa tct att gag ctc ttc att	48
Met Val Leu Lys Asp Asp Asn Ser Glu Lys Ser Ile Glu Leu Phe Ile	
1 5 10 15	
agt att ggt ttg gac gag aaa aca gct cgt aat acc atc aat aat aac	96
Ser Ile Gly Leu Asp Glu Lys Thr Ala Arg Asn Thr Ile Asn Asn Asn	
20 25 30	
aag gtc acc gcc aat ctc acc gcc gtt atc cac gag gct gct gtt act	144
Lys Val Thr Ala Asn Leu Thr Ala Val Ile His Glu Ala Ala Val Thr	
35 40 45	
gat ggg tgc gat cga aat act ggc aat ctg tta tac tcg gtc gct act	192
Asp Gly Cys Asp Arg Asn Thr Gly Asn Leu Leu Tyr Ser Val Ala Thr	
50 55 60	
aag ttc cct aca aat gct ctt gtg cat cgc cct aca ttg ctc aag tac	240
Lys Phe Pro Thr Asn Ala Leu Val His Arg Pro Thr Leu Leu Lys Tyr	
65 70 75 80	
att gtt aac tct aag att aaa act cca gcc caa ttg gaa gct gca ttt	288
Ile Val Asn Ser Lys Ile Lys Thr Pro Ala Gln Leu Glu Ala Ala Phe	
85 90 95	
gcc ttt ttt gcc agt acc ggt cct gag gac ttt aag ctg aat gag ttt	336
Ala Phe Phe Ala Ser Thr Gly Pro Glu Asp Phe Lys Leu Asn Glu Phe	
100 105 110	
gaa gag gca tgt ggt gtt ggg att gaa gtt tcc cca gaa gat att gag	384
Glu Glu Ala Cys Gly Val Gly Ile Glu Val Ser Pro Glu Asp Ile Glu	
115 120 125	
aaa gca gtt aaa gga atc ttt gaa gag aat aag aaa aca ata ttg gag	432
Lys Ala Val Lys Gly Ile Phe Glu Glu Asn Lys Lys Thr Ile Leu Glu	
130 135 140	
cag cgc tat cga act aat gtg ggt gaa tta ttt gga cat gtc cgg aaa	480
Gln Arg Tyr Arg Thr Asn Val Gly Glu Leu Phe Gly His Val Arg Lys	
145 150 155 160	
agt ttg cca tgg gcc gat cct aag att gta aag aaa ctc ata gat gag	528
Ser Leu Pro Trp Ala Asp Pro Lys Ile Val Lys Lys Leu Ile Asp Glu	
165 170 175	

PF59083SeqList PF59083.txt																
aaa	atg	tat	gag	ctg	ctt	ggt	gag	aaa	acc	gct	gct	gat	aat	gaa	aaa	576
Lys	Met	Tyr	Glu	Leu	Leu	Gly	Glu	Lys	Thr	Ala	Ala	Asp	Asn	Glu	Lys	
			180					185					190			
cct	aca	aaa	aag	aag	gag	aag	aag	gag	aag	cct	gcc	aaa	gtc	gag	gaa	624
Pro	Thr	Lys	Lys	Lys	Glu	Lys	Lys	Glu	Lys	Pro	Ala	Lys	Val	Glu	Glu	
		195					200					205				
aag	aaa	gct	gtg	gtg	gaa	act	acc	gca	gag	cca	tct	gaa	gag	gag	ctt	672
Lys	Lys	Ala	Val	Val	Glu	Thr	Thr	Ala	Glu	Pro	Ser	Glu	Glu	Glu	Leu	
	210					215					220					
aat	cca	tat	act	ata	ttc	cct	cag	cca	gaa	caa	aat	ttt	atg	gtt	cac	720
Asn	Pro	Tyr	Thr	Ile	Phe	Pro	Gln	Pro	Glu	Gln	Asn	Phe	Met	Val	His	
225					230					235					240	
aca	gaa	gtg	ttt	ttc	agt	gat	ggc	tct	att	ctc	aga	tgt	agc	aat	aca	768
Thr	Glu	Val	Phe	Phe	Ser	Asp	Gly	Ser	Ile	Leu	Arg	Cys	Ser	Asn	Thr	
				245					250					255		
aag	gaa	gta	ctt	gac	aaa	cat	ctc	aag	gtg	act	gga	ggg	aaa	gtt	tat	816
Lys	Glu	Val	Leu	Asp	Lys	His	Leu	Lys	Val	Thr	Gly	Gly	Lys	Val	Tyr	
			260					265					270			
act	cgg	ttc	ccc	cct	gaa	cca	aat	ggt	tat	ctt	cat	att	gga	cat	gcc	864
Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ala	
		275					280					285				
aag	gct	atg	ttt	gtt	gat	ttt	ggt	ctt	gca	aag	gag	cga	ggg	ggt	tgc	912
Lys	Ala	Met	Phe	Val	Asp	Phe	Gly	Leu	Ala	Lys	Glu	Arg	Gly	Gly	Cys	
	290				295					300						
tgt	tat	cta	agg	tat	gat	aca	aat	cca	gag	gca	gaa	aag	gaa	gag		960
Cys	Tyr	Leu	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys	Glu	Glu	
305					310					315					320	
tat	att	aat	cat	att	gaa	gaa	att	gtt	aag	tgg	atg	ggt	tgg	gaa	ccc	1008
Tyr	Ile	Asn	His	Ile	Glu	Glu	Ile	Val	Lys	Trp	Met	Gly	Trp	Glu	Pro	
				325					330					335		
ttc	aag	att	aca	tac	acc	agt	gat	tat	ttc	cag	gaa	ctg	tat	gat	ttg	1056
Phe	Lys	Ile	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Gln	Glu	Leu	Tyr	Asp	Leu	
			340					345					350			
gca	gtg	gag	ttg	att	cgg	aga	ggt	cat	gct	tat	gtt	gat	cat	cag	act	1104
Ala	Val	Glu	Leu	Ile	Arg	Arg	Gly	His	Ala	Tyr	Val	Asp	His	Gln	Thr	
		355					360					365				
gct	gat	gag	ata	aaa	gag	tac	aga	gag	aag	aaa	atg	aac	agc	ccc	tgg	1152
Ala	Asp	Glu	Ile	Lys	Glu	Tyr	Arg	Glu	Lys	Lys	Met	Asn	Ser	Pro	Trp	
	370				375					380						
agg	gac	aga	cct	att	gaa	gaa	tct	cta	aaa	ctt	ttt	gat	gaa	atg	aga	1200
Arg	Asp	Arg	Pro	Ile	Glu	Glu	Ser	Leu	Lys	Leu	Phe	Asp	Glu	Met	Arg	
385					390					395					400	
cga	ggc	atc	att	gag	gaa	ggg	aag	gca	acc	cta	aga	atg	aag	caa	gat	1248
Arg	Gly	Ile	Ile	Glu	Glu	Gly	Lys	Ala	Thr	Leu	Arg	Met	Lys	Gln	Asp	
				405					410					415		
atg	cag	agt	gac	aat	ttt	aat	atg	tat	gat	ctt	att	gcc	tat	cga	ata	1296
Met	Gln	Ser	Asp	Asn	Phe	Asn	Met	Tyr	Asp	Leu	Ile	Ala	Tyr	Arg	Ile	
			420				425					430				
aag	ttc	gca	cct	cat	cct	aag	gct	ggt	gac	aag	tgg	tgt	atc	tat	ccg	1344
Lys	Phe	Ala	Pro	His	Pro	Lys	Ala	Gly	Asp	Lys	Trp	Cys	Ile	Tyr	Pro	
		435					440					445				
agt	tat	gat	tat	gcc	cac	tgc	act	gtt	gat	tct	ctt	gag	aat	ata	acg	1392
Ser	Tyr	Asp	Tyr	Ala	His	Cys	Thr	Val	Asp	Ser	Leu	Glu	Asn	Ile	Thr	
	450					455					460					
cat	tcg	ctc	tgt	act	ctt	gaa	ttt	gaa	acc	cgg	cgt	gct	tca	tac	tat	1440
His	Ser	Leu	Cys	Thr	Leu	Glu	Phe	Glu	Thr	Arg	Arg	Ala	Ser	Tyr	Tyr	
				470						475					480	
tgg	ctg	tta	cat	tcc	ctg	agt	ctc	tac	atg	cca	tat	gtg	tgg	gaa	tat	1488
Trp	Leu	Leu	His	Ser	Leu	Ser	Leu	Tyr	Met	Pro	Tyr	Val	Trp	Glu	Tyr	
				485					490					495		
tca	cgg	ttg	aat	gtg	aca	aac	act	gta	atg	tcc	aag	cgt	aag	ttg	aat	1536
Ser	Arg	Leu	Asn	Val	Thr	Asn	Thr	Val	Met	Ser	Lys	Arg	Lys	Leu	Asn	
			500					505					510			
tac	ata	gtg	aca	aac	aag	tat	gtt	gat	ggt	tgg	gat	gat	cca	cgt	ctt	1584
Tyr	Ile	Val	Thr	Asn	Lys	Tyr	Val	Asp	Gly	Trp	Asp	Asp	Pro	Arg	Leu	
		515					520					525				
ttg	aca	ctt	tct	ggt	ttg	aga	cgg	agg	ggt	gtg	act	tca	act	gcg	att	1632
Leu	Thr	Leu	Ser	Gly	Leu	Arg	Arg	Arg	Gly	Val	Thr	Ser	Thr	Ala	Ile	
	530					535					540					

PF59083SeqList PF59083.txt

aat	gca	ttt	gta	cga	ggc	att	ggg	att	act	aga	agt	gat	ggt	agc	atg	1680
Asn	Ala	Phe	Val	Arg	Gly	Ile	Gly	Ile	Thr	Arg	Ser	Asp	Gly	Ser	Met	
545					550					555					560	
ata	cac	gta	agt	cgt	ctt	gag	cat	cat	att	aga	gag	gaa	ttg	aat	aaa	1728
Ile	His	Val	Ser	Arg	Leu	Glu	His	His	Ile	Arg	Glu	Glu	Leu	Asn	Lys	
				565					570					575		
aca	gcc	cct	cgc	acc	atg	gtg	gtg	ctt	aat	cct	ctt	aaa	gtg	gtc	atc	1776
Thr	Ala	Pro	Arg	Thr	Met	Val	Val	Leu	Asn	Pro	Leu	Lys	Val	Val	Ile	
				580				585					590			
acc	aat	ttg	gaa	tca	gac	aag	ctt	ata	gag	ctt	gat	gcc	aaa	agg	tgg	1824
Thr	Asn	Leu	Glu	Ser	Asp	Lys	Leu	Ile	Glu	Leu	Asp	Ala	Lys	Arg	Trp	
		595					600					605				
cct	gat	gct	cag	aac	gat	gat	ccc	tca	gca	ttc	tac	aag	gta	ccg	ttc	1872
Pro	Asp	Ala	Gln	Asn	Asp	Asp	Pro	Ser	Ala	Phe	Tyr	Lys	Val	Pro	Phe	
	610					615					620					
tct	aga	gtt	gta	tac	att	gac	caa	tct	gac	ttc	cga	atg	aag	gat	tca	1920
Ser	Arg	Val	Val	Tyr	Ile	Asp	Gln	Ser	Asp	Phe	Arg	Met	Lys	Asp	Ser	
625					630					635					640	
aaa	gat	tat	tat	ggg	ctc	gcc	cct	ggt	aaa	tct	gtt	ttg	cta	aga	tat	1968
Lys	Asp	Tyr	Tyr	Gly	Leu	Ala	Pro	Gly	Lys	Ser	Val	Leu	Leu	Arg	Tyr	
				645				650						655		
gct	ttc	cca	atc	aag	tgc	acc	aat	gtt	gtc	ttt	gct	gat	gac	aat	gaa	2016
Ala	Phe	Pro	Ile	Lys	Cys	Thr	Asn	Val	Val	Phe	Ala	Asp	Asp	Asn	Glu	
			660				665						670			
acc	gtt	cgt	gag	att	cat	gcg	gaa	tat	gac	ccc	gag	aaa	aag	tca	aag	2064
Thr	Val	Arg	Glu	Ile	His	Ala	Glu	Tyr	Asp	Pro	Glu	Lys	Lys	Ser	Lys	
		675					680					685				
cca	aag	ggg	gtt	cta	cac	tgg	gtc	gct	gaa	tct	tcc	cca	gga	gaa	gag	2112
Pro	Lys	Gly	Val	Leu	His	Trp	Val	Ala	Glu	Ser	Ser	Pro	Gly	Glu	Glu	
	690					695					700					
ccc	ata	aag	gtg	gaa	gtc	cga	tta	ttt	gag	aaa	ctc	ttt	aac	tcc	gag	2160
Pro	Ile	Lys	Val	Glu	Val	Arg	Leu	Phe	Glu	Lys	Leu	Phe	Asn	Ser	Glu	
705					710					715					720	
aac	ccg	gct	gaa	ctc	aat	gat	gct	tgg	ctc	act	gac	att	aac	cca	aac	2208
Asn	Pro	Ala	Glu	Leu	Asn	Asp	Ala	Trp	Leu	Thr	Asp	Ile	Asn	Pro	Asn	
				725				730						735		
tct	aaa	atg	gta	att	tct	ggt	gcc	tat	gct	gta	tca	acc	ctt	aaa	gat	2256
Ser	Lys	Met	Val	Ile	Ser	Gly	Ala	Tyr	Ala	Val	Ser	Thr	Leu	Lys	Asp	
			740					745					750			
gct	gca	gtt	ggg	gac	aga	ttc	caa	ttc	gag	agg	cta	ggt	tat	tac	gcg	2304
Ala	Ala	Val	Gly	Asp	Arg	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Tyr	Ala	
		755					760					765				
gtg	gac	aag	gac	tct	gag	cca	gga	aag	ctt	gtg	ttc	aac	cgg	acg	gtc	2352
Val	Asp	Lys	Asp	Ser	Glu	Pro	Gly	Lys	Leu	Val	Phe	Asn	Arg	Thr	Val	
	770					775					780					
aca	ctc	aga	gac	agc	tac	ggg	aaa	ggt	gga	aag	taa					2388
Thr	Leu	Arg	Asp	Ser	Tyr	Gly	Lys	Gly	Gly	Lys						
785					790					795						

<210> 9938

<211> 795

<212> PRT

<213> Arabidopsis thaliana

<400> 9938

Met	Val	Leu	Lys	Asp	Asp	Asn	Ser	Glu	Lys	Ser	Ile	Glu	Leu	Phe	Ile	
1				5					10					15		
Ser	Ile	Gly	Leu	Asp	Glu	Lys	Thr	Ala	Arg	Asn	Thr	Ile	Asn	Asn	Asn	
			20					25					30			
Lys	Val	Thr	Ala	Asn	Leu	Thr	Ala	Val	Ile	His	Glu	Ala	Ala	Val	Thr	
		35					40					45				
Asp	Gly	Cys	Asp	Arg	Asn	Thr	Gly	Asn	Leu	Leu	Tyr	Ser	Val	Ala	Thr	
	50					55					60					
Lys	Phe	Pro	Thr	Asn	Ala	Leu	Val	His	Arg	Pro	Thr	Leu	Leu	Lys	Tyr	
65					70					75					80	
Ile	Val	Asn	Ser	Lys	Ile	Lys	Thr	Pro	Ala	Gln	Leu	Glu	Ala	Ala	Phe	
				85					90					95		
Ala	Phe	Phe	Ala	Ser	Thr	Gly	Pro	Glu	Asp	Phe	Lys	Leu	Asn	Glu	Phe	
			100					105					110			

PF59083SeqList PF59083.txt

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

PF59083SeqList PF59083.txt

```

        660
Thr Val Arg Glu Ile His Ala Glu Tyr Asp Pro Glu Lys Lys Ser Lys
        675
Pro Lys Gly Val Leu His Trp Val Ala Glu Ser Ser Pro Gly Glu Glu
        690
Pro Ile Lys Val Glu Val Arg Leu Phe Glu Lys Leu Phe Asn Ser Glu
        705
Asn Pro Ala Glu Leu Asn Asp Ala Trp Leu Thr Asp Ile Asn Pro Asn
        720
Ser Lys Met Val Ile Ser Gly Ala Tyr Ala Val Ser Thr Leu Lys Asp
        735
Ala Ala Val Gly Asp Arg Phe Gln Phe Glu Arg Leu Gly Tyr Tyr Ala
        750
Val Asp Lys Asp Ser Glu Pro Gly Lys Leu Val Phe Asn Arg Thr Val
        765
Thr Leu Arg Asp Ser Tyr Gly Lys Gly Gly Lys
        780
        785
        790
        795

```

<210> 9939

<211> 2328

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(2328)

<400> 9939

```

atg gct act cca gat tcg cta gcg ctg ttc acc ggc ctt ggc ctt agc      48
Met Ala Thr Pro Asp Ser Leu Ala Leu Phe Thr Gly Leu Gly Leu Ser
1      5      10      15
gag aac aag gcc cgc gag acg ctc aag aac gag gct ctg agc act cag      96
Glu Asn Lys Ala Arg Glu Thr Leu Lys Asn Glu Ala Leu Ser Thr Gln
20      25      30
ctg cgc gag gcg gcg acc cag gca cac cag att ctg ggt tct acc atc      144
Leu Arg Glu Ala Ala Thr Gln Ala His Gln Ile Leu Gly Ser Thr Ile
35      40      45
gac aag gct act ggg gtc ctc cta tat gac ttg gtc tcc cga ctc agg      192
Asp Lys Ala Thr Gly Val Leu Leu Tyr Asp Leu Val Ser Arg Leu Arg
50      55      60
gat act cgg cgt cgt tct ttc ctt gtg agc tat ata gcc aat aag aag      240
Asp Thr Arg Arg Arg Ser Phe Leu Val Ser Tyr Ile Ala Asn Lys Lys
65      70      75      80
att cac acg gga ctc cag ctg agc gct gct ctt gaa tat gtt cgg agt      288
Ile His Thr Gly Leu Gln Leu Ser Ala Leu Glu Tyr Val Arg Ser
85      90      95
cat ccc cag gat ccc att gat acc aag gac ttc gag cag gag tgt ggc      336
His Pro Gln Asp Pro Ile Asp Thr Lys Asp Phe Glu Gln Glu Cys Gly
100      105      110
gtc ggt gtg gtg gtc aca ccg gag cag att gag gaa gct gtg gag tcc      384
Val Gly Val Val Val Thr Pro Glu Gln Ile Glu Glu Ala Val Glu Ser
115      120      125
acc ata aat aag cat cag ttg cag ctc cta gcg gaa cgg tac cgt ttc      432
Thr Ile Asn Lys His Gln Leu Gln Leu Leu Ala Glu Arg Tyr Arg Phe
130      135      140
aac atg ggg ctg cta atg gga gag gct cgg gct gcg ctc aga tgg gca      480
Asn Met Gly Leu Leu Met Gly Glu Ala Arg Ala Ala Leu Arg Trp Ala
145      150      155      160
gac ggc aaa atg atc aag aac gag gtg gat atg cag gtg ctt cac ctt      528
Asp Gly Lys Met Ile Lys Asn Glu Val Asp Met Gln Val Leu His Leu
165      170      175
ttg ggg ccc aag atg gaa gct gat ctg gtg aag aag ccc aag gtg gca      576
Leu Gly Pro Lys Met Glu Ala Asp Leu Val Lys Lys Pro Lys Val Ala
180      185      190
aag gca cgg ctg gaa gaa aca gac cgg aag aca gca aaa gat gtg gtg      624
Lys Ala Arg Leu Glu Glu Thr Asp Arg Lys Thr Ala Lys Asp Val Val
195      200      205
gag aaa ggt gaa gtg gct ggc cag acc ctg tct ctg atg gag cag ctc      672
Glu Lys Gly Glu Val Ala Gly Gln Thr Leu Ser Met Glu Glu Leu

```

PF59083SeqList PF59083.txt

210	cgg	ggg	gag	gca	ctt	aag	ttt	cat	aag	cca	ggt	gag	aac	tac	aag	acg	720
	Arg	Gly	Glu	Ala	Leu	Lys	Phe	His	Lys	Pro	Gly	Glu	Asn	Tyr	Lys	Thr	
225	cca	ggc	tat	gtg	atc	act	cca	tat	acc	atg	gat	ctg	ctg	aag	cag	cac	768
	Pro	Gly	Tyr	Val	Ile	Thr	Pro	Tyr	Thr	Met	Asp	Leu	Leu	Lys	Gln	His	
					245					250					255		
	ctg	gag	atc	act	ggg	gga	cag	gta	cgt	acg	cgg	ttc	cct	cca	gag	ccc	816
	Leu	Glu	Ile	Thr	Gly	Gly	Gln	Val	Arg	Thr	Arg	Phe	Pro	Pro	Glu	Pro	
				260					265					270			
	aat	gga	atc	ctg	cat	att	gga	cac	gcc	aaa	gcc	atc	aat	ttc	aac	ttt	864
	Asn	Gly	Ile	Leu	His	Ile	Gly	His	Ala	Lys	Ala	Ile	Asn	Phe	Asn	Phe	
			275					280					285				
	ggt	tat	gcc	aag	gcc	aac	aat	ggt	atc	tgt	ttt	ctg	cgc	ttt	gat	gac	912
	Gly	Tyr	Ala	Lys	Ala	Asn	Asn	Gly	Ile	Cys	Phe	Leu	Arg	Phe	Asp	Asp	
			290				295					300					
	acc	aac	cct	gag	aaa	gaa	gaa	gca	aaa	ttc	ttc	act	gct	att	tat	gac	960
	Thr	Asn	Pro	Glu	Lys	Glu	Glu	Ala	Lys	Phe	Phe	Thr	Ala	Ile	Tyr	Asp	
	305				310					315						320	
	atg	gtg	acc	tgg	ctg	ggt	tat	aca	cct	tac	aaa	gtg	aca	tat	gct	tct	1008
	Met	Val	Thr	Trp	Leu	Gly	Tyr	Thr	Pro	Tyr	Lys	Val	Thr	Tyr	Ala	Ser	
					325					330					335		
	gac	tat	ttt	gac	cag	ctg	tat	gcc	tgg	gcc	gtg	gaa	ctc	atc	cat	ggg	1056
	Asp	Tyr	Phe	Asp	Gln	Leu	Tyr	Ala	Trp	Ala	Val	Glu	Leu	Ile	His	Gly	
				340					345					350			
	ggt	ctt	gct	tat	gtg	tgt	cac	cag	aga	gtg	gaa	gag	ctc	aaa	ggc	cat	1104
	Gly	Leu	Ala	Tyr	Val	Cys	His	Gln	Arg	Val	Glu	Glu	Leu	Lys	Gly	His	
			355					360					365				
	aac	cct	tta	cct	tct	cca	tgg	agg	gac	agg	cct	aag	gaa	gaa	tca	ttg	1152
	Asn	Pro	Leu	Pro	Ser	Pro	Trp	Arg	Asp	Arg	Pro	Lys	Glu	Glu	Ser	Leu	
			370				375					380					
	ctg	ctc	ttt	gag	gca	atg	cgc	aag	ggc	aaa	ttt	gca	gaa	gga	gag	gcc	1200
	Leu	Leu	Phe	Glu	Ala	Met	Arg	Lys	Gly	Lys	Phe	Ala	Glu	Gly	Glu	Ala	
	385					390					395					400	
	aca	ctt	cga	atg	aag	ttg	gtg	atg	gaa	gat	ggc	aag	atg	gac	ccc	gtg	1248
	Thr	Leu	Arg	Met	Lys	Leu	Val	Met	Glu	Asp	Gly	Lys	Met	Asp	Pro	Val	
					405					410					415		
	gcc	tat	cga	gtc	aag	tac	acg	cca	cac	cat	cgc	aca	ggg	gac	aaa	tgg	1296
	Ala	Tyr	Arg	Val	Lys	Tyr	Thr	Pro	His	His	Arg	Thr	Gly	Asp	Lys	Trp	
				420					425					430			
	tgc	atc	tac	ccc	acc	tat	gac	tac	aca	cat	tgt	ctg	tgt	gac	tcc	att	1344
	Cys	Ile	Tyr	Pro	Thr	Tyr	Asp	Tyr	Thr	His	Cys	Leu	Cys	Asp	Ser	Ile	
			435				440						445				
	gag	cac	att	acc	cac	tcg	ttg	tgt	acc	aag	gag	ttc	cag	gct	cga	cgg	1392
	Glu	His	Ile	Thr	His	Ser	Leu	Cys	Thr	Lys	Glu	Phe	Gln	Ala	Arg	Arg	
			450				455					460					
	tct	tcc	tac	ttt	tgg	tta	tgt	aac	gct	ctg	aaa	gtc	tat	tgt	cct	gtt	1440
	Ser	Ser	Tyr	Phe	Trp	Leu	Cys	Asn	Ala	Leu	Lys	Val	Tyr	Cys	Pro	Val	
	465				470					475						480	
	cag	tgg	gaa	tat	ggt	cgc	ctc	aat	ttg	cac	tat	gct	gtt	gtc	tca	aag	1488
	Gln	Trp	Glu	Tyr	Gly	Arg	Leu	Asn	Leu	His	Tyr	Ala	Val	Val	Ser	Lys	
					485					490					495		
	cgc	aag	att	ctc	cag	ctt	gta	gca	gct	ggt	gct	gtt	cgg	gac	tgg	gac	1536
	Arg	Lys	Ile	Leu	Gln	Leu	Val	Ala	Ala	Gly	Ala	Val	Arg	Asp	Trp	Asp	
				500					505					510			
	gat	cca	cgg	ctc	ttc	aca	ctc	act	gcc	cta	cga	cga	cgg	ggt	ttt	cca	1584
	Asp	Pro	Arg	Leu	Phe	Thr	Leu	Thr	Ala	Leu	Arg	Arg	Arg	Gly	Phe	Pro	
			515					520					525				
	cca	gag	gct	atc	aac	aac	ttc	tgt	gct	cgg	gtt	ggg	gtc	aca	gtg	gca	1632
	Pro	Glu	Ala	Ile	Asn	Asn	Phe	Cys	Ala	Arg	Val	Gly	Val	Thr	Val	Ala	
			530				535					540					
	cag	acc	aca	atg	gaa	cct	cat	ctt	ctg	gaa	gcc	tgt	gtg	cgt	gat	gtg	1680
	Gln	Thr	Thr	Met	Glu	Pro	His	Leu	Leu	Glu	Ala	Cys	Val	Arg	Asp	Val	
	545					550				555						560	
	ctg	aat	gat	gca	gcc	cca	cgt	gcc	atg	gct	gtt	cta	gag	cca	cta	caa	1728
	Leu	Asn	Asp	Ala	Ala	Pro	Arg	Ala	Met	Ala	Val	Leu	Glu	Pro	Leu	Gln	
				565					570						575		
	gtt	gtc	atc	acc	aac	ttt	cct	gct	ccc	aag	ccc	ttg	gac	atc	cga	gtg	1776
	Val	Val	Ile	Thr	Asn	Phe	Pro	Ala	Pro	Lys	Pro	Leu	Asp	Ile	Arg	Val	

PF59083SeqList PF59083.txt

	580	585	590	
cca aat ttc cca gct gat gag acc aag ggt ttc cac cag gtt cct ttt	1824			
Pro Asn Phe Pro Ala Asp Glu Thr Lys Gly Phe His Gln Val Pro Phe				
gct tcc act gtc ttc att gag aga agc gac ttt aag gag gag tca gaa	1872			
Ala Ser Thr Val Phe Ile gag Arg Ser Asp Phe Lys Glu Glu Ser Glu				
cca ggc tat aag cgc cta gct tcg ggc cag cct gtg ggc ctg aga cac	1920			
Pro Gly Tyr Lys Arg Leu Ala Ser Gly Gln Pro Val Gly Leu Arg His				
act ggt tat gtc att gaa ctg cag aat att gtc agg ggc tcc agt ggc	1968			
Thr Gly Tyr Val Ile Glu Leu Gln Asn Ile Val Arg Gly Ser Ser Gly				
tgt gtg gaa cgc ttg gag gtg acc tgt aga cga gct gat gct gga gag	2016			
Cys Val Glu Arg Leu Glu Val Thr Cys Arg Arg Ala Asp Ala Gly Glu				
aag ccc aag gcc ttt att cac tgg gta tca cag cct ttg gtg tgt gag	2064			
Lys Pro Lys Ala Phe Ile His Trp Val Ser Gln Pro Leu Val Cys Glu				
att cgc ctc tat gag cgc cta ttc cag cac aag aac ccc gaa gac cct	2112			
Ile Arg Leu Tyr Glu Arg Leu Phe Gln His Lys Asn Pro Glu Asp Pro				
gtt gaa gtg cct ggt gga ttc cta agt gac ctg aac ccg gcg tca cta	2160			
Val Glu Val Pro Gly Gly Phe Leu Ser Asp Leu Asn Pro Ala Ser Leu				
caa gtg gta gaa gga gca tta gtg gac tgc tct gtg gct ttg gca aag	2208			
Gln Val Val Glu Gly Ala Leu Val Asp Cys Ser Val Ala Leu Ala Lys				
ccc ttt gac aag ttc cag ttt gag cgc ctt ggg tac ttc tct gtg gat	2256			
Pro Phe Asp Lys Phe Gln Phe Glu Arg Leu Gly Tyr Phe Ser Val Asp				
cca gac agc cat caa gga cag att gtc ttc aac cga act gtc aca cta	2304			
Pro Asp Ser His Gln Gly Gln Ile Val Phe Asn Arg Thr Val Thr Leu				
aaa gaa gac cca ggc aaa ata tga	2328			
Lys Glu Asp Pro Gly Lys Ile				

<210> 9940

<211> 775

<212> PRT

<213> Mus musculus

<400> 9940

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

PF59083SeqList PF59083.txt

		195				200				205					
Glu	Lys	Gly	Glu	Val	Ala	Gly	Gln	Thr	Leu	Ser	Leu	Met	Glu	Gln	Leu
	210					215					220				
Arg	Gly	Glu	Ala	Leu	Lys	Phe	His	Lys	Pro	Gly	Glu	Asn	Tyr	Lys	Thr
225					230					235					240
Pro	Gly	Tyr	Val	Ile	Thr	Pro	Tyr	Thr	Met	Asp	Leu	Leu	Lys	Gln	His
				245					250					255	
Leu	Glu	Ile	Thr	Gly	Gly	Gln	Val	Arg	Thr	Arg	Phe	Pro	Pro	Glu	Pro
			260					265					270		
Asn	Gly	Ile	Leu	His	Ile	Gly	His	Ala	Lys	Ala	Ile	Asn	Phe	Asn	Phe
		275					280					285			
Gly	Tyr	Ala	Lys	Ala	Asn	Asn	Gly	Ile	Cys	Phe	Leu	Arg	Phe	Asp	Asp
	290					295					300				
Thr	Asn	Pro	Glu	Lys	Glu	Glu	Ala	Lys	Phe	Phe	Thr	Ala	Ile	Tyr	Asp
305					310					315					320
Met	Val	Thr	Trp	Leu	Gly	Tyr	Thr	Pro	Tyr	Lys	Val	Thr	Tyr	Ala	Ser
				325					330					335	
Asp	Tyr	Phe	Asp	Gln	Leu	Tyr	Ala	Trp	Ala	Val	Glu	Leu	Ile	His	Gly
			340					345					350		
Gly	Leu	Ala	Tyr	Val	Cys	His	Gln	Arg	Val	Glu	Glu	Leu	Lys	Gly	His
		355					360					365			
Asn	Pro	Leu	Pro	Ser	Pro	Trp	Arg	Asp	Arg	Pro	Lys	Glu	Glu	Ser	Leu
	370					375					380				
Leu	Leu	Phe	Glu	Ala	Met	Arg	Lys	Gly	Lys	Phe	Ala	Glu	Gly	Glu	Ala
385					390					395					400
Thr	Leu	Arg	Met	Lys	Leu	Val	Met	Glu	Asp	Gly	Lys	Met	Asp	Pro	Val
				405					410					415	
Ala	Tyr	Arg	Val	Lys	Tyr	Thr	Pro	His	His	Arg	Thr	Gly	Asp	Lys	Trp
			420					425					430		
Cys	Ile	Tyr	Pro	Thr	Tyr	Asp	Tyr	Thr	His	Cys	Leu	Cys	Asp	Ser	Ile
		435					440					445			
Glu	His	Ile	Thr	His	Ser	Leu	Cys	Thr	Lys	Glu	Phe	Gln	Ala	Arg	Arg
	450					455					460				
Ser	Ser	Tyr	Phe	Trp	Leu	Cys	Asn	Ala	Leu	Lys	Val	Tyr	Cys	Pro	Val
465					470					475					480
Gln	Trp	Glu	Tyr	Gly	Arg	Leu	Asn	Leu	His	Tyr	Ala	Val	Val	Ser	Lys
				485					490					495	
Arg	Lys	Ile	Leu	Gln	Leu	Val	Ala	Ala	Gly	Ala	Val	Arg	Asp	Trp	Asp
			500					505					510		
Asp	Pro	Arg	Leu	Phe	Thr	Leu	Thr	Ala	Leu	Arg	Arg	Arg	Gly	Phe	Pro
		515					520						525		
Pro	Glu	Ala	Ile	Asn	Asn	Phe	Cys	Ala	Arg	Val	Gly	Val	Thr	Val	Ala
	530					535					540				
Gln	Thr	Thr	Met	Glu	Pro	His	Leu	Leu	Glu	Ala	Cys	Val	Arg	Asp	Val
545					550					555					560
Leu	Asn	Asp	Ala	Ala	Pro	Arg	Ala	Met	Ala	Val	Leu	Glu	Pro	Leu	Gln
				565					570					575	
Val	Val	Ile	Thr	Asn	Phe	Pro	Ala	Pro	Lys	Pro	Leu	Asp	Ile	Arg	Val
			580					585					590		
Pro	Asn	Phe	Pro	Ala	Asp	Glu	Thr	Lys	Gly	Phe	His	Gln	Val	Pro	Phe
		595					600					605			
Ala	Ser	Thr	Val	Phe	Ile	Glu	Arg	Ser	Asp	Phe	Lys	Glu	Glu	Ser	Glu
	610					615				620					
Pro	Gly	Tyr	Lys	Arg	Leu	Ala	Ser	Gly	Gln	Pro	Val	Gly	Leu	Arg	His
625					630					635					640
Thr	Gly	Tyr	Val	Ile	Glu	Leu	Gln	Asn	Ile	Val	Arg	Gly	Ser	Ser	Gly
				645					650					655	
Cys	Val	Glu	Arg	Leu	Glu	Val	Thr	Cys	Arg	Arg	Ala	Asp	Ala	Gly	Glu
			660					665					670		
Lys	Pro	Lys	Ala	Phe	Ile	His	Trp	Val	Ser	Gln	Pro	Leu	Val	Cys	Glu
		675					680					685			
Ile	Arg	Leu	Tyr	Glu	Arg	Leu	Phe	Gln	His	Lys	Asn	Pro	Glu	Asp	Pro
	690					695					700				
Val	Glu	Val	Pro	Gly	Gly	Phe	Leu	Ser	Asp	Leu	Asn	Pro	Ala	Ser	Leu
705					710					715					720
Gln	Val	Val	Glu	Gly	Ala	Leu	Val	Asp	Cys	Ser	Val	Ala	Leu	Ala	Lys
				725					730					735	
Pro	Phe	Asp	Lys	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Phe	Ser	Val	Asp
			740					745					750		

PF59083SeqList PF59083.txt

Pro Asp Ser His Gln Gly Gln Ile Val Phe Asn Arg Thr Val Thr Leu
 755 760 765
 Lys Glu Asp Pro Gly Lys Ile
 770 775

<210> 9941
 <211> 2397
 <212> DNA
 <213> Eremothecium gossypii

<220>
 <221> CDS
 <222> (1)..(2397)

<400> 9941
 atg tca tct gtt gag gag cta agc cag ctg ttc gca gat gtg ggg ttt 48
 Met Ser Ser Val Glu Glu Leu Ser Gln Leu Phe Ala Asp Val Gly Phe
 1 5 10 15
 gag gaa gcg aag gtg aag gag ata gtc aag aac aag aag gtt gca cac 96
 Glu Glu Ala Lys Val Lys Glu Ile Val Lys Asn Lys Lys Val Ala His
 20 25 30
 tcg ctg gaa gaa ctg gtt cgc gaa gca ggg gcg agg gcc gaa tgg gac 144
 Ser Leu Glu Glu Leu Val Arg Glu Ala Gly Ala Arg Ala Glu Trp Asp
 35 40 45
 aag ggt aag cgt gcg cta ctg cac acg ctt gca agc tcc ttg aag ggg 192
 Lys Gly Lys Arg Ala Leu Leu His Thr Leu Ala Ser Ser Leu Lys Gly
 50 55 60
 gcc acg gtc acc ggg cag aac ctg gtt gcc gag ggc atc cgc agc ggt 240
 Ala Thr Val Thr Gly Gln Asn Leu Val Ala Glu Gly Ile Arg Ser Gly
 65 70 75 80
 gaa ctg aag aca tcg ttg cag gtg gat gcg gcc ctg aag tat gtc aag 288
 Glu Leu Lys Thr Ser Leu Gln Val Asp Ala Ala Leu Lys Tyr Val Lys
 85 90 95
 cgg gcg ggc gag gga gcc aca gtg gcc gag atg cac gct gag agc ggc 336
 Arg Ala Gly Glu Gly Ala Thr Val Ala Glu Met His Ala Glu Ser Gly
 100 105 110
 gta ggc gtc cag gtg acg gaa gac cag gtg cag gcg cgc gtg gtg cag 384
 Val Gly Val Gln Val Thr Glu Asp Gln Val Gln Ala Arg Val Val Gln
 115 120 125
 tat ctc gaa gag aac cgc gcg aag atc gaa agc gag cgt tac aag ttg 432
 Tyr Leu Glu Glu Asn Arg Ala Lys Ile Glu Ser Glu Arg Tyr Lys Leu
 130 135 140
 gtt cca ggc atc ttt gcg cag atc aag gcg ttg ccc gag ctg aag tgg 480
 Val Pro Gly Ile Phe Ala Gln Ile Lys Ala Leu Pro Glu Leu Lys Trp
 145 150 155 160
 gcg gac ccg cgg ctg ttc aag cct att att gat cgc gag gta ttg aaa 528
 Ala Asp Pro Arg Leu Phe Lys Pro Ile Ile Asp Arg Glu Val Leu Lys
 165 170 175
 atc ctt ggg ccc aag gat gag cgc gat gtt gtt aag aag gaa aag aag 576
 Ile Leu Gly Pro Lys Asp Glu Arg Asp Val Val Lys Lys Glu Lys Lys
 180 185 190
 aaa gag cct aaa acg aac gac aaa aag aag gcc gcg gtg gag gag gct 624
 Lys Glu Pro Lys Thr Asn Asp Lys Lys Lys Ala Ala Val Glu Glu Ala
 195 200 205
 cct aag cgc acg atg ttc tcc gaa ggt ttt cta gcc gac ctg cac aaa 672
 Pro Lys Arg Thr Met Phe Ser Glu Gly Phe Leu Gly Asp Leu His Lys
 210 215 220
 gtt gga gag aac cca cag gcc tac cca gag ctg atg gta gaa cac ttg 720
 Val Gly Glu Asn Pro Gln Ala Tyr Pro Glu Leu Met Val Glu His Leu
 225 230 235 240
 aaa gcc act ggc ggc aag gtg cac acg cgt ttc cca cct gag cca aac 768
 Lys Ala Thr Gly Gly Lys Val His Thr Arg Phe Pro Pro Glu Pro Asn
 245 250 255
 gga tac cta cac atc ggt cac tcg aag gcc atc atg gtg aac ttt ggc 816
 Gly Tyr Leu His Ile Gly His Ser Lys Ala Ile Met Val Asn Phe Gly
 260 265 270
 tat gcg aag cat cac ggc ggt gtc tgc tac ttg cgt ttt gac gat acc 864
 Tyr Ala Lys His His Gly Gly Val Cys Tyr Leu Arg Phe Asp Asp Thr
 275 280 285

PF59083SeqList PF59083.txt

aac	cca	gag	gca	gaa	gca	cca	gaa	tat	ttt	gaa	agt	att	gag	aga	atg	912
Asn	Pro	Glu	Ala	Glu	Ala	Pro	Glu	Tyr	Phe	Glu	Ser	Ile	Glu	Arg	Met	
	290					295				300						
gtg	gca	ttg	ttg	ggg	ttc	agt	cca	ttg	aag	atc	aca	tac	tcg	agc	gac	960
Val	Ala	Trp	Leu	Gly	Phe	Ser	Pro	Trp	Lys	Ile	Thr	Tyr	Ser	Ser	Asp	
305				310						315					320	
tac	ttt	gac	cag	cta	tat	gaa	ctt	gcc	gaa	gtt	ctg	atc	aag	aat	ggt	1008
Tyr	Phe	Asp	Gln	Leu	Tyr	Glu	Leu	Ala	Glu	Val	Leu	Ile	Lys	Asn	Gly	
			325					330						335		
aag	gga	tac	atc	tgt	cac	tgt	act	gcg	gaa	gag	ata	aga	cgt	gga	cgg	1056
Lys	Gly	Tyr	Ile	Cys	His	Cys	Thr	Ala	Glu	Glu	Ile	Arg	Arg	Gly	Arg	
			340					345					350			
ggt	atc	aag	gag	gac	ggt	aca	cca	ggt	ggc	gag	aga	ctg	cca	tgt	gcc	1104
Gly	Ile	Lys	Glu	Asp	Gly	Thr	Pro	Gly	Gly	Glu	Arg	Leu	Pro	Cys	Ala	
		355					360					365				
cac	cgt	gaa	cgg	ccc	att	gag	gag	aac	ctt	gct	gag	ttc	agg	aac	atg	1152
His	Arg	Glu	Arg	Pro	Ile	Glu	Glu	Asn	Leu	Ala	Glu	Phe	Arg	Asn	Met	
	370					375					380					
cgc	gat	ggc	aaa	tat	gct	ccc	gga	gag	gct	att	ctc	cgt	atg	aag	cag	1200
Arg	Asp	Gly	Lys	Tyr	Ala	Pro	Gly	Glu	Ala	Ile	Leu	Arg	Met	Lys	Gln	
385				390						395					400	
gat	ctg	tct	tct	cct	tct	ccg	cag	atg	ttg	gat	tta	gtt	gcc	tac	aga	1248
Asp	Leu	Ser	Ser	Pro	Ser	Pro	Gln	Met	Trp	Asp	Leu	Val	Ala	Tyr	Arg	
				405				410						415		
gtc	ttg	aac	gct	cca	cac	cca	aga	acg	ggg	tcc	aaa	ttg	cgc	atc	tat	1296
Val	Leu	Asn	Ala	Pro	His	Pro	Arg	Thr	Gly	Ser	Lys	Trp	Arg	Ile	Tyr	
			420					425					430			
cct	acc	tat	gac	ttc	aca	cac	tgt	ctt	gtt	gat	tct	ctg	gag	aac	att	1344
Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys	Leu	Val	Asp	Ser	Leu	Glu	Asn	Ile	
		435					440					445				
acc	cat	tct	ctg	tgc	acc	gcc	gag	ttc	tat	tta	tcg	cgc	gag	tcg	tat	1392
Thr	His	Ser	Leu	Cys	Thr	Ala	Glu	Phe	Tyr	Leu	Ser	Arg	Glu	Ser	Tyr	
	450					455					460					
gaa	ttg	ttg	tgc	gat	caa	gtg	cat	gtc	ttc	aga	cct	gct	caa	agg	gag	1440
Glu	Trp	Leu	Cys	Asp	Gln	Val	His	Val	Phe	Arg	Pro	Ala	Gln	Arg	Glu	
465				470						475					480	
tat	ggt	cgt	ctg	aat	atc	aca	ggc	act	gta	ttg	tct	aag	cgc	aag	atc	1488
Tyr	Gly	Arg	Leu	Asn	Ile	Thr	Gly	Thr	Val	Leu	Ser	Lys	Arg	Lys	Ile	
				485				490						495		
gcc	aag	ctt	gtc	cac	gag	aaa	tac	gtc	cgt	ggc	ttg	gat	gat	ccc	cgt	1536
Ala	Lys	Leu	Val	His	Glu	Lys	Tyr	Val	Arg	Gly	Trp	Asp	Asp	Pro	Arg	
			500					505					510			
ctc	ttc	acc	ctt	gag	gct	att	cgc	agg	cgc	ggt	gtc	cca	cct	gga	gcc	1584
Leu	Phe	Thr	Leu	Glu	Ala	Ile	Arg	Arg	Arg	Gly	Val	Pro	Pro	Gly	Ala	
		515					520					525				
atc	ctc	tcc	ttc	att	aat	acg	ctg	ggt	gtc	acc	act	agt	act	aca	aac	1632
Ile	Leu	Ser	Phe	Ile	Asn	Thr	Leu	Gly	Val	Thr	Thr	Ser	Thr	Thr	Asn	
		530				535				540						
atc	cag	gtt	gtc	cgt	ttt	gag	agt	gca	atc	aga	aag	tac	ctc	gaa	gac	1680
Ile	Gln	Val	Val	Arg	Phe	Glu	Ser	Ala	Ile	Arg	Lys	Tyr	Leu	Glu	Asp	
545					550					555					560	
acc	act	gca	cgc	ttg	atg	ttt	gtc	tta	gat	ccc	ata	gaa	gtc	atc	gtg	1728
Thr	Thr	Ala	Arg	Leu	Met	Phe	Val	Leu	Asp	Pro	Ile	Glu	Val	Ile	Val	
				565					570					575		
gac	aac	ttg	cca	gag	gac	tat	gag	gag	ctt	gta	tcg	att	cct	tac	cgc	1776
Asp	Asn	Leu	Pro	Glu	Asp	Tyr	Glu	Glu	Leu	Val	Ser	Ile	Pro	Tyr	Arg	
			580					585					590			
cca	ggc	acg	cca	gag	ttc	gga	gag	agg	acg	gtt	ccc	ttc	agc	aag	cgt	1824
Pro	Gly	Thr	Pro	Glu	Phe	Gly	Glu	Arg	Thr	Val	Pro	Phe	Ser	Lys	Arg	
		595				600						605				
ttc	tac	atc	gag	cgt	tcc	gat	ttc	tct	gag	gac	acc	tct	gac	aaa	gag	1872
Phe	Tyr	Ile	Glu	Arg	Ser	Asp	Phe	Ser	Glu	Asp	Thr	Ser	Asp	Lys	Glu	
		610				615					620					
ttc	ttc	cgt	ctc	acg	cct	gct	caa	tcg	gta	ggg	ctc	atc	aag	gtg	cca	1920
Phe	Phe	Arg	Leu	Thr	Pro	Ala	Gln	Ser	Val	Gly	Leu	Ile	Lys	Val	Pro	
625					630					635					640	
tac	act	atc	gcc	ttc	aag	agc	cta	gag	cgt	gat	gcg	aac	gga	aag	atc	1968
Tyr	Thr	Ile	Ala	Phe	Lys	Ser	Leu	Glu	Arg	Asp	Ala	Asn	Gly	Lys	Ile	
				645					650					655		

PF59083SeqList PF59083.txt

acg	cgt	att	cac	gcc	cac	tat	gag	aac	gac	aca	cct	gat	ggg	aag	cct		2016
Thr	Arg	Ile	His	Ala	His	Tyr	Glu	Asn	Asp	Thr	Pro	Asp	Gly	Lys	Pro		
			660					665					670				
cgc	aag	cca	aag	acc	tac	atc	cag	tgg	gtt	cct	att	gca	cct	cgc	cat		2064
Arg	Lys	Pro	Lys	Thr	Tyr	Ile	Gln	Trp	Val	Pro	Ile	Ala	Pro	Arg	His		
			675					680					685				
ggg	tct	cct	atc	cca	gtt	gca	gaa	acg	cgt	gtt	tac	aac	cag	ctg	ttc		2112
Gly	Ser	Pro	Ile	Pro	Val	Ala	Glu	Thr	Arg	Val	Tyr	Asn	Gln	Leu	Phe		
			690				695					700					
act	tca	gag	aac	cca	agc	gga	gac	cca	gcc	gac	atc	aac	cct	tac	agt		2160
Thr	Ser	Glu	Asn	Pro	Ser	Gly	Asp	Pro	Ala	Asp	Ile	Asn	Pro	Tyr	Ser		
																720	
gag	gtc	ata	tat	cct	tcc	gcg	gtc	gtc	gag	cac	aac	ttc	cgt	cat	gtc		2208
Glu	Val	Ile	Tyr	Pro	Ser	Ala	Val	Val	Glu	His	Asn	Phe	Arg	His	Val		
																735	
gtc	tct	aac	tct	ccg	tgg	gtc	gtc	gaa	agc	gcc	aag	cag	tcc	gag	ttc		2256
Val	Ser	Asn	Ser	Pro	Trp	Val	Val	Glu	Ser	Ala	Lys	Gln	Ser	Glu	Phe		
																750	
tac	gtc	cca	gag	gaa	cat	gat	cgc	aaa	gag	gtc	tgc	cgt	ttc	cag	gct		2304
Tyr	Val	Pro	Glu	Glu	His	Asp	Arg	Lys	Glu	Val	Cys	Arg	Phe	Gln	Ala		
																765	
atg	cgc	gta	ggc	tac	ttc	acg	ctt	gac	aag	gac	agt	acc	cat	gac	cgc		2352
Met	Arg	Val	Gly	Tyr	Phe	Thr	Leu	Asp	Lys	Asp	Ser	Thr	His	Asp	Arg		
																780	
atc	atc	ctc	aac	cgc	att	gtc	agc	ctc	aaa	gat	ggc	tcc	aag	tag			2397
Ile	Ile	Leu	Asn	Arg	Ile	Val	Ser	Leu	Lys	Asp	Gly	Ser	Lys				
																795	

<210> 9942

<211> 798

<212> PRT

<213> Erethothecium gossypii

<400> 9942

Met	Ser	Ser	Val	Glu	Glu	Leu	Ser	Gln	Leu	Phe	Ala	Asp	Val	Gly	Phe		
1				5				10						15			
Glu	Glu	Ala	Lys	Val	Lys	Glu	Ile	Val	Lys	Asn	Lys	Lys	Val	Ala	His		
				20				25						30			
Ser	Leu	Glu	Glu	Leu	Val	Arg	Glu	Ala	Gly	Ala	Arg	Ala	Glu	Trp	Asp		
				35				40					45				
Lys	Gly	Lys	Arg	Ala	Leu	Leu	His	Thr	Leu	Ala	Ser	Ser	Leu	Lys	Gly		
				50				55				60					
Ala	Thr	Val	Thr	Gly	Gln	Asn	Leu	Val	Ala	Glu	Gly	Ile	Arg	Ser	Gly		
65					70					75				80			
Glu	Leu	Lys	Thr	Ser	Leu	Gln	Val	Asp	Ala	Leu	Lys	Tyr	Val	Lys			
				85					90					95			
Arg	Ala	Gly	Glu	Gly	Ala	Thr	Val	Ala	Glu	Met	His	Ala	Glu	Ser	Gly		
				100				105					110				
Val	Gly	Val	Gln	Val	Thr	Glu	Asp	Gln	Val	Gln	Ala	Arg	Val	Val	Gln		
				115				120					125				
Tyr	Leu	Glu	Glu	Asn	Arg	Ala	Lys	Ile	Glu	Ser	Glu	Arg	Tyr	Lys	Leu		
				130				135				140					
Val	Pro	Gly	Ile	Phe	Ala	Gln	Ile	Lys	Ala	Leu	Pro	Glu	Leu	Lys	Trp		
145					150				155					160			
Ala	Asp	Pro	Arg	Leu	Phe	Lys	Pro	Ile	Ile	Asp	Arg	Glu	Val	Leu	Lys		
				165					170					175			
Ile	Leu	Gly	Pro	Lys	Asp	Glu	Arg	Asp	Val	Val	Lys	Lys	Glu	Lys	Lys		
				180				185						190			
Lys	Glu	Pro	Lys	Thr	Asn	Asp	Lys	Lys	Ala	Ala	Val	Glu	Glu	Ala			
				195				200						205			
Pro	Lys	Arg	Thr	Met	Phe	Ser	Glu	Gly	Phe	Leu	Gly	Asp	Leu	His	Lys		
				210				215				220					
Val	Gly	Glu	Asn	Pro	Gln	Ala	Tyr	Pro	Glu	Leu	Met	Val	Glu	His	Leu		
225					230					235					240		
Lys	Ala	Thr	Gly	Gly	Lys	Val	His	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn		
				245					250					255			
Gly	Tyr	Leu	His	Ile	Gly	His	Ser	Lys	Ala	Ile	Met	Val	Asn	Phe	Gly		
				260				265						270			
Tyr	Ala	Lys	His	His	Gly	Gly	Val	Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr		

PF59083SeqList PF59083.txt

		275				280				285					
Asn	Pro	Glu	Ala	Glu	Ala	Pro	Glu	Tyr	Phe	Glu	Ser	Ile	Glu	Arg	Met
	290					295				300					
Val	Ala	Trp	Leu	Gly	Phe	Ser	Pro	Trp	Lys	Ile	Thr	Tyr	Ser	Ser	Asp
305					310					315					320
Tyr	Phe	Asp	Gln	Leu	Tyr	Glu	Leu	Ala	Glu	Val	Leu	Ile	Lys	Asn	Gly
				325					330					335	
Lys	Gly	Tyr	Ile	Cys	His	Cys	Thr	Ala	Glu	Glu	Ile	Arg	Arg	Gly	Arg
			340					345					350		
Gly	Ile	Lys	Glu	Asp	Gly	Thr	Pro	Gly	Gly	Glu	Arg	Leu	Pro	Cys	Ala
		355					360					365			
His	Arg	Glu	Arg	Pro	Ile	Glu	Glu	Asn	Leu	Ala	Glu	Phe	Arg	Asn	Met
	370					375					380				
Arg	Asp	Gly	Lys	Tyr	Ala	Pro	Gly	Glu	Ala	Ile	Leu	Arg	Met	Lys	Gln
385					390					395					400
Asp	Leu	Ser	Ser	Pro	Ser	Pro	Gln	Met	Trp	Asp	Leu	Val	Ala	Tyr	Arg
				405					410					415	
Val	Leu	Asn	Ala	Pro	His	Pro	Arg	Thr	Gly	Ser	Lys	Trp	Arg	Ile	Tyr
			420					425					430		
Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys	Leu	Val	Asp	Ser	Leu	Glu	Asn	Ile
		435					440					445			
Thr	His	Ser	Leu	Cys	Thr	Ala	Glu	Phe	Tyr	Leu	Ser	Arg	Glu	Ser	Tyr
	450				455						460				
Glu	Trp	Leu	Cys	Asp	Gln	Val	His	Val	Phe	Arg	Pro	Ala	Gln	Arg	Glu
465					470					475					480
Tyr	Gly	Arg	Leu	Asn	Ile	Thr	Gly	Thr	Val	Leu	Ser	Lys	Arg	Lys	Ile
				485					490					495	
Ala	Lys	Leu	Val	His	Glu	Lys	Tyr	Val	Arg	Gly	Trp	Asp	Asp	Pro	Arg
			500					505					510		
Leu	Phe	Thr	Leu	Glu	Ala	Ile	Arg	Arg	Arg	Gly	Val	Pro	Pro	Gly	Ala
		515					520					525			
Ile	Leu	Ser	Phe	Ile	Asn	Thr	Leu	Gly	Val	Thr	Thr	Ser	Thr	Thr	Asn
	530				535						540				
Ile	Gln	Val	Val	Arg	Phe	Glu	Ser	Ala	Ile	Arg	Lys	Tyr	Leu	Glu	Asp
545					550					555					560
Thr	Thr	Ala	Arg	Leu	Met	Phe	Val	Leu	Asp	Pro	Ile	Glu	Val	Ile	Val
				565					570					575	
Asp	Asn	Leu	Pro	Glu	Asp	Tyr	Glu	Glu	Leu	Val	Ser	Ile	Pro	Tyr	Arg
			580					585					590		
Pro	Gly	Thr	Pro	Glu	Phe	Gly	Glu	Arg	Thr	Val	Pro	Phe	Ser	Lys	Arg
		595					600					605			
Phe	Tyr	Ile	Glu	Arg	Ser	Asp	Phe	Ser	Glu	Asp	Thr	Ser	Asp	Lys	Glu
	610					615					620				
Phe	Phe	Arg	Leu	Thr	Pro	Ala	Gln	Ser	Val	Gly	Leu	Ile	Lys	Val	Pro
625					630					635					640
Tyr	Thr	Ile	Ala	Phe	Lys	Ser	Leu	Glu	Arg	Asp	Ala	Asn	Gly	Lys	Ile
				645					650					655	
Thr	Arg	Ile	His	Ala	His	Tyr	Glu	Asn	Asp	Thr	Pro	Asp	Gly	Lys	Pro
			660					665					670		
Arg	Lys	Pro	Lys	Thr	Tyr	Ile	Gln	Trp	Val	Pro	Ile	Ala	Pro	Arg	His
		675					680					685			
Gly	Ser	Pro	Ile	Pro	Val	Ala	Glu	Thr	Arg	Val	Tyr	Asn	Gln	Leu	Phe
	690					695					700				
Thr	Ser	Glu	Asn	Pro	Ser	Gly	Asp	Pro	Ala	Asp	Ile	Asn	Pro	Tyr	Ser
705					710					715					720
Glu	Val	Ile	Tyr	Pro	Ser	Ala	Val	Val	Glu	His	Asn	Phe	Arg	His	Val
				725					730					735	
Val	Ser	Asn	Ser	Pro	Trp	Val	Val	Glu	Ser	Ala	Lys	Gln	Ser	Glu	Phe
			740					745					750		
Tyr	Val	Pro	Glu	Glu	His	Asp	Arg	Lys	Glu	Val	Cys	Arg	Phe	Gln	Ala
		755					760					765			
Met	Arg	Val	Gly	Tyr	Phe	Thr	Leu	Asp	Lys	Asp	Ser	Thr	His	Asp	Arg
	770					775					780				
Ile	Ile	Leu	Asn	Arg	Ile	Val	Ser	Leu	Lys	Asp	Gly	Ser	Lys		
785					790					795					

<210> 9943
 <211> 2325
 <212> DNA

<213> Anopheles gambiae str. PEST

<220>

<221> CDS

<222> (1)..(2325)

<400> 9943

atg acc acg atg gaa cat ctc gtt tct ctc ggt cta aat gag caa aaa	48
Met Thr Thr Met Glu His Leu Val Ser Leu Gly Leu Asn Glu Gln Lys	
1 5 10 15	
atc aag gaa acg ctt aaa aac gca acc ctt act agc aca att aca cgt	96
Ile Lys Glu Thr Leu Lys Asn Ala Thr Leu Thr Ser Thr Ile Thr Arg	
20 25 30	
gcc ttc tct tac gtc ccg ccg ggt gtg gag tta agt tca gca caa aaa	144
Ala Phe Ser Tyr Val Pro Pro Gly Val Glu Leu Ser Ser Ala Gln Lys	
35 40 45	
ccg ctg ata ttt cag gca tgc tca aag ata aaa ccg cag acg gct cac	192
Pro Leu Ile Phe Gln Ala Cys Ser Lys Ile Lys Pro Gln Thr Ala His	
50 55 60	
cat ttg gaa ctt ata gtg aga aaa att ttg gat aac agt ttg gac act	240
His Leu Glu Leu Ile Val Arg Lys Ile Leu Asp Asn Ser Leu Asp Thr	
65 70 75 80	
agt cta cgt gtt gac acc gca ctg gaa tat gtt ctg gct aac gtg acg	288
Ser Leu Arg Val Asp Thr Ala Leu Glu Tyr Val Leu Ala Asn Val Thr	
85 90 95	
aaa gcc act atc gac gaa gct act ttc gat gcg gct tgc ggt gtg gga	336
Lys Ala Thr Ile Asp Glu Ala Thr Phe Asp Ala Ala Cys Gly Val Gly	
100 105 110	
gta gtt gtg aca ccg gaa gaa atc gag cgg gcg gtt gaa ata acc gtt	384
Val Val Val Thr Pro Glu Glu Ile Glu Arg Ala Val Glu Ile Thr Val	
115 120 125	
gcc aaa tat cgt agc gat atc gtc gac caa cgt tat cgt ttt aat gtc	432
Ala Lys Tyr Arg Ser Asp Ile Val Asp Gln Arg Tyr Arg Phe Asn Val	
130 135 140	
gga aaa ttg ttg agc gaa att cga agt gct ttg cca tgg gtg gat ggt	480
Gly Lys Leu Ser Glu Ile Arg Ser Ala Leu Pro Trp Val Asp Gly	
145 150 155 160	
aaa gcc ctt aaa agt gag gtg gat gtg caa atg ttt gat tta ctt ggc	528
Lys Ala Leu Lys Ser Glu Val Asp Val Gln Met Phe Asp Leu Leu Gly	
165 170 175	
ccc aaa acg gat gcc gat ggc gag aaa gtg ggt aaa aaa cgt cgg gaa	576
Pro Lys Thr Asp Ala Asp Gly Glu Lys Val Gly Lys Lys Arg Arg Glu	
180 185 190	
acc cca gcc tca gat act gca ccc aaa gca acc tct gtc gtt gaa cca	624
Thr Pro Ala Ser Asp Thr Ala Pro Lys Ala Thr Ser Val Val Glu Pro	
195 200 205	
tca gcc gtc aat gct aat aat cga cca gaa ggc cct cga acg atg gtt	672
Ser Ala Val Asn Ala Asn Asn Arg Pro Glu Gly Pro Arg Thr Met Val	
210 215 220	
gat ctg atg cgt aat gtc gat ttc cat cgt cca ggc gaa aat ttc aaa	720
Asp Leu Met Arg Asn Val Asp Phe His Arg Pro Gly Glu Asn Phe Lys	
225 230 235 240	
act gat ggg tat att att act ccc gat acg gaa cgt ctc ttg aag gat	768
Thr Asp Gly Tyr Ile Ile Thr Pro Asp Thr Glu Arg Leu Leu Lys Asp	
245 250 255	
cat tta cag cga act ggt ggc aaa gtg cgt acc cgc ttc cct cct gag	816
His Leu Gln Arg Thr Gly Gly Lys Val Arg Thr Arg Phe Pro Pro Glu	
260 265 270	
ccg aat gga att ctg cac att ggc cac gct aaa gct atc aac atc aac	864
Pro Asn Gly Ile Leu His Ile Gly His Ala Lys Ala Ile Asn Ile Asn	
275 280 285 290	
ttt gct tac gcg gca gcg aac gat ggc atc tgc ttc ctt cgt tac gat	912
Phe Ala Tyr Ala Ala Asn Asp Gly Ile Cys Phe Leu Arg Tyr Asp	
295 300 305	
gac acc aat ccc gag aag gag gaa aaa ttt gtt aaa ggc ata cgc	960
Asp Thr Asn Pro Glu Lys Glu Glu Glu Lys Phe Val Lys Gly Ile Arg	
310 315 320	
gac att gtc gaa tgg ctc ggt tat aag cca ttc aaa att act tac tct	1008
Asp Ile Val Glu Trp Leu Gly Tyr Lys Pro Phe Lys Ile Thr Tyr Ser	

PF59083SeqList PF59083.txt

				325				330				335					
tcg	gac	tac	ttc	caa	cag	ttg	tac	gaa	ttt	gct	gtg	cag	ctc	ata	aga		1056
Ser	Asp	Tyr	Phe	Gln	Gln	Leu	Tyr	Glu	Phe	Ala	Val	Gln	Leu	Ile	Arg		
			340					345				350					
aaa	gat	atg	gct	tac	gtg	tgt	cat	caa	act	gct	gat	caa	atg	aag	gga		1104
Lys	Asp	Met	Ala	Tyr	Val	Cys	His	Gln	Thr	Ala	Asp	Gln	Met	Lys	Gly		
			355					360				365					
ttt	aca	acc	gaa	cca	tcc	aag	tgg	cgt	aat	cgt	cca	atc	gag	gaa	agc		1152
Phe	Thr	Thr	Glu	Pro	Ser	Lys	Trp	Arg	Asn	Arg	Pro	Ile	Glu	Glu	Ser		
			370								380						
ctg	cag	ctg	ttc	gaa	gac	atg	aaa	aat	ggg	aaa	att	gat	gaa	ggt	gcg		1200
Leu	Gln	Leu	Phe	Glu	Asp	Met	Lys	Asn	Gly	Lys	Ile	Asp	Glu	Gly	Ala		
					390					395					400		
gca	aca	tta	cgc	atg	aaa	atc	acg	ctg	gag	gag	gga	aaa	atg	gac	ccg		1248
Ala	Thr	Leu	Arg	Met	Lys	Ile	Thr	Leu	Glu	Glu	Gly	Lys	Met	Asp	Pro		
					405					410					415		
gta	gcc	tac	cgg	atc	aag	ttt	att	cca	cac	cat	cgg	acc	gga	aca	aag		1296
Val	Ala	Tyr	Arg	Ile	Lys	Phe	Ile	Pro	His	His	Arg	Thr	Gly	Thr	Lys		
			420					425							430		
tgg	tgc	atc	tat	ccg	acg	tac	gac	tac	aca	cat	tgt	ttg	tgc	gat	agt		1344
Trp	Cys	Ile	Tyr	Pro	Thr	Tyr	Asp	Tyr	Thr	His	Cys	Leu	Cys	Asp	Ser		
			435					440									
ctg	gag	gat	atc	acc	cat	tcg	ctt	tgc	acc	aag	gag	ttc	caa	tcg	aga		1392
Leu	Glu	Asp	Ile	Thr	His	Ser	Leu	Cys	Thr	Lys	Glu	Phe	Gln	Ser	Arg		
						455					460						
aga	tcg	tcg	tat	tat	tgg	ctc	tgt	aat	gca	ctc	aat	ata	tac	tgc	cca		1440
Arg	Ser	Ser	Tyr	Tyr	Trp	Leu	Cys	Asn	Ala	Leu	Asn	Ile	Tyr	Cys	Pro		
					470					475					480		
gtg	caa	tgg	gaa	tat	gcg	cgg	ctt	aat	gtt	aac	tac	acc	gta	gtt	tct		1488
Val	Gln	Trp	Glu	Tyr	Ala	Arg	Leu	Asn	Val	Asn	Tyr	Thr	Val	Val	Ser		
					485					490					495		
aag	cgc	aaa	att	aac	aag	ctg	atc	act	gaa	aat	att	gtt	aac	gac	tgg		1536
Lys	Arg	Lys	Ile	Asn	Lys	Leu	Ile	Thr	Glu	Asn	Ile	Val	Asn	Asp	Trp		
			500					505							510		
gat	gat	cct	aga	tta	ttc	acc	ctg	tct	gct	ttg	cga	cgc	aag	ggt	tat		1584
Asp	Asp	Pro	Arg	Leu	Phe	Thr	Leu	Ser	Ala	Leu	Arg	Arg	Lys	Gly	Tyr		
			515					520									
cca	gcc	gaa	gca	atc	aac	aat	ttt	tgt	gcc	cag	atg	ggt	ctc	acc	ggt		1632
Pro	Ala	Glu	Ala	Ile	Asn	Asn	Phe	Cys	Ala	Gln	Met	Gly	Leu	Thr	Gly		
						535					540						
gcc	caa	acg	tcc	att	gac	cct	gct	gca	ctg	gaa	gcg	tct	gcc	aga	gat		1680
Ala	Gln	Thr	Ser	Ile	Asp	Pro	Ala	Ala	Leu	Glu	Ala	Ser	Ala	Arg	Asp		
					550					555					560		
gta	ttg	aat	ctt	gca	gca	tca	cgt	aca	atg	gca	gta	tta	gaa	cct	ctg		1728
Val	Leu	Asn	Leu	Ala	Ala	Ser	Arg	Thr	Met	Ala	Val	Leu	Glu	Pro	Leu		
					565					570					575		
aag	att	act	ata	ctt	gat	tat	ccg	cat	gac	ggg	cca	att	caa	cta	tca		1776
Lys	Ile	Thr	Ile	Leu	Asp	Tyr	Pro	His	Asp	Gly	Pro	Ile	Gln	Leu	Ser		
			580					585							590		
gtg	ccc	aat	ttt	cca	aac	gtg	ccg	gag	aaa	ggc	gag	cac	atg	att	tgg		1824
Val	Pro	Asn	Phe	Pro	Asn	Val	Pro	Glu	Lys	Gly	Glu	His	Met	Ile	Trp		
			595					600							605		
ttc	gat	cgt	gtt	gta	tat	ata	gag	cga	acc	gat	ttc	atg	gaa	aat	gct		1872
Phe	Asp	Arg	Val	Val	Tyr	Ile	Glu	Arg	Thr	Asp	Phe	Met	Glu	Asn	Ala		
						615					620						
gac	aaa	tct	ttc	cgt	cga	cta	acg	cca	gga	caa	ccg	gtt	gga	ctg	aaa		1920
Asp	Lys	Ser	Phe	Arg	Arg	Leu	Thr	Pro	Gly	Gln	Pro	Val	Gly	Leu	Lys		
					630					635					640		
tac	att	ggg	tcc	atg	ctt	aga	gta	gaa	agt	gtt	gtt	cga	aaa	tcg	ggc		1968
Tyr	Ile	Gly	Ser	Met	Leu	Arg	Val	Glu	Ser	Val	Val	Arg	Lys	Ser	Gly		
					645					650					655		
acc	gtc	gag	gaa	cta	gta	tgt	cgc	ata	gaa	ccg	tgt	act	gca	acc	gaa		2016
Thr	Val	Glu	Glu	Leu	Val	Cys	Arg	Ile	Glu	Pro	Cys	Thr	Ala	Thr	Glu		
						660				665					670		
aaa	cct	aaa	gcg	tat	gta	cac	tgg	gta	gct	aaa	ccc	tgt	cca	gta	gag		2064
Lys	Pro	Lys	Ala	Tyr	Val	His	Trp	Val	Ala	Lys	Pro	Cys	Pro	Val	Glu		
							680								685		
gta	cgt	ttg	tat	gag	aag	ctg	ttt	atg	cac	aag	aac	cca	gaa	gac	agt		2112
Val	Arg	Leu	Tyr	Glu	Lys	Leu	Phe	Met	His	Lys	Asn	Pro	Glu	Asp	Ser		

PF59083SeqList PF59083.txt

690	aac gat gtt ccc aat ggg ttt ttg agc gac tgt gct tcg gac acg att	2160
Asn Asp Val Pro Asn Gly Phe Leu Ser Asp Cys Ala Ser Asp Thr Ile		
705	cgt tca ctg tgc ggc tat gtc gat gca cat gtc atg aac agt aaa gtg	2208
Arg Ser Leu Cys Gly Tyr Val Asp Ala His Val Met Asn Ser Lys Val		
725	tac gat aaa tat caa ttc gaa cgc att ggt tac ttc tcc gtg gat ccg	2256
Tyr Asp Lys Tyr Gln Phe Glu Arg Ile Gly Tyr Phe Ser Val Asp Pro		
740	gat agc aga aac ggc cag ctt gtt ttc aat cgt acc gtc acg ctt aaa	2304
Asp Ser Arg Asn Gly Gln Leu Val Phe Asn Arg Thr Val Thr Leu Lys		
755	gaa gat act ggt aaa aat tag	2325
Glu Asp Thr Gly Lys Asn		
770		

<210> 9944

<211> 774

<212> PRT

<213> Anopheles gambiae str. PEST

<400> 9944

Met Thr Thr Met Glu His Leu Val Ser Leu Gly Leu Asn Glu Gln Lys	
1 5 10 15	
Ile Lys Glu Thr Leu Lys Asn Ala Thr Leu Thr Ser Thr Ile Thr Arg	
20 25 30	
Ala Phe Ser Tyr Val Pro Pro Gly Val Glu Leu Ser Ser Ala Gln Lys	
35 40 45	
Pro Leu Ile Phe Gln Ala Cys Ser Lys Ile Lys Pro Gln Thr Ala His	
50 55 60	
His Leu Glu Leu Ile Val Arg Lys Ile Leu Asp Asn Ser Leu Asp Thr	
65 70 75 80	
Ser Leu Arg Val Asp Thr Ala Leu Glu Tyr Val Leu Ala Asn Val Thr	
85 90 95	
Lys Ala Thr Ile Asp Glu Ala Thr Phe Asp Ala Ala Cys Gly Val Gly	
100 105 110	
Val Val Val Thr Pro Glu Glu Ile Glu Arg Ala Val Glu Ile Thr Val	
115 120 125	
Ala Lys Tyr Arg Ser Asp Ile Val Asp Gln Arg Tyr Arg Phe Asn Val	
130 135 140	
Gly Lys Leu Leu Ser Glu Ile Arg Ser Ala Leu Pro Trp Val Asp Gly	
145 150 155 160	
Lys Ala Leu Lys Ser Glu Val Asp Val Gln Met Phe Asp Leu Leu Gly	
165 170 175	
Pro Lys Thr Asp Ala Asp Gly Glu Lys Val Gly Lys Lys Arg Arg Glu	
180 185 190	
Thr Pro Ala Ser Asp Thr Ala Pro Lys Ala Thr Ser Val Val Glu Pro	
195 200 205	
Ser Ala Val Asn Ala Asn Asn Arg Pro Glu Gly Pro Arg Thr Met Val	
210 215 220	
Asp Leu Met Arg Asn Val Asp Phe His Arg Pro Gly Glu Asn Phe Lys	
225 230 235 240	
Thr Asp Gly Tyr Ile Thr Pro Asp Thr Glu Arg Leu Leu Lys Asp	
245 250 255	
His Leu Gln Arg Thr Gly Gly Lys Val Arg Thr Arg Phe Pro Pro Glu	
260 265 270	
Pro Asn Gly Ile Leu His Ile Gly His Ala Lys Ala Ile Asn Ile Asn	
275 280 285	
Phe Ala Tyr Ala Ala Ala Asn Asp Gly Ile Cys Phe Leu Arg Tyr Asp	
290 295 300	
Asp Thr Asn Pro Glu Lys Glu Glu Glu Lys Phe Val Lys Gly Ile Arg	
305 310 315 320	
Asp Ile Val Glu Trp Leu Gly Tyr Lys Pro Phe Lys Ile Thr Tyr Ser	
325 330 335	
Ser Asp Tyr Phe Gln Gln Leu Tyr Glu Phe Ala Val Gln Leu Ile Arg	
340 345 350	
Lys Asp Met Ala Tyr Val Cys His Gln Thr Ala Asp Gln Met Lys Gly	
355 360 365	

PF59083SeqList PF59083.txt

Phe Thr Thr Glu Pro Ser Lys Trp Arg Asn Arg Pro Ile Glu Glu Ser
 370 375 380
 Leu Gln Leu Phe Glu Asp Met Lys Asn Gly Lys Ile Asp Glu Gly Ala
 385 390 395 400
 Ala Thr Leu Arg Met Lys Ile Thr Leu Glu Gly Lys Met Asp Pro
 405 410 415
 Val Ala Tyr Arg Ile Lys Phe Ile Pro His His Arg Thr Gly Thr Lys
 420 425 430
 Trp Cys Ile Tyr Pro Thr Tyr Asp Tyr Thr His Cys Leu Cys Asp Ser
 435 440 445
 Leu Glu Asp Ile Thr His Ser Leu Cys Thr Lys Glu Phe Gln Ser Arg
 450 455 460
 Arg Ser Ser Tyr Tyr Trp Leu Cys Asn Ala Leu Asn Ile Tyr Cys Pro
 465 470 475 480
 Val Gln Trp Glu Tyr Ala Arg Leu Asn Val Asn Tyr Thr Val Val Ser
 485 490 495
 Lys Arg Lys Ile Asn Lys Leu Ile Thr Glu Asn Ile Val Asn Asp Trp
 500 505 510
 Asp Asp Pro Arg Leu Phe Thr Leu Ser Ala Leu Arg Arg Lys Gly Tyr
 515 520 525
 Pro Ala Glu Ala Ile Asn Asn Phe Cys Ala Gln Met Gly Leu Thr Gly
 530 535 540
 Ala Gln Thr Ser Ile Asp Pro Ala Ala Leu Glu Ala Ser Ala Arg Asp
 545 550 555 560
 Val Leu Asn Leu Ala Ser Arg Thr Met Ala Val Leu Glu Pro Leu
 565 570 575
 Lys Ile Thr Ile Leu Asp Tyr Pro His Asp Gly Pro Ile Gln Leu Ser
 580 585 590
 Val Pro Asn Phe Pro Asn Val Pro Glu Lys Gly Glu His Met Ile Trp
 595 600 605
 Phe Asp Arg Val Val Tyr Ile Glu Arg Thr Asp Phe Met Glu Asn Ala
 610 615 620
 Asp Lys Ser Phe Arg Arg Leu Thr Pro Gly Gln Pro Val Gly Leu Lys
 625 630 635 640
 Tyr Ile Gly Ser Met Leu Arg Val Glu Ser Val Val Arg Lys Ser Gly
 645 650 655
 Thr Val Glu Glu Leu Val Cys Arg Ile Glu Pro Cys Thr Ala Thr Glu
 660 665 670
 Lys Pro Lys Ala Tyr Val His Trp Val Ala Lys Pro Cys Pro Val Glu
 675 680 685
 Val Arg Leu Tyr Glu Lys Leu Phe Met His Lys Asn Pro Glu Asp Ser
 690 695 700
 Asn Asp Val Pro Asn Gly Phe Leu Ser Asp Cys Ala Ser Asp Thr Ile
 705 710 715 720
 Arg Ser Leu Cys Gly Tyr Val Asp Ala His Val Met Asn Ser Lys Val
 725 730 735
 Tyr Asp Lys Tyr Gln Phe Glu Arg Ile Gly Tyr Phe Ser Val Asp Pro
 740 745 750
 Asp Ser Arg Asn Gly Gln Leu Val Phe Asn Arg Thr Val Thr Leu Lys
 755 760 765
 Glu Asp Thr Gly Lys Asn
 770

<210> 9945

<211> 2388

<212> DNA

<213> Candida glabrata CBS 138

<220>

<221> CDS

<222> (1)..(2388)

<400> 9945

atg tct ttg gag aag ttt ggg tac gag gag gcg aag atc aag gag att
 Met Ser Leu Glu Lys Phe Gly Tyr Glu Glu Ala Lys Ile Lys Glu Ile
 1 5 10 15
 acc aag aat cag aag att ctg agt gag ttg gag aag ctt ttg ggc gag
 Thr Lys Asn Gln Lys Ile Leu Ser Glu Leu Glu Lys Leu Leu Gly Glu
 20 25 30

48

96

PF59083SeqList PF59083.txt																
gtc	cag	gtc	ggg	gag	ttg	gac	aag	acg	cag	agg	gct	ata	ttg	cac	cag	144
Val	Gln	Val	Gly	Glu	Leu	Asp	Lys	Thr	Gln	Arg	Ala	Ile	Leu	His	Gln	
		35					40					45				
ttt	gcg	acg	cta	ctg	gcc	aag	cgg	aag	gat	gcc	ggt	gag	gtg	agc	act	192
Phe	Ala	Thr	Leu	Leu	Ala	Lys	Arg	Lys	Asp	Ala	Gly	Glu	Val	Ser	Thr	
	50					55					60					
gct	ctg	gtt	gtg	gag	aat	gtt	gtg	aac	ggt	ggt	atc	aag	acc	aac	ttg	240
Ala	Leu	Val	Val	Glu	Asn	Val	Val	Asn	Gly	Gly	Ile	Lys	Thr	Asn	Leu	
65					70				75						80	
cag	ata	gac	gct	gcg	ttc	aag	tat	gtg	gtg	gca	cac	ccg	gat	gtg	gac	288
Gln	Ile	Asp	Ala	Ala	Phe	Lys	Tyr	Val	Val	Ala	His	Pro	Asp	Val	Asp	
				85				90						95		
cag	gag	acg	ctg	gcc	gcc	gag	gct	ggt	att	ggt	gtg	cat	gtc	ggc	gag	336
Gln	Glu	Thr	Leu	Ala	Ala	Glu	Ala	Gly	Ile	Gly	Val	His	Val	Gly	Glu	
			100					105					110			
gag	gat	gtc	aga	cgc	aaa	gtt	gtg	gag	tat	atc	gag	agc	aac	aag	agc	384
Glu	Asp	Val	Arg	Arg	Lys	Val	Val	Glu	Tyr	Ile	Glu	Ser	Asn	Lys	Ser	
		115				120						125				
aag	att	gaa	gag	cag	aga	tac	aag	ctt	gtg	cca	ggg	atc	atg	gcg	gat	432
Lys	Ile	Glu	Glu	Gln	Arg	Tyr	Lys	Leu	Val	Pro	Gly	Ile	Met	Ala	Asp	
	130					135					140					
gtc	aag	aag	atg	cca	gag	ttg	aag	tgg	gct	gaa	cca	cgt	ttg	ttc	aag	480
Val	Lys	Lys	Met	Pro	Glu	Leu	Lys	Trp	Ala	Glu	Pro	Arg	Leu	Phe	Lys	
145					150				155						160	
cct	atc	att	gat	gaa	gag	atc	ctg	aag	gcc	att	ggt	cct	aag	gac	gag	528
Pro	Ile	Ile	Asp	Glu	Glu	Ile	Leu	Lys	Ala	Ile	Gly	Pro	Lys	Asp	Glu	
				165					170					175		
aga	gat	gtg	gtc	aag	aag	cag	cct	aag	gca	aag	aag	aat	gcc	aag	aag	576
Arg	Asp	Val	Val	Lys	Lys	Gln	Pro	Lys	Ala	Lys	Lys	Asn	Ala	Lys	Lys	
			180					185					190			
gat	gac	agt	ggc	gac	aag	agc	tct	gat	tca	aag	ggt	gag	aag	aga	acc	624
Asp	Asp	Ser	Gly	Asp	Lys	Ser	Ser	Asp	Ser	Lys	Gly	Glu	Lys	Arg	Thr	
		195				200						205				
atg	ttc	act	gaa	ggt	ttc	cta	ggt	gac	ctg	cac	aaa	gtc	ggt	gag	aac	672
Met	Phe	Thr	Glu	Gly	Phe	Leu	Gly	Asp	Leu	His	Lys	Val	Gly	Glu	Asn	
	210					215					220					
cca	caa	gct	tac	cct	gag	ttg	atg	gca	gaa	cac	ttg	aaa	gcc	act	ggt	720
Pro	Gln	Ala	Tyr	Pro	Glu	Leu	Met	Ala	Glu	His	Leu	Lys	Ala	Thr	Gly	
225					230				235						240	
ggc	aaa	gtc	cac	acc	aga	ttc	cca	cct	gag	cca	aat	ggt	tac	tta	cat	768
Gly	Lys	Val	His	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	
				245					250					255		
atc	ggt	cat	tcc	aag	gct	atc	atg	gtc	aac	ttc	ggt	tac	gcc	aag	tac	816
Ile	Gly	His	Ser	Lys	Ala	Ile	Met	Val	Asn	Phe	Gly	Tyr	Ala	Lys	Tyr	
			260					265					270			
cac	gac	ggt	gtg	tgc	tac	ttg	aga	ttt	gac	gat	acc	aat	cca	gaa	gct	864
His	Asp	Gly	Val	Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	
		275				280					285					
gaa	gcc	cca	gag	tac	ttt	gag	tcc	att	aag	aga	atg	ggt	tcg	tgg	ctg	912
Glu	Ala	Pro	Glu	Tyr	Phe	Glu	Ser	Ile	Lys	Arg	Met	Val	Ser	Trp	Leu	
	290					295					300					
ggc	ttt	aag	cca	tgg	aag	gtt	acg	tac	tcc	agt	gat	tac	ttc	gat	aag	960
Gly	Phe	Lys	Pro	Trp	Lys	Val	Thr	Tyr	Ser	Ser	Asp	Tyr	Phe	Asp	Lys	
305					310				315						320	
ctg	tac	gaa	ttg	gct	gag	gtt	tta	ata	aag	aat	ggc	aag	ggt	tac	gtt	1008
Leu	Tyr	Glu	Leu	Ala	Glu	Val	Leu	Ile	Lys	Asn	Gly	Lys	Gly	Tyr	Val	
				325				330						335		
tgt	cac	tgt	act	gct	gaa	gaa	atc	aag	cgt	ggt	cgt	ggt	atc	aaa	gag	1056
Cys	His	Cys	Thr	Ala	Glu	Glu	Ile	Lys	Arg	Gly	Arg	Gly	Ile	Lys	Glu	
			340					345					350			
gat	ggt	act	cca	ggt	ggt	gaa	aga	cat	gcc	tgc	aaa	cac	aga	gat	cag	1104
Asp	Gly	Thr	Pro	Gly	Gly	Glu	Arg	His	Ala	Cys	Lys	His	Arg	Asp	Gln	
		355				360						365				
agt	gta	gaa	aag	aac	ttg	gaa	gaa	ttc	aga	gct	atg	aga	gat	ggt	aag	1152
Ser	Val	Glu	Lys	Asn	Leu	Glu	Glu	Phe	Arg	Ala	Met	Arg	Asp	Gly	Lys	
	370					375					380					
tac	aag	cca	ggt	gaa	gct	att	ctg	aga	atg	aag	caa	aac	cta	gaa	tct	1200
Tyr	Lys	Pro	Gly	Glu	Ala	Ile	Leu	Arg	Met	Lys	Gln	Asn	Leu	Glu	Ser	
385					390					395					400	

PF59083SeqList PF59083.txt

cca	tct	cca	cag	atg	tgg	gat	ttg	att	gcc	tac	aga	gtg	cta	aac	gct	1248
Pro	Ser	Pro	Gln	Met	Trp	Asp	Leu	Ile	Ala	Tyr	Arg	Val	Leu	Asn	Ala	
			405						410					415		
cca	cat	cca	aga	act	ggt	acc	aaa	tgg	aag	att	tac	cca	aca	tac	gat	1296
Pro	His	Pro	Arg	Thr	Gly	Thr	Lys	Trp	Lys	Ile	Tyr	Pro	Thr	Tyr	Asp	
			420					425					430			
ttc	aca	cac	tgt	ttg	ggt	gat	tct	ttc	gaa	aac	atc	aca	cac	tct	cta	1344
Phe	Thr	His	Cys	Leu	Val	Asp	Ser	Phe	Glu	Asn	Ile	Thr	His	Ser	Leu	
		435					440				445					
tgt	act	act	gaa	ttt	tac	tta	tcg	agg	gag	agt	tat	gaa	tgg	cta	tgt	1392
Cys	Thr	Thr	Glu	Phe	Tyr	Leu	Ser	Arg	Glu	Ser	Tyr	Glu	Trp	Leu	Cys	
	450					455					460					
gac	cag	ggt	cac	gtc	ttt	aga	cca	gca	cag	aga	gag	tat	ggt	cgt	cta	1440
Asp	Gln	Val	His	Val	Phe	Arg	Pro	Ala	Gln	Arg	Glu	Tyr	Gly	Arg	Leu	
465					470				475						480	
aac	atc	acc	ggt	acg	ggt	tta	tcc	aag	cgt	aag	att	gct	aag	ctt	ggt	1488
Asn	Ile	Thr	Gly	Thr	Val	Leu	Ser	Lys	Arg	Lys	Ile	Ala	Lys	Leu	Val	
			485					490						495		
gat	gaa	cat	ttc	ggt	aga	ggt	tgg	gat	gac	cca	aga	tta	ttt	act	ttg	1536
Asp	Glu	His	Phe	Val	Arg	Gly	Trp	Asp	Asp	Pro	Arg	Leu	Phe	Thr	Leu	
			500					505					510			
gaa	gcc	att	cgt	aga	cgt	ggt	ggt	cca	cca	ggt	gca	atc	tta	tct	ttc	1584
Glu	Ala	Ile	Arg	Arg	Arg	Gly	Val	Pro	Pro	Gly	Ala	Ile	Leu	Ser	Phe	
	515					520					525					
atc	aat	aca	ctt	ggt	gtc	aca	aca	agc	aca	acc	aat	att	caa	ggt	ggt	1632
Ile	Asn	Thr	Leu	Gly	Val	Thr	Thr	Ser	Thr	Thr	Asn	Ile	Gln	Val	Val	
	530					535					540					
aga	ttt	gag	agc	gca	atc	aga	aag	tac	ttg	gaa	gat	tct	act	cca	aga	1680
Arg	Phe	Glu	Ser	Ala	Ile	Arg	Lys	Tyr	Leu	Glu	Asp	Ser	Thr	Pro	Arg	
545					550					555					560	
ttg	atg	atg	att	ctt	gat	cca	att	gag	gtc	ggt	ggt	gaa	aac	cta	cca	1728
Leu	Met	Met	Ile	Leu	Asp	Pro	Ile	Glu	Val	Val	Val	Glu	Asn	Leu	Pro	
			565					570						575		
gag	gac	tat	gaa	gaa	ctt	ggt	act	att	cca	tac	aga	gct	ggt	acc	aaa	1776
Glu	Asp	Tyr	Glu	Glu	Leu	Val	Thr	Ile	Pro	Tyr	Arg	Ala	Gly	Thr	Lys	
			580				585						590			
gaa	ttc	ggt	gac	aga	aat	gtc	cca	ttc	act	aat	aag	ttt	tac	att	gaa	1824
Glu	Phe	Gly	Asp	Arg	Asn	Val	Pro	Phe	Thr	Asn	Lys	Phe	Tyr	Ile	Glu	
	595					600					605					
agg	gca	gat	ttc	tcc	gaa	aat	aca	gaa	gac	aag	gaa	ttc	aga	ctt		1872
Arg	Ala	Asp	Phe	Ser	Glu	Asn	Thr	Glu	Asp	Lys	Glu	Phe	Phe	Arg	Leu	
	610				615						620					
act	cca	aac	caa	ccg	ggt	ggt	ttg	att	aaa	ggt	cca	tac	act	ggt	tct	1920
Thr	Pro	Asn	Gln	Pro	Val	Gly	Leu	Ile	Lys	Val	Pro	Tyr	Thr	Val	Ser	
625					630					635					640	
ttc	aag	agt	ggt	gag	aag	gat	gct	gat	ggt	aag	atc	act	aga	att	cat	1968
Phe	Lys	Ser	Val	Glu	Lys	Asp	Ala	Asp	Gly	Lys	Ile	Thr	Arg	Ile	His	
			645					650						655		
ggt	aag	tac	gat	aat	gaa	gac	aag	cca	gtg	aag	cca	aga	act	tac	atc	2016
Val	Lys	Tyr	Asp	Asn	Glu	Asp	Lys	Pro	Val	Lys	Pro	Arg	Thr	Tyr	Ile	
			660					665					670			
caa	tgg	ggt	cct	atc	tcc	aag	aag	tac	aac	tcc	cca	gta	cgt	ggt	tct	2064
Gln	Trp	Val	Pro	Ile	Ser	Lys	Lys	Tyr	Asn	Ser	Pro	Val	Arg	Val	Ser	
	675					680						685				
gaa	acc	aga	ggt	tat	aac	caa	ctc	ttc	aag	tct	gaa	aat	cca	tcc	gct	2112
Glu	Thr	Arg	Val	Tyr	Asn	Gln	Leu	Phe	Lys	Ser	Glu	Asn	Pro	Ser	Ala	
	690				695						700					
cat	cca	gat	ggt	tat	ttg	aaa	gac	atc	aac	cct	gaa	agt	gag	gtc	att	2160
His	Pro	Asp	Gly	Tyr	Leu	Lys	Asp	Ile	Asn	Pro	Glu	Ser	Glu	Val	Ile	
705					710					715					720	
tat	gat	aag	tct	gtc	att	gaa	cat	aat	ttc	gac	cac	ggt	atc	aag	aac	2208
Tyr	Asp	Lys	Ser	Val	Ile	Glu	His	Asn	Phe	Asp	His	Val	Ile	Lys	Asn	
			725					730						735		
tcc	cca	tgg	ggt	ggt	gat	tcc	ggt	aag	aat	tct	gaa	ttt	tat	ggt	aaa	2256
Ser	Pro	Trp	Val	Val	Asp	Ser	Val	Lys	Asn	Ser	Glu	Phe	Tyr	Val	Lys	
			740				745						750			
gaa	gat	aag	tcc	gga	aag	gaa	att	tgt	aga	ttc	cag	gct	atg	aga	ggt	2304
Glu	Asp	Lys	Ser	Gly	Lys	Glu	Ile	Cys	Arg	Phe	Gln	Ala	Met	Arg	Val	
		755					760					765				

PF59083SeqList PF59083.txt

ggt	tac	ttc	act	ctt	gac	aag	gag	agc	act	gat	gat	aag	atc	att	cta	2352
Gly	Tyr	Phe	Thr	Leu	Asp	Lys	Glu	Ser	Thr	Asp	Asp	Lys	Ile	Ile	Leu	
	770					775					780					
aat	aga	att	gtc	tcc	cta	aaa	gac	aac	act	aaa	taa					2388
Asn	Arg	Ile	Val	Ser	Leu	Lys	Asp	Asn	Thr	Lys						
785					790					795						

<210> 9946

<211> 795

<212> PRT

<213> Candida glabrata CBS 138

<400> 9946

Met	Ser	Leu	Glu	Lys	Phe	Gly	Tyr	Glu	Glu	Ala	Lys	Ile	Lys	Glu	Ile	
1				5				10						15		
Thr	Lys	Asn	Gln	Lys	Ile	Leu	Ser	Glu	Leu	Glu	Lys	Leu	Leu	Gly	Glu	
			20					25					30			
Val	Gln	Val	Gly	Glu	Leu	Asp	Lys	Thr	Gln	Arg	Ala	Ile	Leu	His	Gln	
		35					40					45				
Phe	Ala	Thr	Leu	Leu	Ala	Lys	Arg	Lys	Asp	Ala	Gly	Glu	Val	Ser	Thr	
	50					55					60					
Ala	Leu	Val	Val	Glu	Asn	Val	Val	Asn	Gly	Gly	Ile	Lys	Thr	Asn	Leu	
65					70				75						80	
Gln	Ile	Asp	Ala	Ala	Phe	Lys	Tyr	Val	Val	Ala	His	Pro	Asp	Val	Asp	
				85				90						95		
Gln	Glu	Thr	Leu	Ala	Ala	Glu	Ala	Gly	Ile	Gly	Val	His	Val	Gly	Glu	
			100					105					110			
Glu	Asp	Val	Arg	Arg	Lys	Val	Val	Glu	Tyr	Ile	Glu	Ser	Asn	Lys	Ser	
		115					120					125				
Lys	Ile	Glu	Glu	Gln	Arg	Tyr	Lys	Leu	Val	Pro	Gly	Ile	Met	Ala	Asp	
		130				135					140					
Val	Lys	Lys	Met	Pro	Glu	Leu	Lys	Trp	Ala	Glu	Pro	Arg	Leu	Phe	Lys	
145					150				155						160	
Pro	Ile	Ile	Asp	Glu	Ile	Leu	Lys	Ala	Ile	Gly	Pro	Lys	Asp	Glu		
				165				170					175			
Arg	Asp	Val	Val	Lys	Lys	Gln	Pro	Lys	Ala	Lys	Lys	Asn	Ala	Lys	Lys	
			180					185					190			
Asp	Asp	Ser	Gly	Asp	Lys	Ser	Ser	Asp	Ser	Lys	Gly	Glu	Lys	Arg	Thr	
		195					200					205				
Met	Phe	Thr	Glu	Gly	Phe	Leu	Gly	Asp	Leu	His	Lys	Val	Gly	Glu	Asn	
	210					215					220					
Pro	Gln	Ala	Tyr	Pro	Glu	Leu	Met	Ala	Glu	His	Leu	Lys	Ala	Thr	Gly	
225					230				235						240	
Gly	Lys	Val	His	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	
				245					250					255		
Ile	Gly	His	Ser	Lys	Ala	Ile	Met	Val	Asn	Phe	Gly	Tyr	Ala	Lys	Tyr	
			260				265						270			
His	Asp	Gly	Val	Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	
		275					280					285				
Glu	Ala	Pro	Glu	Tyr	Phe	Glu	Ser	Ile	Lys	Arg	Met	Val	Ser	Trp	Leu	
	290					295					300					
Gly	Phe	Lys	Pro	Trp	Lys	Val	Thr	Tyr	Ser	Ser	Asp	Tyr	Phe	Asp	Lys	
305					310					315					320	
Leu	Tyr	Glu	Leu	Ala	Glu	Val	Leu	Ile	Lys	Asn	Gly	Lys	Gly	Tyr	Val	
				325					330					335		
Cys	His	Cys	Thr	Ala	Glu	Glu	Ile	Lys	Arg	Gly	Arg	Gly	Ile	Lys	Glu	
			340					345					350			
Asp	Gly	Thr	Pro	Gly	Gly	Glu	Arg	His	Ala	Cys	Lys	His	Arg	Asp	Gln	
		355					360					365				
Ser	Val	Glu	Lys	Asn	Leu	Glu	Glu	Phe	Arg	Ala	Met	Arg	Asp	Gly	Lys	
	370					375					380					
Tyr	Lys	Pro	Gly	Glu	Ala	Ile	Leu	Arg	Met	Lys	Gln	Asn	Leu	Glu	Ser	
385					390					395					400	
Pro	Ser	Pro	Gln	Met	Trp	Asp	Leu	Ile	Ala	Tyr	Arg	Val	Leu	Asn	Ala	
				405					410					415		
Pro	His	Pro	Arg	Thr	Gly	Thr	Lys	Trp	Lys	Ile	Tyr	Pro	Thr	Tyr	Asp	
			420					425					430			
Phe	Thr	His	Cys	Leu	Val	Asp	Ser	Phe	Glu	Asn	Ile	Thr	His	Ser	Leu	
		435					440					445				

PF59083SeqList PF59083.txt

Cys Thr Thr Glu Phe Tyr Leu Ser Arg Glu Ser Tyr Glu Trp Leu Cys
 450 455 460
 Asp Gln Val His Val Phe Arg Pro Ala Gln Arg Glu Tyr Gly Arg Leu
 465 470 475
 Asn Ile Thr Gly Thr Val Leu Ser Lys Arg Lys Ile Ala Lys Leu Val
 485 490 495
 Asp Glu His Phe Val Arg Gly Trp Asp Asp Pro Arg Leu Phe Thr Leu
 500 505 510
 Glu Ala Ile Arg Arg Arg Gly Val Pro Pro Gly Ala Ile Leu Ser Phe
 515 520 525
 Ile Asn Thr Leu Gly Val Thr Ser Thr Thr Asn Ile Gln Val Val
 530 535 540
 Arg Phe Glu Ser Ala Ile Arg Lys Tyr Leu Glu Asp Ser Thr Pro Arg
 545 550 555
 Leu Met Met Ile Leu Asp Pro Ile Glu Val Val Glu Asn Leu Pro
 565 570 575
 Glu Asp Tyr Glu Glu Leu Val Thr Ile Pro Tyr Arg Ala Gly Thr Lys
 580 585 590
 Glu Phe Gly Asp Arg Asn Val Pro Phe Thr Asn Lys Phe Tyr Ile Glu
 595 600 605
 Arg Ala Asp Phe Ser Glu Asn Thr Glu Asp Lys Glu Phe Phe Arg Leu
 610 615 620
 Thr Pro Asn Gln Pro Val Gly Leu Ile Lys Val Pro Tyr Thr Val Ser
 625 630 635
 Phe Lys Ser Val Glu Lys Asp Ala Asp Gly Lys Ile Thr Arg Ile His
 645 650 655
 Val Lys Tyr Asp Asn Glu Asp Lys Pro Val Lys Pro Arg Thr Tyr Ile
 660 665 670
 Gln Trp Val Pro Ile Ser Lys Lys Tyr Asn Ser Pro Val Arg Val Ser
 675 680 685
 Glu Thr Arg Val Tyr Asn Gln Leu Phe Lys Ser Glu Asn Pro Ser Ala
 690 695 700
 His Pro Asp Gly Tyr Leu Lys Asp Ile Asn Pro Glu Ser Glu Val Ile
 705 710 715
 Tyr Asp Lys Ser Val Ile Glu His Asn Phe Asp His Val Ile Lys Asn
 725 730 735
 Ser Pro Trp Val Val Asp Ser Val Lys Asn Ser Glu Phe Tyr Val Lys
 740 745 750
 Glu Asp Lys Ser Gly Lys Glu Ile Cys Arg Phe Gln Ala Met Arg Val
 755 760 765
 Gly Tyr Phe Thr Leu Asp Lys Glu Ser Thr Asp Asp Lys Ile Ile Leu
 770 775 780
 Asn Arg Ile Val Ser Leu Lys Asp Asn Thr Lys
 785 790 795

<210> 9947

<211> 2415

<212> DNA

<213> Kluyveromyces lactis NRRL Y-1140

<220>

<221> CDS

<222> (1)..(2415)

<400> 9947

atg tca tct gta gac gag ttg acc aat cta ttt tcc aag att ggg ttc	48
Met Ser Ser Val Asp Glu Leu Thr Asn Leu Phe Ser Lys Ile Gly Phe	
1 5 10 15	
gaa gaa gct aaa gta aag gaa atc tta aag aat gct aaa gta tcc agc	96
Glu Glu Ala Lys Val Lys Glu Ile Leu Lys Asn Ala Lys Val Ser Ser	
20 25 30	
tcc cta gag tcc tta gta aac ttg gca tct gat gat ttc cca tgg aac	144
Ser Leu Glu Ser Leu Val Asn Leu Ala Ser Asp Asp Phe Pro Trp Asn	
35 40 45	
aag aat tct aga gct tta att cac acg tta gca gcc tct tta aag gga	192
Lys Asn Ser Arg Ala Leu Ile His Thr Leu Ala Ala Ser Leu Lys Gly	
50 55 60	
gct gaa gtt cct cat ttg caa tat atc gtt gat ggt att ggt aag aat	240
Ala Glu Val Pro His Leu Gln Tyr Ile Val Asp Gly Ile Gly Lys Asn	

PF59083SeqList PF59083.txt

65	gat	ttg	aag	act	gca	ttg	cag	ata	gat	gca	gct	ttg	aag	tac	ttg	aag	288
	Asp	Leu	Lys	Thr	Ala	Leu	Gln	Ile	Asp	Ala	Ala	Leu	Lys	Tyr	Leu	Lys	
				85						90					95		
	acc	aag	ggt	gag	gat	gcc	act	ggt	gtg	gac	ttg	aac	aaa	gag	tcc	ggt	336
	Thr	Lys	Gly	Glu	Asp	Ala	Thr	Val	Val	Asp	Leu	Asn	Lys	Glu	Ser	Gly	
				100					105					110			
	gtc	ggt	att	gaa	ggt	act	gaa	gat	caa	ggt	aga	aac	cgt	ggt	gct	aag	384
	Val	Gly	Ile	Glu	Val	Thr	Glu	Asp	Gln	Val	Arg	Asn	Arg	Val	Ala	Lys	
			115					120					125				
	tac	ggt	gag	gat	aac	aaa	gat	acc	att	ttg	aag	gaa	aga	tac	aag	tta	432
	Tyr	Val	Glu	Asp	Asn	Lys	Asp	Thr	Ile	Leu	Lys	Glu	Arg	Tyr	Lys	Leu	
							135					140					
	gtg	cct	ggt	cta	ttt	gcc	aaa	atc	aaa	gct	ctc	ccc	gaa	tta	aaa	tgg	480
	Val	Pro	Gly	Leu	Phe	Ala	Lys	Ile	Lys	Ala	Leu	Pro	Glu	Leu	Lys	Trp	
						150					155					160	
	gct	gaa	cca	cgt	ttg	ttc	aaa	cca	atc	att	gac	gaa	gaa	atc	ttg	aag	528
	Ala	Glu	Pro	Arg	Leu	Phe	Lys	Pro	Ile	Ile	Asp	Glu	Glu	Ile	Leu	Lys	
					165				170						175		
	ggt	ttg	ggt	cca	aaa	gat	gaa	aga	gat	atc	gta	aag	aag	gaa	aag	aaa	576
	Val	Leu	Gly	Pro	Lys	Asp	Glu	Arg	Asp	Ile	Val	Lys	Lys	Glu	Lys	Lys	
				180					185					190			
	cca	aag	gct	gaa	aag	aag	gct	aat	ggc	aaa	gca	agc	aag	gac	caa	aca	624
	Pro	Lys	Ala	Glu	Lys	Lys	Ala	Asn	Gly	Lys	Ala	Ser	Lys	Asp	Gln	Thr	
			195					200					205				
	gaa	gaa	gat	ggt	cca	aag	aga	tct	atg	ttc	aca	gaa	ggt	ttc	ttg	ggt	672
	Glu	Glu	Asp	Gly	Pro	Lys	Arg	Ser	Met	Phe	Thr	Glu	Gly	Phe	Leu	Gly	
							215					220					
	gac	ttg	cat	aag	ggt	gga	gaa	aat	gag	cag	gcc	tac	cca	gaa	cta	atg	720
	Asp	Leu	His	Lys	Val	Gly	Glu	Asn	Glu	Gln	Ala	Tyr	Pro	Glu	Leu	Met	
						230					235					240	
	gct	gag	cat	ctc	aag	gct	acc	ggt	ggt	aaa	gta	cac	act	aga	ttc	cca	768
	Ala	Glu	His	Leu	Lys	Ala	Thr	Gly	Gly	Lys	Val	His	Thr	Arg	Phe	Pro	
					245				250						255		
	cca	gaa	cct	aac	gga	tat	tta	cat	att	ggt	cat	tct	aag	gcc	att	atg	816
	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ser	Lys	Ala	Ile	Met	
				260					265					270			
	ggt	aac	ttt	ggc	ttc	gct	aaa	tac	cat	aac	ggg	gta	tgt	tat	cta	aga	864
	Val	Asn	Phe	Gly	Phe	Ala	Lys	Tyr	His	Asn	Gly	Val	Cys	Tyr	Leu	Arg	
			275					280					285				
	ttt	gat	gat	acc	aac	cct	gaa	gca	gaa	gct	ccg	gaa	tat	ttc	gag	agt	912
	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Ala	Pro	Glu	Tyr	Phe	Glu	Ser	
							295					300					
	atc	aaa	agc	atg	gta	tca	tggt	ttg	ggg	ttc	aaa	cca	tggt	aaa	act	acc	960
	Ile	Lys	Ser	Met	Val	Ser	Trp	Leu	Gly	Phe	Lys	Pro	Trp	Lys	Thr	Thr	
						310					315					320	
	tat	tcc	tct	gat	tac	ttc	gat	gag	tta	tac	caa	tta	gct	gaa	act	ttg	1008
	Tyr	Ser	Ser	Asp	Tyr	Phe	Asp	Glu	Leu	Tyr	Gln	Leu	Ala	Glu	Thr	Leu	
					325				330					335			
	att	aag	aac	gga	aag	gct	tat	gtc	tgt	cac	tgc	tct	gca	gaa	gaa	ata	1056
	Ile	Lys	Asn	Gly	Lys	Ala	Tyr	Val	Cys	His	Cys	Ser	Ala	Glu	Glu	Ile	
				340					345					350			
	aaa	cgt	ggc	cgt	ggt	atc	aaa	gaa	gat	ggt	aca	cct	ggt	ggt	gaa	aga	1104
	Lys	Arg	Gly	Arg	Gly	Ile	Lys	Glu	Asp	Gly	Thr	Pro	Gly	Gly	Glu	Arg	
				355				360					365				
	aaa	gct	tgt	gtc	tcc	aga	gaa	aga	cct	att	gag	gaa	agc	tta	act	gag	1152
	Lys	Ala	Cys	Val	Ser	Arg	Glu	Arg	Pro	Ile	Glu	Glu	Ser	Leu	Thr	Glu	
						375					380						
	ttc	aga	aag	atg	aga	gac	gga	ttc	tac	aaa	cca	ggt	gaa	gca	atc	tta	1200
	Phe	Arg	Lys	Met	Arg	Asp	Gly	Phe	Tyr	Lys	Pro	Gly	Glu	Ala	Ile	Leu	
						390					395					400	
	aga	atg	aaa	caa	gat	ttg	aac	tct	cca	tca	cca	caa	atg	tggt	gat	ttg	1248
	Arg	Met	Lys	Gln	Asp	Leu	Asn	Ser	Pro	Ser	Pro	Gln	Met	Trp	Asp	Leu	
				405					410					415			
	att	gct	tat	agg	gtc	ttg	gat	gct	cca	cat	cca	aga	act	ggt	gac	aaa	1296
	Ile	Ala	Tyr	Arg	Val	Leu	Asp	Ala	Pro	His	Pro	Arg	Thr	Gly	Asp	Lys	
				420				425						430			
	tggt	aaa	att	tac	cca	aca	tac	gac	ttc	act	cac	tgt	tta	gtc	gat	tcc	1344
	Trp	Lys	Ile	Tyr	Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys	Leu	Val	Asp	Ser	

PF59083SeqList PF59083.txt

tta	gaa	aac	att	acc	cac	tcc	ttg	tgt	acc	aca	gaa	ttt	tac	ttg	tct	1392
Leu	Glu	Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Thr	Glu	Phe	Tyr	Leu	Ser	
	450					455					460					
aga	gaa	agt	tac	gaa	tgg	cta	tgt	gac	caa	gtg	cac	gtc	ttc	aga	cca	1440
Arg	Glu	Ser	Tyr	Glu	Trp	Leu	Cys	Asp	Gln	Val	His	Val	Phe	Arg	Pro	
465					470					475					480	
gct	caa	aga	gaa	tat	ggg	aga	ttg	aac	atc	acc	ggg	acc	gtt	cta	tct	1488
Ala	Gln	Arg	Glu	Tyr	Gly	Arg	Leu	Asn	Ile	Thr	Gly	Thr	Val	Leu	Ser	
				485					490					495		
aag	aga	aaa	att	gct	aaa	ctt	gtt	act	ggg	gga	tac	gtc	agc	gga	tgg	1536
Lys	Arg	Lys	Ile	Ala	Lys	Leu	Val	Thr	Gly	Gly	Tyr	Val	Ser	Gly	Trp	
			500					505					510			
aat	gat	cct	cgt	tta	ttc	aca	ttg	gaa	gct	atc	cgt	aga	cgt	ggg	gtt	1584
Asn	Asp	Pro	Arg	Leu	Phe	Thr	Leu	Glu	Ala	Ile	Arg	Arg	Arg	Gly	Val	
			515				520					525				
cca	ccg	gga	gcc	att	cta	tct	ttc	att	aac	act	ttg	ggg	gtg	acc	acc	1632
Pro	Pro	Gly	Ala	Ile	Leu	Ser	Phe	Ile	Asn	Thr	Leu	Gly	Val	Thr	Thr	
	530					535					540					
agt	acc	act	aat	atc	caa	gtc	gta	aga	ttc	gaa	agt	gct	att	aga	aag	1680
Ser	Thr	Thr	Asn	Ile	Gln	Val	Val	Arg	Phe	Glu	Ser	Ala	Ile	Arg	Lys	
545					550					555					560	
tac	ttg	gaa	gac	act	aca	ccc	aga	ctc	atg	ttc	att	ttg	gat	cca	gtg	1728
Tyr	Leu	Glu	Asp	Thr	Thr	Pro	Arg	Leu	Met	Phe	Ile	Leu	Asp	Pro	Val	
				565					570					575		
gaa	gtg	gtt	gtg	gac	aat	gtc	gat	gaa	gat	ttc	gtt	gag	cta	tgt	aac	1776
Glu	Val	Val	Val	Asp	Asn	Val	Asp	Glu	Asp	Phe	Val	Glu	Leu	Cys	Asn	
				580				585					590			
atc	cca	tac	agg	cca	aac	act	cca	gag	ttc	ggg	gat	aga	acc	gtc	cca	1824
Ile	Pro	Tyr	Arg	Pro	Asn	Thr	Pro	Glu	Phe	Gly	Asp	Arg	Thr	Val	Pro	
			595				600					605				
ttc	acc	aag	aga	ttc	tac	atc	gaa	aga	agc	gac	ttc	tcg	gaa	gac	gtt	1872
Phe	Thr	Lys	Arg	Phe	Tyr	Ile	Glu	Arg	Ser	Asp	Phe	Ser	Glu	Asp	Val	
	610					615					620					
gac	aac	aag	gag	ttc	ttc	aga	tta	aca	cct	aac	caa	tca	gtt	ggg	tta	1920
Asp	Asn	Lys	Glu	Phe	Phe	Arg	Leu	Thr	Pro	Asn	Gln	Ser	Val	Gly	Leu	
625					630					635					640	
atc	aaa	gta	cca	tac	acc	gta	tcc	tac	caa	tct	tta	gag	aag	gat	gcg	1968
Ile	Lys	Val	Pro	Tyr	Thr	Val	Ser	Tyr	Gln	Ser	Leu	Glu	Lys	Asp	Ala	
				645					650					655		
aac	ggg	aag	atc	act	aaa	att	cat	gtt	aaa	tat	gag	aac	gag	gaa	gcc	2016
Asn	Gly	Lys	Ile	Thr	Lys	Ile	His	Val	Lys	Tyr	Glu	Asn	Glu	Glu	Ala	
			660				665						670			
aaa	cca	aag	aaa	cca	aag	acc	tac	att	caa	tgg	gtg	cca	atc	tcc	gaa	2064
Lys	Pro	Lys	Lys	Pro	Lys	Thr	Tyr	Ile	Gln	Trp	Val	Pro	Ile	Ser	Glu	
			675				680						685			
aag	cac	gac	tcc	cca	gta	aga	att	gcg	gaa	act	aga	gtt	tac	aac	caa	2112
Lys	His	Asp	Ser	Pro	Val	Arg	Ile	Ala	Glu	Thr	Arg	Val	Tyr	Asn	Gln	
	690					695					700					
ttg	ttc	aag	tcc	gaa	aac	cca	gcg	cac	cca	gat	ggg	tac	tta	tct		2160
Leu	Phe	Lys	Ser	Glu	Asn	Pro	Ser	Ala	His	Pro	Asp	Gly	Tyr	Leu	Ser	
705					710					715					720	
gat	att	aac	cca	gac	agc	att	atc	gtg	tac	aag	agt	tct	gtc	gct	gaa	2208
Asp	Ile	Asn	Pro	Asp	Ser	Ile	Ile	Val	Tyr	Lys	Ser	Ser	Val	Ala	Glu	
				725					730					735		
tac	aac	atc	aac	agc	att	ata	aag	aac	tcg	cca	tgg	gtc	gtg	gac	agt	2256
Tyr	Asn	Ile	Asn	Ser	Ile	Ile	Lys	Asn	Ser	Pro	Trp	Val	Val	Asp	Ser	
				740					745					750		
gca	aag	aag	tct	gaa	ttc	tat	gtg	gaa	gaa	gaa	aag	gga	aga	aag	gaa	2304
Ala	Lys	Lys	Ser	Glu	Phe	Tyr	Val	Glu	Glu	Glu	Lys	Gly	Arg	Lys	Glu	
			755				760					765				
gtc	tcg	aga	ttc	caa	gcc	atg	aga	gtt	ggg	tat	ttc	acc	ttg	gac	tct	2352
Val	Cys	Arg	Phe	Gln	Ala	Met	Arg	Val	Gly	Tyr	Phe	Thr	Leu	Asp	Ser	
	770					775					780					
gat	agc	aca	gat	gaa	aag	atc	gtc	ttg	aac	agg	atc	gtt	tcc	ttg	aaa	2400
Asp	Ser	Thr	Asp	Glu	Lys	Ile	Val	Leu	Asn	Arg	Ile	Val	Ser	Leu	Lys	
					790					795					800	
gac	ggg	act	aaa	tga												2415
Asp	Gly	Thr	Lys													

PF59083SeqList PF59083.txt

<210> 9948
 <211> 804
 <212> PRT
 <213> Kluyveromyces lactis NRRL Y-1140

<400> 9948

```

Met Ser Ser Val Asp Glu Leu Thr Asn Leu Phe Ser Lys Ile Gly Phe
1      5      10      15
Glu Glu Ala Lys Val Lys Glu Ile Leu Lys Asn Ala Lys Val Ser Ser
      20      25      30
Ser Leu Glu Ser Leu Val Asn Leu Ala Ser Asp Asp Phe Pro Trp Asn
      35      40      45
Lys Asn Ser Arg Ala Leu Ile His Thr Leu Ala Ala Ser Leu Lys Gly
      50      55      60
Ala Glu Val Pro His Leu Gln Tyr Ile Val Asp Gly Ile Gly Lys Asn
65      70      75      80
Asp Leu Lys Thr Ala Leu Gln Ile Asp Ala Leu Lys Tyr Leu Lys
      85      90      95
Thr Lys Gly Glu Asp Ala Thr Val Val Asp Leu Asn Lys Glu Ser Gly
      100      105
Val Gly Ile Glu Val Thr Glu Asp Gln Val Arg Asn Arg Val Ala Lys
      110      115      120      125
Tyr Val Glu Asp Asn Lys Asp Thr Ile Leu Lys Glu Arg Tyr Lys Leu
      130      135      140
Val Pro Gly Leu Phe Ala Lys Ile Lys Ala Leu Pro Glu Leu Lys Trp
145      150      155      160
Ala Glu Pro Arg Leu Phe Lys Pro Ile Ile Asp Glu Glu Ile Leu Lys
      165      170      175
Val Leu Gly Pro Lys Asp Glu Arg Asp Ile Val Lys Lys Glu Lys Lys
      180      185      190
Pro Lys Ala Glu Lys Lys Ala Asn Gly Lys Ala Ser Lys Asp Gln Thr
      195      200      205
Glu Glu Asp Gly Pro Lys Arg Ser Met Phe Thr Glu Gly Phe Leu Gly
210      215      220
Asp Leu His Lys Val Gly Glu Asn Glu Gln Ala Tyr Pro Glu Leu Met
225      230      235      240
Ala Glu His Leu Lys Ala Thr Gly Gly Lys Val His Thr Arg Phe Pro
      245      250      255
Pro Glu Pro Asn Gly Tyr Leu His Ile Gly His Ser Lys Ala Ile Met
      260      265      270
Val Asn Phe Gly Phe Ala Lys Tyr His Asn Gly Val Cys Tyr Leu Arg
      275      280      285
Phe Asp Thr Asn Pro Glu Ala Glu Ala Pro Glu Tyr Phe Glu Ser
290      295      300
Ile Lys Ser Met Val Ser Trp Leu Gly Phe Lys Pro Trp Lys Thr Thr
305      310      315      320
Tyr Ser Ser Asp Tyr Phe Asp Glu Leu Tyr Gln Leu Ala Glu Thr Leu
      325      330      335
Ile Lys Asn Gly Lys Ala Tyr Val Cys His Cys Ser Ala Glu Glu Ile
      340      345      350      355
Lys Arg Gly Arg Gly Ile Lys Glu Asp Gly Thr Pro Gly Gly Glu Arg
      360      365      370
Lys Ala Cys Val Ser Arg Glu Arg Pro Ile Glu Glu Ser Leu Thr Glu
375      380
Phe Arg Lys Met Arg Asp Gly Phe Tyr Lys Pro Gly Glu Ala Ile Leu
385      390      395      400
Arg Met Lys Gln Asp Leu Asn Ser Pro Ser Pro Gln Met Trp Asp Leu
      405      410      415
Ile Ala Tyr Arg Val Leu Asp Ala Pro His Pro Arg Thr Gly Asp Lys
      420      425      430
Trp Lys Ile Tyr Pro Thr Tyr Asp Phe Thr His Cys Leu Val Asp Ser
      435      440      445
Leu Glu Asn Ile Thr His Ser Leu Cys Thr Thr Glu Phe Tyr Leu Ser
450      455      460
Arg Glu Ser Tyr Glu Trp Leu Cys Asp Gln Val His Val Phe Arg Pro
465      470      475      480
Ala Gln Arg Glu Tyr Gly Arg Leu Asn Ile Thr Gly Thr Val Leu Ser

```


PF59083SeqList PF59083.txt

485 490 495
 Lys Arg Lys Ile Ala Lys Leu Val Thr Gly Gly Tyr Val Ser Gly Trp
 500 505 510
 Asn Asp Pro Arg Leu Phe Thr Leu Glu Ala Ile Arg Arg Arg Gly Val
 515 520 525
 Pro Pro Gly Ala Ile Leu Ser Phe Ile Asn Thr Leu Gly Val Thr Thr
 530 535 540
 Ser Thr Thr Asn Ile Gln Val Val Arg Phe Glu Ser Ala Ile Arg Lys
 545 550 555 560
 Tyr Leu Glu Asp Thr Thr Pro Arg Leu Met Phe Ile Leu Asp Pro Val
 565 570 575
 Glu Val Val Val Asp Asn Val Asp Glu Asp Phe Val Glu Leu Cys Asn
 580 585 590
 Ile Pro Tyr Arg Pro Asn Thr Pro Glu Phe Gly Asp Arg Thr Val Pro
 595 600 605
 Phe Thr Lys Arg Phe Tyr Ile Glu Arg Ser Asp Phe Ser Glu Asp Val
 610 615 620
 Asp Asn Lys Glu Phe Phe Arg Leu Thr Pro Asn Gln Ser Val Gly Leu
 625 630 635 640
 Ile Lys Val Pro Tyr Thr Val Ser Tyr Gln Ser Leu Glu Lys Asp Ala
 645 650 655
 Asn Gly Lys Ile Thr Lys Ile His Val Lys Tyr Glu Asn Glu Glu Ala
 660 665 670
 Lys Pro Lys Lys Pro Lys Thr Tyr Ile Gln Trp Val Pro Ile Ser Glu
 675 680 685
 Lys His Asp Ser Pro Val Arg Ile Ala Glu Thr Arg Val Tyr Asn Gln
 690 695 700
 Leu Phe Lys Ser Glu Asn Pro Ser Ala His Pro Asp Gly Tyr Leu Ser
 705 710 715 720
 Asp Ile Asn Pro Asp Ser Ile Ile Val Tyr Lys Ser Ser Val Ala Glu
 725 730 735
 Tyr Asn Ile Asn Ser Ile Ile Lys Asn Ser Pro Trp Val Val Asp Ser
 740 745 750
 Ala Lys Lys Ser Glu Phe Tyr Val Glu Glu Glu Lys Gly Arg Lys Glu
 755 760 765
 Val Cys Arg Phe Gln Ala Met Arg Val Gly Tyr Phe Thr Leu Asp Ser
 770 775 780
 Asp Ser Thr Asp Glu Lys Ile Val Leu Asn Arg Ile Val Ser Leu Lys
 785 790 795 800
 Asp Gly Thr Lys

<210> 9949
 <211> 2385
 <212> DNA
 <213> Debaryomyces hansenii CBS767

<220>
 <221> CDS
 <222> (1)..(2385)

<400> 9949	
atg gcg tca gaa gaa gaa ttg atc aac ttg ttt agc aaa gtt ggg ttc	48
Met Ala Ser Glu Glu Glu Leu Ile Asn Leu Phe Ser Lys Val Gly Phe	
1 5 10 15	
aat gat aag aaa tct aaa gaa gtt tgc aaa aat aaa aag gtt tcc caa	96
Asn Asp Lys Lys Ser Lys Glu Val Cys Lys Asn Lys Lys Val Ser Gln	
20 25 30	
tca tta gca gaa atc atc aat gag tca aag gtg gaa gaa aca gat gaa	144
Ser Leu Ala Glu Ile Ile Asn Glu Ser Lys Val Glu Glu Thr Asp Glu	
35 40 45	
aag aag ctt tct ttg ttg cat gcg tta gcc gtt gag agt aaa gga gga	192
Lys Lys Leu Ser Leu Leu His Ala Leu Ala Val Glu Ser Lys Gly Gly	
50 55 60	
gat gtt cct aga cgt gaa tta att acg aag gct att att gat ggt aga	240
Asp Val Pro Arg Arg Glu Leu Ile Thr Lys Ala Ile Ile Asp Gly Arg	
65 70 75 80	
ttg aag act aac tta cag gtc acc gaa gca ttc aaa tat gtc aag gaa	288
Leu Lys Thr Asn Leu Gln Val Thr Glu Ala Phe Lys Tyr Val Lys Glu	

PF59083SeqList PF59083.txt

															85																90																95				
aac	ccc	gaa	act	gcc	aac	aac	gaa	acc	atg	gaa	gaa	aag	tca	ggg	ggt	336																																			
Asn	Pro	Glu	Thr	Ala	Asn	Asn	Glu	Thr	Met	Glu	Glu	Lys	Ser	Gly	Val																																				
																100																	105																	110	
ggt	att	gag	ctc	agt	gat	tcc	gat	ggt	gaa	aga	gag	att	aaa	aag	tac	384																																			
Gly	Ile	Glu	Leu	Ser	Asp	Ser	Asp	Val	Glu	Arg	Glu	Ile	Lys	Lys	Tyr																																				
																115																	120																	125	
atg	gaa	gcc	cat	aag	tct	gat	att	gag	act	aag	aga	tac	tcg	att	ggt	432																																			
Met	Glu	Ala	His	Lys	Ser	Asp	Ile	Glu	Thr	Lys	Arg	Tyr	Ser	Ile	Val																																				
																130																	135																	140	
cct	agt	cta	tta	ggt	gac	gtc	aag	aag	gta	cca	gaa	ttg	aaa	tgg	gcc	480																																			
Pro	Ser	Leu	Leu	Gly	Asp	Val	Lys	Lys	Val	Pro	Glu	Leu	Lys	Trp	Ala																																				
145																150																	155																	160	
aag	cca	aac	tta	ttc	aag	cca	att	att	gac	agt	ttg	gtc	ttg	gag	atg	528																																			
Lys	Pro	Asn	Leu	Phe	Lys	Pro	Ile	Ile	Asp	Ser	Leu	Val	Leu	Glu	Met																																				
																165																	170																	175	
att	gga	cca	aag	gat	gag	aga	gat	gtc	ggt	aag	aag	gaa	aag	aag	aag	576																																			
Ile	Gly	Pro	Lys	Asp	Glu	Arg	Asp	Val	Val	Lys	Lys	Glu	Lys	Lys	Lys																																				
																180																	185																	190	
ctg	act	aaa	aag	caa	ggt	gaa	acc	aag	aag	gaa	gca	cag	att	gag	aga	624																																			
Leu	Thr	Lys	Lys	Gln	Val	Glu	Thr	Lys	Lys	Glu	Ala	Gln	Ile	Glu	Arg																																				
																195																	200																	205	
tcg	atg	ttt	tcc	gaa	ggg	ttt	ttg	ggt	gac	tta	cac	aag	cct	ggt	gaa	672																																			
Ser	Met	Phe	Ser	Glu	Gly	Phe	Leu	Gly	Asp	Leu	His	Lys	Pro	Gly	Glu																																				
																210																	215																	220	
aat	cca	caa	aaa	tat	cct	gaa	tta	atg	aaa	gaa	cat	tta	gaa	ttc	acc	720																																			
Asn	Pro	Gln	Lys	Tyr	Pro	Glu	Leu	Met	Lys	Glu	His	Leu	Glu	Phe	Thr																																				
225																230																	235																	240	
aag	cgt	aaa	gta	ttc	act	aga	ttc	cca	cca	gaa	cca	aac	gga	tat	ttg	768																																			
Lys	Arg	Lys	Val	Phe	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu																																				
																245																	250																	255	
cac	atc	ggg	cat	tcg	aag	gca	att	atg	ggt	aat	ttt	gga	tat	gct	aag	816																																			
His	Ile	Gly	His	Ser	Lys	Ala	Ile	Met	Val	Asn	Phe	Gly	Tyr	Ala	Lys																																				
																260																	265																	270	
tac	aat	ggt	ggt	aac	tcg	tac	tta	aga	ttc	gac	gac	acc	aac	cct	gaa	864																																			
Tyr	Asn	Gly	Gly	Asn	Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu																																				
																275																	280																	285	
gcg	gaa	gaa	gaa	gtg	tat	ttc	aag	tca	att	gaa	aaa	atg	att	gac	tgg	912																																			
Ala	Glu	Glu	Glu	Val	Tyr	Phe	Lys	Ser	Ile	Glu	Lys	Met	Ile	Asp	Trp																																				
																290																	295																	300	
tta	gga	tat	gaa	cca	tgg	aaa	ggt	act	cat	tca	tcc	gac	tat	ttt	gat	960																																			
Leu	Gly	Tyr	Glu	Pro	Trp	Lys	Val	Thr	His	Ser	Ser	Asp	Tyr	Phe	Asp																																				
305																310																	315																	320	
gag	tta	tac	gat	tta	gct	gag	aga	tta	atc	agc	tta	ggt	aaa	ggt	tat	1008																																			
Glu	Leu	Tyr	Asp	Leu	Ala	Glu	Arg	Leu	Ile	Ser	Leu	Gly	Lys	Gly	Tyr																																				
																325																	330																	335	
ggt	tgc	cat	tgt	acg	gcg	gaa	gaa	ggt	aag	gct	caa	aga	ggg	ttg	aag	1056																																			
Val	Cys	His	Cys	Thr	Ala	Glu	Glu	Val	Lys	Ala	Gln	Arg	Gly	Leu	Lys																																				
																340																	345																	350	
gaa	gat	ggt	acc	tta	ggt	gga	gaa	agg	ttt	gca	tgt	aag	cat	cgt	tca	1104																																			
Glu	Asp	Gly	Thr	Leu	Gly	Gly	Glu	Arg	Phe	Ala	Cys	Lys	His	Arg	Ser																																				
																355																	360																	365	
aga	agc	ggt	gaa	gat	agt	atg	gct	gaa	ttc	cgt	aag	atg	aag	aac	ggt	1152																																			
Arg	Ser	Val	Glu	Asp	Ser	Met	Ala	Glu	Phe	Arg	Lys	Met	Lys	Asn	Gly																																				
																370																	375																	380	
gaa	tat	aag	agt	gga	gag	gct	acc	ttg	aga	atg	aag	caa	gac	ttg	gaa	1200																																			
Glu	Tyr	Lys	Ser	Gly	Glu	Ala	Thr	Leu	Arg	Met	Lys	Gln	Asp	Leu	Glu																																				
385																390																	395																	400	
tcg	cca	tct	cca	caa	atg	tgg	gat	ctt	ggt	gcg	tac	aga	gtc	tta	aac	1248																																			
Ser	Pro	Ser	Pro	Gln	Met	Trp	Asp	Leu	Val	Ala	Tyr	Arg	Val	Leu	Asn																																				
																405																	410																	415	
aag	ccc	cac	cac	agg	act	gga	gac	aaa	tgg	aag	atc	tac	cca	aca	tac	1296																																			
Lys	Pro	His	His	Arg	Thr	Gly	Asp	Lys	Trp	Lys	Ile	Tyr	Pro	Thr	Tyr																																				
																420																	425																	430	
gat	ttt	act	cac	tgt	ctt	ggt	gat	tct	ttt	gaa	aac	att	agt	cat	tca	1344																																			
Asp	Phe	Thr	His	Cys	Leu	Val	Asp	Ser	Phe	Glu	Asn	Ile	Ser	His	Ser																																				
																435																	440																	445	
tta	tgt	act	act	gaa	ttt	aga	ctt	tct	aga	gag	tct	tac	gaa	tgg	ttg	1392																																			
Leu	Cys	Thr	Thr	Glu	Phe	Arg	Leu	Ser	Arg	Glu	Ser	Tyr	Glu	Trp	Leu																																				

PF59083SeqList PF59083.txt

450	tgt gac gag cta cac gtt	455	tac aga cca gca caa aga gaa tat ggt aga	1440
Cys Asp Glu Leu His Val	Tyr Arg Pro Ala Gln Arg Glu Tyr Gly Arg	460		
465	tta aat att act ggt acc ata ttg agt aag aga aag att gct aaa tta	475		1488
Leu Asn Ile Thr Gly Thr Ile Leu Ser Lys Arg Lys Ile Ala Lys Leu		480		
485	gtc aac gaa ggt att gtt aga gga tgg gat gat cct aga ttg tac acg	490		1536
Val Asn Glu Gly Ile Val Arg Gly Trp Asp Asp Pro Arg Leu Tyr Thr		495		
500	tta gaa gct atc cgt cgt cgt ggg gtt cca ccg ggc gct att tta agt	505		1584
Leu Glu Ala Ile Arg Arg Arg Gly Val Pro Pro Gly Ala Ile Leu Ser		510		
515	ttc atc aac acg tta ggg gtc acc act tca act act aat att caa gca	520		1632
Phe Ile Asn Thr Leu Gly Val Thr Thr Ser Thr Asn Ile Gln Ala		525		
530	gtg aga ctc gac agt gct atc aga gca ttc ttg gac caa acg acc cca	535		1680
Val Arg Leu Asp Ser Ala Ile Arg Ala Phe Leu Asp Gln Thr Thr Pro		540		
545	aga ttg atg atg att ctt gac cct gtc gaa gtc gaa gtt gag aac tta	545		1728
Arg Leu Met Met Ile Leu Asp Pro Val Glu Val Glu Val Glu Asn Leu		550		
555	cca gaa ggg tac gag gaa atg gtc gag gtg cca tac aaa ccg ggt gac	555		1776
Pro Glu Gly Tyr Glu Glu Met Val Glu Val Pro Tyr Lys Pro Gly Asp		560		
565	acc gtt aag ttc gga acc aga aag gtt ccg ttc acc aag cgt ttc tat	570		1824
Thr Val Lys Phe Gly Thr Arg Lys Val Pro Phe Thr Lys Arg Phe Tyr		575		
580	att gac aga tct gac tac aga gac tct act tcc gac gac tac ttt aga	585		1872
Ile Asp Arg Ser Asp Tyr Arg Asp Ser Thr Ser Asp Tyr Phe Arg		590		
585	tta gcc cct ggc caa cca gtt ggg tta att agg gta cca ttc aat gtt	595		1920
Leu Ala Pro Gly Gln Pro Val Gly Leu Ile Arg Val Pro Phe Asn Val		600		
605	tct gtc aag gac gtt gtc aag gat gac gca ggt aag gtg acg aag atc	605		1968
Ser Val Lys Asp Val Val Lys Asp Asp Ala Gly Lys Val Thr Lys Ile		610		
615	atc gcg cac tac gac aac gac ggt acg ttc aaa aag cct aag act tat	615		2016
Ile Ala His Tyr Asp Asn Asp Gly Thr Phe Lys Lys Pro Lys Thr Tyr		620		
625	atc caa tgg gtc cca aaa tcg gcc tct tca cca atc aag gtc aac gag	625		2064
Ile Gln Trp Val Pro Lys Ser Ala Ser Ser Pro Ile Lys Val Asn Glu		630		
635	gtg agg att cag aac caa ttg ttc aac agc gag aac cca tca gct cac	635		2112
Val Arg Ile Gln Asn Gln Leu Phe Asn Ser Glu Asn Pro Ser Ala His		640		
645	cca gac gga ttc ttg aac gat ctc aac gag caa tcg gaa gag atc tac	645		2160
Pro Asp Gly Phe Leu Asn Asp Leu Asn Glu Gln Ser Glu Glu Ile Tyr		650		
655	cgc gat gcg att gtc gag tcg gct ttc act gaa att aag gag aaa tcg	655		2208
Arg Asp Ala Ile Val Glu Ser Ala Phe Thr Glu Ile Lys Glu Lys Ser		660		
665	cca ttg aat att cct atc gaa gga agc gag ttc aac atc aag gag aag	665		2256
Pro Leu Asn Ile Pro Ile Glu Gly Ser Glu Phe Asn Ile Lys Glu Lys		670		
675	ccg agt gtc gaa acg gtg aga ttc cag gcc ttg aga gtg gga tac ttc	675		2304
Pro Ser Val Glu Thr Val Arg Phe Gln Ala Leu Arg Val Gly Tyr Phe		680		
685	tgc atg gac aag gat tcg agc gcg gac aaa ttg gtg ttg aac cgt att	685		2352
Cys Met Asp Lys Asp Ser Ser Ala Asp Lys Leu Val Leu Asn Arg Ile		690		
695	gtc act ttg aag gag gac tcg tcg aaa aat tga	695		2385
Val Thr Leu Lys Glu Asp Ser Ser Lys Asn		700		
705		705		
710		710		
715		715		
720		720		
725		725		
730		730		
735		735		
740		740		
745		745		
750		750		
755		755		
760		760		
765		765		
770		770		
775		775		
780		780		
785		785		
790		790		

<210> 9950

<211> 794

<212> PRT

<213> Debaryomyces hansenii CBS767

PF59083SeqList PF59083.txt

<400> 9950

```

Met Ala Ser Glu Glu Glu Leu Ile Asn Leu Phe Ser Lys Val Gly Phe
1      5      10      15
Asn Asp Lys Lys Ser Lys Glu Val Cys Lys Asn Lys Lys Val Ser Gln
      20      25      30
Ser Leu Ala Glu Ile Ile Asn Glu Ser Lys Val Glu Glu Thr Asp Glu
      35      40      45
Lys Lys Leu Ser Leu Leu His Ala Leu Ala Val Glu Ser Lys Gly Gly
50      55      60
Asp Val Pro Arg Arg Glu Leu Ile Thr Lys Ala Ile Ile Asp Gly Arg
65      70      75      80
Leu Lys Thr Asn Leu Gln Val Thr Glu Ala Phe Lys Tyr Val Lys Glu
      85      90      95
Asn Pro Glu Thr Ala Asn Asn Glu Thr Met Glu Glu Lys Ser Gly Val
100      105      110
Gly Ile Glu Leu Ser Asp Ser Asp Val Glu Arg Glu Ile Lys Lys Tyr
115      120      125
Met Glu Ala His Lys Ser Asp Ile Glu Thr Lys Arg Tyr Ser Ile Val
130      135      140
Pro Ser Leu Leu Gly Asp Val Lys Lys Val Pro Glu Leu Lys Trp Ala
145      150      155      160
Lys Pro Asn Leu Phe Lys Pro Ile Ile Asp Ser Leu Val Leu Glu Met
165      170      175
Ile Gly Pro Lys Asp Glu Arg Asp Val Lys Lys Glu Lys Lys Lys
180      185      190
Leu Thr Lys Lys Gln Val Glu Thr Lys Lys Glu Ala Gln Ile Glu Arg
195      200      205
Ser Met Phe Ser Glu Gly Phe Leu Gly Asp Leu His Lys Pro Gly Glu
210      215      220
Asn Pro Gln Lys Tyr Pro Glu Leu Met Lys Glu His Leu Glu Phe Thr
225      230      235      240
Lys Arg Lys Val Phe Thr Arg Phe Pro Pro Glu Pro Asn Gly Tyr Leu
245      250      255
His Ile Gly His Ser Lys Ala Ile Met Val Asn Phe Gly Tyr Ala Lys
260      265      270
Tyr Asn Gly Gly Asn Cys Tyr Leu Arg Phe Asp Asp Thr Asn Pro Glu
275      280      285
Ala Glu Glu Glu Val Tyr Phe Lys Ser Ile Glu Lys Met Ile Asp Trp
290      295      300
Leu Gly Tyr Glu Pro Trp Lys Val Thr His Ser Ser Asp Tyr Phe Asp
305      310      315      320
Glu Leu Tyr Asp Leu Ala Glu Arg Leu Ile Ser Leu Gly Lys Gly Tyr
325      330      335
Val Cys His Cys Thr Ala Glu Glu Val Lys Ala Gln Arg Gly Leu Lys
340      345      350
Glu Asp Gly Thr Leu Gly Gly Glu Arg Phe Ala Cys Lys His Arg Ser
355      360      365
Arg Ser Val Glu Asp Ser Met Ala Glu Phe Arg Lys Met Lys Asn Gly
370      375      380
Glu Tyr Lys Ser Gly Glu Ala Thr Leu Arg Met Lys Gln Asp Leu Glu
385      390      395      400
Ser Pro Ser Pro Gln Met Trp Asp Leu Val Ala Tyr Arg Val Leu Asn
405      410      415
Lys Pro His His Arg Thr Gly Asp Lys Trp Lys Ile Tyr Pro Thr Tyr
420      425      430
Asp Phe Thr His Cys Leu Val Asp Ser Phe Glu Asn Ile Ser His Ser
435      440      445
Leu Cys Thr Thr Glu Phe Arg Leu Ser Arg Glu Ser Tyr Glu Trp Leu
450      455      460
Cys Asp Glu Leu His Val Tyr Arg Pro Ala Gln Arg Glu Tyr Gly Arg
465      470      475      480
Leu Asn Ile Thr Gly Thr Ile Leu Ser Lys Arg Lys Ile Ala Lys Leu
485      490      495
Val Asn Glu Gly Ile Val Arg Gly Trp Asp Asp Pro Arg Leu Tyr Thr
500      505      510
Leu Glu Ala Ile Arg Arg Arg Gly Val Pro Pro Gly Ala Ile Leu Ser
515      520      525
Phe Ile Asn Thr Leu Gly Val Thr Thr Ser Thr Thr Ile Gln Ala

```

PF59083SeqList PF59083.txt

530
 Val Arg Leu Asp Ser Ala 535
 545 Arg Leu Met Met Ile 550
 Pro Glu Gly Tyr 565
 Thr Val Lys Phe Gly Thr Arg Lys Val 570
 Ile Asp Arg Ser Asp Tyr Arg Asp Ser Thr Ser Asp Tyr Phe Arg 585
 Leu Ala Pro Gly Gln Pro Val Gly Leu Ile Arg Val Pro Phe Asn Val 590
 625 Ser Val Lys Asp Val Val Lys Asp Asp Ala Gly Lys Val Thr Lys Ile 605
 Ile Ala His Tyr 660
 Ile Gln Trp Val Pro Lys Ser Ala Ser Ser Pro Ile Lys Val Asn Glu 670
 Val Arg Ile Gln Asn Gln Leu Phe Asn Ser Glu Asn Pro Ser Ala His 685
 Pro Asp Gly Phe Leu Asn Asp Leu Asn Glu Gln Ser Glu Glu Ile Tyr 700
 705 Arg Asp Ala Ile Val Glu Ser Ala Phe Thr Glu Ile Lys Glu Lys Ser 715
 Pro Leu Asn Ile Pro Ile Glu Gly Ser Glu Phe Asn Ile Lys Glu Lys 730
 Pro Ser Val Glu Thr Val Arg Phe Gln Ala Leu Arg Val Gly Tyr Phe 745
 Cys Met Asp Lys Asp Ser Ser Ala Asp Lys Leu Val Leu Asn Arg Ile 760
 770 Val Thr Leu Lys Glu Asp Ser Ser Lys Asn 780
 785

<210> 9951

<211> 2382

<212> DNA

<213> Yarrowia lipolytica CLIB122

<220>

<221> CDS

<222> (1)..(2382)

<400> 9951

atg tcc gac gtt gcc gag ctc agc acc aag ctg gaa cat ctc ggt ttt	48
Met Ser Asp Val Ala Glu Leu Ser Thr Lys Leu Glu His Leu Gly Phe	
1 5 10 15	
gcc gag ccc aag atc aag gag gtg ttg aaa aac aaa aag gtc gcc gcc	96
Ala Glu Pro Lys Ile Lys Glu Val Leu Lys Asn Lys Lys Val Ala Ala	
20 25 30	
tcc ttc aac gac att ctc aac gta gtg aac gtg ggc aag gac gag aag	144
Ser Phe Asn Asp Ile Leu Asn Val Val Asn Val Gly Lys Asp Glu Lys	
35 40 45	
cga gct gct cta ctc cac aac ctc gcc tcg tcc tcc aag gac gcc aag	192
Arg Ala Ala Leu Leu His Asn Leu Ala Ser Ser Ser Lys Asp Ala Lys	
50 55 60	
gat gaa gcc gtg atc aag aag cga aat gag gtc gcc tct gcc att gcc	240
Asp Glu Ala Val Ile Lys Lys Arg Asn Glu Val Ala Ser Ala Ile Ala	
65 70 75 80	
gac ggc cga atc aag acc aac gtg cag ctg gac gcc gcc tgg aag tgg	288
Asp Gly Arg Ile Lys Thr Asn Val Gln Leu Asp Ala Ala Trp Lys Trp	
85 90 95	
gcc cag gac cta cac agc tcc gag agc ctc gat cag gct gct ggc gtg	336
Ala Gln Asp Leu His Ser Ser Glu Ser Leu Asp Gln Ala Ala Gly Val	
100 105 110	
ggc att gag gtc acc cgg gac gac gtt tat cgt gag att gcc gcc tac	384
Gly Ile Glu Val Thr Arg Asp Asp Val Tyr Arg Glu Ile Ala Ala Tyr	
115 120 125	
att gcc gca aac aag gct cag ctc gag gag gag cga tac aag gcc ctg	432

PF59083SeqList PF59083.txt

Ile	Ala	Ala	Asn	Lys	Ala	Gln	Leu	Glu	Glu	Glu	Arg	Tyr	Lys	Ala	Leu	
130	130					135					140					
cct	ggt	gtc	atg	gtg	gct	gcc	aag	aag	atc	cct	gct	ctc	aag	tgg	gcc	480
Pro	Gly	Val	Met	Val	Ala	Ala	Lys	Lys	Ile	Pro	Ala	Leu	Lys	Trp	Ala	
145					150					155					160	
aac	cct	gcc	gac	ttt	aag	ccc	gtg	atc	gac	gag	cag	ctc	aag	gag	ctt	528
Asn	Pro	Ala	Asp	Phe	Lys	Pro	Val	Ile	Asp	Glu	Gln	Leu	Lys	Glu	Leu	
				165					170						175	
ctg	gga	ccc	aag	gat	gag	cga	gat	ctc	gtc	aag	aag	aag	gcg	ccc	aag	576
Leu	Gly	Pro	Lys	Asp	Glu	Arg	Asp	Leu	Val	Lys	Lys	Lys	Ala	Pro	Lys	
				180					185						190	
gcc	aag	cct	gct	gcc	aag	gat	gct	gcc	aag	aag	gag	gag	cct	gag	aag	624
Ala	Lys	Pro	Ala	Ala	Lys	Asp	Ala	Ala	Lys	Lys	Glu	Glu	Pro	Glu	Lys	
				195					200						205	
gtg	tct	gcc	acc	gcc	atg	ttc	acc	acc	ggg	ttc	ctg	ggc	aac	ctg	cac	672
Val	Ser	Ala	Thr	Ala	Met	Phe	Thr	Thr	Gly	Phe	Leu	Gly	Asn	Leu	His	
				210											220	
aag	act	gga	gag	aac	cct	cag	gcc	aac	atg	gag	cga	atg	ggt	gag	cat	720
Lys	Thr	Gly	Glu	Asn	Pro	Gln	Ala	Asn	Met	Glu	Arg	Met	Val	Glu	His	
225					230					235					240	
ctc	aag	gcc	acc	aag	ggc	cag	gtt	ttc	acc	cgg	ttc	cct	ccc	gaa	cct	768
Leu	Lys	Ala	Thr	Lys	Gly	Gln	Val	Phe	Thr	Arg	Phe	Pro	Pro	Glu	Pro	
				245					250						255	
aac	gga	tac	ctg	cac	att	ggc	cac	tcc	aag	gcc	atc	acc	ggt	aac	ttt	816
Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ser	Lys	Ala	Ile	Thr	Val	Asn	Phe	
				260					265						270	
ggc	tat	gcc	cag	ttc	aac	aag	ggg	aag	tgc	tac	ctg	cga	ttt	gac	gac	864
Gly	Tyr	Ala	Gln	Phe	Asn	Lys	Gly	Lys	Cys	Tyr	Leu	Arg	Phe	Asp	Asp	
				275					280						285	
acg	aac	cct	gag	gcc	gag	gag	gag	cga	ttc	ttc	act	tcc	att	cga	gag	912
Thr	Asn	Pro	Glu	Ala	Glu	Glu	Glu	Arg	Phe	Phe	Thr	Ser	Ile	Arg	Glu	
				290											300	
acc	att	gag	tgg	ctg	ggc	ttc	gag	ccc	tac	aag	gtc	acc	tac	tcg	tcg	960
Thr	Ile	Glu	Trp	Leu	Gly	Phe	Glu	Pro	Tyr	Lys	Val	Thr	Tyr	Ser	Ser	
305					310					315					320	
gac	tac	ttc	cag	gag	ctg	tac	gac	cta	gct	gag	aag	ctg	atc	gag	tgt	1008
Asp	Tyr	Phe	Gln	Glu	Leu	Tyr	Asp	Leu	Ala	Glu	Lys	Leu	Ile	Glu	Cys	
				325					330						335	
gga	ggt	gcg	ttt	gtg	tgt	cac	cag	acc	gcc	gag	gag	atg	aag	gct	tcc	1056
Gly	Gly	Ala	Phe	Val	Cys	His	Gln	Thr	Ala	Glu	Glu	Met	Lys	Ala	Ser	
				340					345						350	
cga	gga	gtg	tct	gag	gga	tct	cga	gga	ggc	gag	cga	gtg	cct	tct	ccc	1104
Arg	Gly	Val	Ser	Glu	Gly	Ser	Arg	Gly	Gly	Glu	Arg	Val	Pro	Ser	Pro	
				355					360						365	
tgg	aga	aac	aga	acc	gtg	gag	gag	aac	ctg	gtg	gag	ttc	cga	aag	atg	1152
Trp	Arg	Asn	Arg	Thr	Val	Glu	Glu	Asn	Leu	Val	Glu	Phe	Arg	Lys	Met	
					375										380	
cga	gac	ggc	cac	tac	aag	ccc	gga	gag	gca	gtt	ttg	cga	atg	aag	caa	1200
Arg	Asp	Gly	His	Tyr	Lys	Pro	Gly	Glu	Ala	Val	Leu	Arg	Met	Lys	Gln	
385					390					395					400	
gat	ctc	aac	aac	ccc	aac	ccc	caa	atg	tgg	gat	ctg	gtt	gcc	tac	cga	1248
Asp	Leu	Asn	Asn	Pro	Asn	Pro	Gln	Met	Trp	Asp	Leu	Val	Ala	Tyr	Arg	
				405					410						415	
gta	ctc	aac	gct	ccc	cat	cac	cga	act	gcc	gac	aag	tgg	aag	att	tac	1296
Val	Leu	Asn	Ala	Pro	His	His	Arg	Thr	Ala	Asp	Lys	Trp	Lys	Ile	Tyr	
				420					425						430	
cct	acc	tac	gac	ttc	acc	cac	tgt	ctg	gtt	gat	tcg	ctg	gag	aat	att	1344
Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys	Leu	Val	Asp	Ser	Leu	Glu	Asn	Ile	
				435					440						445	
tcg	cat	tcg	ctt	tgt	acc	acc	gag	ttc	tac	ctc	tcc	cgt	gag	tca	tac	1392
Ser	His	Ser	Leu	Cys	Thr	Thr	Glu	Phe	Tyr	Leu	Ser	Arg	Glu	Ser	Tyr	
					455										460	
gag	tgg	ctg	tgt	gac	gct	gtg	gac	gtc	tac	cga	cca	gcc	cag	cga	gag	1440
Glu	Trp	Leu	Cys	Asp	Ala	Val	Asp	Val	Tyr	Arg	Pro	Ala	Gln	Arg	Glu	
465					470					475					480	
tat	ggc	cga	ctt	aac	atc	act	gga	acc	gtt	ctt	tcc	aag	cga	aag	att	1488
Tyr	Gly	Arg	Leu	Asn	Ile	Thr	Gly	Thr	Val	Leu	Ser	Lys	Arg	Lys	Ile	
				485					490						495	
gcc	aag	ctc	ggt	tct	gag	ggt	cat	gtt	cga	ggc	tgg	gat	gat	ccc	cgt	1536

PF59083SeqList PF59083.txt

Ala	Lys	Leu	Val	Ser	Glu	Gly	His	Val	Arg	Gly	Trp	Asp	Asp	Pro	Arg	
ctc	ttc	act	ctg	gtc	gct	att	cga	cgg	cga	ggg	att	cct	cct	gga	gcc	1584
Leu	Phe	Thr	Leu	Val	Ala	Ile	Arg	Arg	Arg	Gly	Ile	Pro	Pro	Gly	Ala	
		515					520					525				
att	ctc	aac	ttt	gtc	tcc	act	ctc	ggg	gtc	acc	act	gcc	gag	tcc	aac	1632
Ile	Leu	Asn	Phe	Val	Ser	Thr	Leu	Gly	Val	Thr	Thr	Ala	Glu	Ser	Asn	
		530				535					540					
att	cag	cat	tct	cga	ttt	gag	aac	aat	gtg	cgg	aag	tac	ctt	gag	gac	1680
Ile	Gln	His	Ser	Arg	Phe	Glu	Asn	Asn	Val	Arg	Lys	Tyr	Leu	Glu	Asp	
		545			550				555						560	
act	act	cct	cgt	ctc	atg	atg	gtg	ctg	gac	ccc	gtc	aag	gtg	acc	att	1728
Thr	Thr	Pro	Arg	Leu	Met	Met	Val	Leu	Asp	Pro	Val	Lys	Val	Thr	Ile	
				565					570					575		
gag	aac	ctg	cct	gag	gac	cac	ttt	gaa	gag	ttt	gac	atg	ccc	ttt	ggc	1776
Glu	Asn	Leu	Pro	Glu	Asp	His	Phe	Glu	Glu	Phe	Asp	Met	Pro	Phe	Gly	
				580				585						590		
aag	aat	gac	gag	cgg	tcg	cga	aag	gtg	ccc	ttc	acc	cga	gag	ctg	tac	1824
Lys	Asn	Asp	Glu	Arg	Ser	Arg	Lys	Val	Pro	Phe	Thr	Arg	Glu	Leu	Tyr	
		595					600					605				
att	gac	cga	agc	gac	ttt	gag	gag	tct	gct	ggc	aag	gag	ttc	ttc	cga	1872
Ile	Asp	Arg	Ser	Asp	Phe	Glu	Glu	Ser	Ala	Gly	Lys	Glu	Phe	Phe	Arg	
		610				615					620					
ctc	act	gct	act	cag	ccc	gtg	ggg	ctg	ctc	aag	gtg	ccc	cac	aac	att	1920
Leu	Thr	Ala	Thr	Gln	Pro	Val	Gly	Leu	Leu	Lys	Val	Pro	His	Asn	Ile	
		625			630					635					640	
tct	ctc	aag	gag	gtc	aag	aag	gat	gct	gct	gga	aac	atc	acc	gag	ctg	1968
Ser	Leu	Lys	Glu	Val	Lys	Lys	Asp	Ala	Ala	Gly	Asn	Ile	Thr	Glu	Leu	
				645				650						655		
att	tgc	cat	ctc	gac	aac	gac	att	ccc	ttc	aag	aag	ccc	aag	aca	tac	2016
Ile	Cys	His	Leu	Asp	Asn	Asp	Ile	Pro	Phe	Lys	Lys	Pro	Lys	Thr	Tyr	
				660				665						670		
atc	cag	tgg	gtc	ccc	gag	tgt	gct	gcc	aag	aag	tct	ccc	gtc	aag	att	2064
Ile	Gln	Trp	Val	Pro	Glu	Cys	Ala	Ala	Lys	Lys	Ser	Pro	Val	Lys	Ile	
		675					680							685		
tcc	gag	acc	cga	atc	ttc	aag	cag	ctc	ttc	aag	tcc	gag	aac	cct	cag	2112
Ser	Glu	Thr	Arg	Ile	Phe	Lys	Gln	Leu	Phe	Lys	Ser	Glu	Asn	Pro	Gln	
		690				695					700					
ggc	cac	ccc	gat	gga	tac	ctt	gca	gat	ctt	gct	gag	gag	tcc	gag	gtc	2160
Gly	His	Pro	Asp	Gly	Tyr	Leu	Ala	Asp	Leu	Ala	Glu	Glu	Ser	Glu	Val	
		705			710				715						720	
atc	cac	aag	cat	gct	ctt	gtc	gag	ccc	ggc	ttc	tac	gac	gtc	aag	gag	2208
Ile	His	Lys	His	Ala	Leu	Val	Glu	Pro	Gly	Phe	Tyr	Asp	Val	Lys	Glu	
				725				730						735		
aac	tct	cct	tgg	gtc	act	ggg	gag	cat	act	ggc	aag	gag	aag	aag	gga	2256
Asn	Ser	Pro	Trp	Val	Thr	Gly	Glu	His	Thr	Gly	Lys	Glu	Lys	Lys	Gly	
				740				745						750		
tcc	ccc	gag	agt	gtg	cgg	ttc	cag	gct	ctt	cga	gtg	gga	tac	ttt	tgc	2304
Ser	Pro	Glu	Ser	Val	Arg	Phe	Gln	Ala	Leu	Arg	Val	Gly	Tyr	Phe	Cys	
		755					760							765		
atg	gat	aag	gat	tct	act	gag	aag	gat	att	gtt	ctg	aac	cag	att	gtt	2352
Met	Asp	Lys	Asp	Ser	Thr	Glu	Lys	Asp	Ile	Val	Leu	Asn	Gln	Ile	Val	
		770				775					780					
tct	ctg	aag	gag	gat	aac	cag	aag	aag	taa							2382
Ser	Leu	Lys	Glu	Asp	Asn	Gln	Lys	Lys								
					790											

<210> 9952

<211> 793

<212> PRT

<213> Yarrowia lipolytica CLIB122

<400> 9952

Met	Ser	Asp	Val	Ala	Glu	Leu	Ser	Thr	Lys	Leu	Glu	His	Leu	Gly	Phe
1				5					10					15	
Ala	Glu	Pro	Lys	Ile	Lys	Glu	Val	Leu	Lys	Asn	Lys	Lys	Val	Ala	Ala
			20					25					30		
Ser	Phe	Asn	Asp	Ile	Leu	Asn	Val	Val	Asn	Val	Gly	Lys	Asp	Glu	Lys
		35					40					45			

PF59083SeqList PF59083.txt

Arg Ala Ala Leu Leu His Asn 50 55 Leu Ala Ser Ser 60 Lys Asp Ala Lys
 Asp Glu Ala Val Ile Lys 65 70 Lys Arg Asn Glu Val 75 Ala Ser Ala Ile Ala
 Asp Gly Arg Ile Lys 85 Thr Asn Val Gln Leu 90 Asp Ala Ala Trp Lys 95 Trp
 Ala Gln Asp Leu His Ser Ser Glu Ser Leu Asp Gln Ala Ala Gly Val
 Gly Ile Glu Val Thr Arg Asp Asp Val Tyr Arg Glu Ile Ala Ala Tyr
 Ile Ala 115 130 Asn Lys Ala Gln 120 135 Leu Glu Glu Glu Arg 140 Tyr Lys Ala Leu
 Pro Gly Val Met Val Ala 150 155 Lys Lys Ile Pro Ala Leu Lys Trp Ala
 Asn Pro Ala Asp Phe 165 Lys Pro Val Ile Asp 170 Glu Gln Leu Lys Glu Leu
 Leu Gly Pro Lys Asp Glu Arg Asp Leu Val Lys Lys Lys Ala Pro Lys
 Ala Lys Pro Ala Ala Lys Asp Ala 185 200 Ala Lys Lys Glu Glu Pro Glu Lys
 Val Ser 210 Ala Thr Ala Met Phe 215 Thr Thr Gly Phe Leu 220 Gly Asn Leu His
 Lys Thr Gly Glu Asn Pro 230 Gln Ala Asn Met Glu Arg Met Val Glu His
 Leu Lys Ala Thr Lys 245 Gly Gln Val Phe Thr 250 Arg Phe Pro Pro Glu Pro
 Asn Gly Tyr Leu His Ile Gly His Ser Lys Ala Ile Thr Val Asn Phe
 Gly Tyr Ala Gln Phe Asn Lys Gly 280 Lys Cys Tyr Leu Arg Phe Asp Asp
 Thr Asn 290 Pro Glu Ala Glu Glu 295 Glu Arg Phe Phe Thr Ser Ile Arg Glu
 Thr Ile Glu Trp Leu Gly 310 Phe Glu Pro Tyr Lys Val Thr Tyr Ser Ser
 Asp Tyr Phe Gln Glu 325 Leu Tyr Asp Leu Ala 330 Glu Lys Leu Ile Glu Cys
 Gly Gly Ala Phe Val Cys His Gln Thr Ala Glu Glu Met Lys Ala Ser
 Arg Gly Val Ser Glu Gly Ser Arg Gly Gly Glu Arg Val Pro Ser Pro
 Trp Arg Asn Arg Thr Val Glu Glu Asn Leu Val Glu Phe Arg Lys Met
 Arg Asp Gly His Tyr Lys 390 Pro Gly Glu Ala Val 395 Leu Arg Met Lys Gln
 Asp Leu Asn Asn Pro 405 Asn Pro Gln Met Trp 410 Asp Leu Val Ala Tyr Arg
 Val Leu Asn Ala Pro His His Arg Thr Ala Asp Lys Trp Lys Ile Tyr
 Pro Thr Tyr Asp Phe Thr His Cys Leu Val Asp Ser Leu Glu Asn Ile
 Ser His Ser Leu Cys Thr Thr 455 Glu Phe Tyr Leu Ser Arg Glu Ser Tyr
 Glu Trp Leu Cys Asp Ala Val Asp Val Tyr Arg 475 Pro Ala Gln Arg Glu
 Tyr Gly Arg Leu Asn 485 Ile Thr Gly Thr Val 490 Leu Ser Lys Arg Lys Ile
 Ala Lys Leu Val Ser Glu Gly His Val Arg Gly Trp Asp Asp Pro Arg
 Leu Phe Thr 515 Leu Val Ala Ile Arg Arg Arg Gly Ile Pro Pro Gly Ala
 Ile Leu Asn Phe Val Ser Thr 535 Leu Gly Val Thr Thr Ala Glu Ser Asn
 Ile Gln His Ser Arg Phe 550 Glu Asn Asn Val Arg 555 Lys Tyr Leu Glu Asp
 Thr Thr Pro Arg Leu 565 Met Met Val Leu Asp 570 Pro Val Lys Val Thr Ile
 Glu Asn Leu Pro Glu Asp His Phe Glu Glu Phe Asp Met Pro Phe Gly
 Lys Asn Asp Glu Arg Ser Arg Lys Val Pro Phe Thr Arg Glu Leu Tyr

PF59083SeqList PF59083.txt

595
 Ile Asp Arg Ser Asp Phe Glu Glu Ser Ala Gly Lys Glu Phe Phe Arg
 610 615 620
 Leu Thr Ala Thr Gln Pro Val Gly Leu Leu Lys Val Pro His Asn Ile
 625 630 635 640
 Ser Leu Lys Glu Val Lys Lys Asp Ala Ala Gly Asn Ile Thr Glu Leu
 645 650 655
 Ile Cys His Leu Asp Asn Asp Ile Pro Phe Lys Lys Pro Lys Thr Tyr
 660 665 670
 Ile Gln Trp Val Pro Glu Cys Ala Ala Lys Lys Ser Pro Val Lys Ile
 675 680 685
 Ser Glu Thr Arg Ile Phe Lys Gln Leu Phe Lys Ser Glu Asn Pro Gln
 690 695 700
 Gly His Pro Asp Gly Tyr Leu Ala Asp Leu Ala Glu Glu Ser Glu Val
 705 710 715 720
 Ile His Lys His Ala Leu Val Glu Pro Gly Phe Tyr Asp Val Lys Glu
 725 730 735
 Asn Ser Pro Trp Val Thr Gly Glu His Thr Gly Lys Glu Lys Lys Gly
 740 745 750
 Ser Pro Glu Ser Val Arg Phe Gln Ala Leu Arg Val Gly Tyr Phe Cys
 755 760 765
 Met Asp Lys Asp Ser Thr Glu Lys Asp Ile Val Leu Asn Gln Ile Val
 770 775 780
 Ser Leu Lys Glu Asp Asn Gln Lys Lys
 785 790

<210> 9953

<211> 2391

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(2391)

<400> 9953

atg ggc acc gga ggc ggc gag ggg gac aag tcg gcc gtg ctg ccg ctg	48
Met Gly Thr Gly Gly Gly Glu Gly Asp Lys Ser Ala Val Leu Pro Leu	
1 5 10 15	
gag gcg ctg ctg gcg ctg ggg ctc gac cag cgc acg gcg gag aac gct	96
Glu Ala Leu Leu Ala Leu Gly Leu Asp Gln Arg Thr Ala Glu Asn Ala	
20 25 30	
ctg gtc aac agc aag gtc acc gcc aac ctc gcc gcc gtc ata gcc gag	144
Leu Val Asn Ser Lys Val Thr Ala Asn Leu Ala Ala Val Ile Ala Glu	
35 40 45	
gct ggt ata agt gga tgt gat aag acg gtt ggg aac ctc ctg tac acg	192
Ala Gly Ile Ser Gly Cys Asp Lys Thr Val Gly Asn Leu Leu Tyr Thr	
50 55 60	
gtt gcc act aaa tac cca acc aat gcg ctt gtc cat cgt cct gta ctc	240
Val Ala Thr Lys Tyr Pro Thr Asn Ala Leu Val His Arg Pro Val Leu	
65 70 75 80	
att gac tat att gtg tca acg aag ata aag aat cct gca caa cta gat	288
Ile Asp Tyr Ile Val Ser Thr Lys Ile Lys Asn Pro Ala Gln Leu Asp	
85 90 95	
gct gct ctg tca ttc ctt act aat act ggc cct gac tct tta gat act	336
Ala Ala Leu Ser Phe Leu Thr Asn Thr Gly Pro Asp Ser Leu Asp Thr	
100 105 110	
ggg aag ttt gaa gaa gcc tgt ggt gta ggt gtg gtt gtt tca att gaa	384
Gly Lys Phe Glu Glu Ala Cys Gly Val Gly Val Val Val Ser Ile Glu	
115 120 125	
gag att aaa tca aca gtc aat gag gta tta aag cat aat atg gag gct	432
Glu Ile Lys Ser Thr Val Asn Glu Val Leu Lys His Asn Met Glu Ala	
130 135 140	
ata ttg gag cag cga tat cat att aat gtt ggt aac cta tgc gga cag	480
Ile Leu Glu Gln Arg Tyr His Ile Asn Val Gly Asn Leu Cys Gly Gln	
145 150 155 160	
gtt agg aag agg cac ccc tgg ggt gat gct aag gcg acc aag gat gaa	528
Val Arg Lys Arg His Pro Trp Gly Asp Ala Lys Ala Thr Lys Asp Glu	
165 170 175	

PF59083SeqList PF59083.txt

att	gac	aag	aag	ctt	gca	gag	ata	tta	ggt	cca	aag	aca	gat	gct	gac	576
Ile	Asp	Lys	Lys	Leu	Ala	Glu	Ile	Leu	Gly	Pro	Lys	Thr	Asp	Ala	Asp	
			180					185					190			
aat	gta	aaa	cca	gtg	aaa	aag	aaa	aag	gaa	aaa	gca	gca	aaa	gtt	gag	624
Asn	Val	Lys	Pro	Val	Lys	Lys	Lys	Lys	Glu	Lys	Ala	Ala	Lys	Val	Glu	
		195					200					205				
gag	aaa	aaa	gct	gca	gta	gtc	act	gct	gca	ccg	cca	tct	gag	gag	gaa	672
Glu	Lys	Lys	Ala	Ala	Val	Val	Thr	Ala	Ala	Pro	Pro	Ser	Glu	Glu	Glu	
	210					215					220					
ttg	aat	cca	tac	tct	ata	ttt	cct	cag	cca	gag	gaa	aat	ttt	aag	gtt	720
Leu	Asn	Pro	Tyr	Ser	Ile	Phe	Pro	Gln	Pro	Glu	Glu	Asn	Phe	Lys	Val	
225					230					235					240	
cat	aca	gaa	ata	ttc	tat	agt	gat	ggg	aac	ata	tgg	aga	gcg	cat	aac	768
His	Thr	Glu	Ile	Phe	Tyr	Ser	Asp	Gly	Asn	Ile	Trp	Arg	Ala	His	Asn	
			245					250						255		
agt	aag	gag	att	tta	gag	aaa	cac	ctt	aag	gca	acc	ggt	gga	aaa	gtg	816
Ser	Lys	Glu	Ile	Leu	Glu	Lys	His	Leu	Lys	Ala	Thr	Gly	Gly	Lys	Val	
		260					265					270				
atg	acc	cgt	ttc	cca	cca	gaa	cct	aat	gga	tat	ctt	cat	att	ggt	cat	864
Met	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	
		275					280					285				
gcc	aag	gct	atg	ttt	att	gat	ttt	gga	ctg	gcg	aaa	gag	aga	aat	ggt	912
Ala	Lys	Ala	Met	Phe	Ile	Asp	Phe	Gly	Leu	Ala	Lys	Glu	Arg	Asn	Gly	
	290					295				300						
cat	tgt	tac	ctt	agg	ttt	gat	gac	aca	aat	cca	gaa	gcc	gaa	aag	aaa	960
His	Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys	Lys	
305					310					315					320	
gag	tat	att	gac	cac	att	cag	gaa	atc	gta	cac	tgg	atg	gga	tgg	gag	1008
Glu	Tyr	Ile	Asp	His	Ile	Gln	Glu	Ile	Val	His	Trp	Met	Gly	Trp	Glu	
			325						330					335		
ccc	tac	aaa	gtt	aca	tat	aca	agt	gat	tat	ttc	cag	gct	tta	tat	gag	1056
Pro	Tyr	Lys	Val	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Gln	Ala	Leu	Tyr	Glu	
		340					345					350				
cat	gca	gtt	gag	tta	ata	cga	aaa	ggg	cta	gcc	tat	gtg	gat	cac	cag	1104
His	Ala	Val	Glu	Leu	Ile	Arg	Lys	Gly	Leu	Ala	Tyr	Val	Asp	His	Gln	
		355					360					365				
acc	gca	gaa	gaa	atc	aag	gaa	tac	agg	gaa	aag	aaa	atg	aat	agt	cca	1152
Thr	Ala	Glu	Glu	Ile	Lys	Glu	Tyr	Arg	Glu	Lys	Lys	Met	Asn	Ser	Pro	
	370					375					380					
tgg	agg	gat	aga	ccc	att	gaa	gaa	tca	ctg	aaa	cta	ttt	gaa	gac	atg	1200
Trp	Arg	Asp	Arg	Pro	Ile	Glu	Glu	Ser	Leu	Lys	Leu	Phe	Glu	Asp	Met	
385					390					395					400	
aga	cgt	ggg	ttg	att	gct	gaa	ggt	gca	gca	aca	ctc	cga	atg	aaa	caa	1248
Arg	Arg	Gly	Leu	Ile	Ala	Glu	Gly	Ala	Ala	Thr	Leu	Arg	Met	Lys	Gln	
			405					410						415		
gat	atg	cag	aat	gat	aac	aag	aat	atg	tct	gat	tta	ata	gca	tat	aga	1296
Asp	Met	Gln	Asn	Asp	Asn	Lys	Asn	Met	Ser	Asp	Leu	Ile	Ala	Tyr	Arg	
		420					425					430				
ata	aaa	ttc	act	cct	cat	cca	cat	gct	ggt	gat	aag	tgg	tgc	atc	tat	1344
Ile	Lys	Phe	Thr	Pro	His	Pro	His	Ala	Gly	Asp	Lys	Trp	Cys	Ile	Tyr	
		435					440					445				
cca	agc	tat	gac	tat	gct	cac	tgc	atg	gtg	gat	tct	ctt	gag	aac	att	1392
Pro	Ser	Tyr	Asp	Tyr	Ala	His	Cys	Met	Val	Asp	Ser	Leu	Glu	Asn	Ile	
	450					455					460					
aca	cat	tcg	ctg	tgc	acg	ctc	gag	ttt	gac	ata	cgt	cgc	ccg	tca	tac	1440
Thr	His	Ser	Leu	Cys	Thr	Leu	Glu	Phe	Asp	Ile	Arg	Arg	Pro	Ser	Tyr	
465					470					475					480	
tac	tgg	cta	ctt	gtt	gcc	ttg	ggc	ctg	tac	cag	cca	tat	gtt	tgg	gag	1488
Tyr	Trp	Leu	Leu	Val	Ala	Leu	Gly	Leu	Tyr	Gln	Pro	Tyr	Val	Trp	Glu	
			485					490						495		
tat	tcg	agg	cta	aac	ata	tcg	aat	act	gtg	atg	tct	aaa	aga	aag	ttg	1536
Tyr	Ser	Arg	Leu	Asn	Ile	Ser	Asn	Thr	Val	Met	Ser	Lys	Arg	Lys	Leu	
		500					505					510				
aat	cga	ctt	gtg	aca	gaa	aag	tgg	gta	gat	ggg	tgg	gat	gac	cct	cgt	1584
Asn	Arg	Leu	Val	Thr	Glu	Lys	Trp	Val	Asp	Gly	Trp	Asp	Asp	Pro	Arg	
		515					520					525				
ttg	ttg	aca	cta	gca	gga	ttg	cgg	cga	cgt	gga	gtg	tca	tca	act	gca	1632
Leu	Leu	Thr	Leu	Ala	Gly	Leu	Arg	Arg	Arg	Gly	Val	Ser	Ser	Thr	Ala	
	530					535					540					

PF59083SeqList PF59083.txt

att	aat	tcg	ttt	att	tgt	gga	att	gga	ata	aca	aga	agt	gac	aat	agc	1680
Ile	Asn	Ser	Phe	Ile	Cys	Gly	Ile	Gly	Ile	Thr	Arg	Ser	Asp	Asn	Ser	
545					550					555					560	
tta	att	cgg	gtt	gac	cgt	ctt	gaa	tat	cat	atc	aga	gaa	gag	ctt	aat	1728
Leu	Ile	Arg	Val	Asp	Arg	Leu	Glu	Tyr	His	Ile	Arg	Glu	Glu	Leu	Asn	
				565					570					575		
aaa	aca	gct	tcc	cgt	gcc	atg	gtt	gtg	ttg	aat	cct	cta	aag	gtt	gta	1776
Lys	Thr	Ala	Ser	Arg	Ala	Met	Val	Val	Leu	Asn	Pro	Leu	Lys	Val	Val	
			580					585					590			
ata	act	aac	ttg	gag	gat	gaa	aaa	gtc	ata	gac	ctt	gat	gga	aaa	atg	1824
Ile	Thr	Asn	Leu	Glu	Asp	Glu	Lys	Val	Ile	Asp	Leu	Asp	Gly	Lys	Met	
			595				600					605				
tgg	cct	gat	gct	cct	gca	gac	gat	gct	tca	tcc	tac	tac	aag	gtt	cct	1872
Trp	Pro	Asp	Ala	Pro	Ala	Asp	Asp	Ala	Ser	Ser	Tyr	Tyr	Lys	Val	Pro	
	610					615					620					
ttc	tca	aga	atc	gtt	tac	atc	gaa	aaa	act	gat	ttt	cgt	cta	aag	gac	1920
Phe	Ser	Arg	Ile	Val	Tyr	Ile	Glu	Lys	Thr	Asp	Phe	Arg	Leu	Lys	Asp	
625					630					635					640	
tcg	aaa	gat	tac	tac	ggg	cta	gct	cct	ggg	aaa	tct	gcc	ctg	cta	aga	1968
Ser	Lys	Asp	Tyr	Tyr	Gly	Leu	Ala	Pro	Gly	Lys	Ser	Ala	Leu	Leu	Arg	
				645					650					655		
tat	gca	ttc	ccc	att	aaa	tgt	acc	gag	gtt	gtt	tat	ggg	gac	aat	cca	2016
Tyr	Ala	Phe	Pro	Ile	Lys	Cys	Thr	Glu	Val	Val	Tyr	Gly	Asp	Asn	Pro	
			660				665						670			
gat	gac	atc	att	gaa	att	cga	gct	gaa	tat	gac	cct	tca	aag	act	act	2064
Asp	Asp	Ile	Ile	Glu	Ile	Arg	Ala	Glu	Tyr	Asp	Pro	Ser	Lys	Thr	Thr	
			675				680					685				
aaa	cct	aag	ggg	gtt	ctg	cac	tgg	gtt	gct	cag	cca	gca	cct	gga	gtt	2112
Lys	Pro	Lys	Gly	Val	Leu	His	Trp	Val	Ala	Gln	Pro	Ala	Pro	Gly	Val	
	690					695				700						
gaa	cca	ctt	aag	gtg	gaa	gta	aga	tta	ttt	gat	aaa	tta	ttc	ctc	tct	2160
Glu	Pro	Leu	Lys	Val	Glu	Val	Arg	Leu	Phe	Asp	Lys	Leu	Phe	Leu	Ser	
705					710					715					720	
gag	aat	cct	gct	gaa	ctg	gag	gat	tgg	ctg	ggg	gat	ctt	aac	ccg	aac	2208
Glu	Asn	Pro	Ala	Glu	Leu	Glu	Asp	Trp	Leu	Gly	Asp	Leu	Asn	Pro	Asn	
				725					730					735		
tca	aaa	gag	gtg	atc	aag	ggg	gcc	tac	gcc	gtg	cca	tcg	ctt	gcg	act	2256
Ser	Lys	Glu	Val	Ile	Lys	Gly	Ala	Tyr	Ala	Val	Pro	Ser	Leu	Ala	Thr	
			740					745					750			
gcg	gtt	ctt	ggg	gac	aag	ttc	cag	ttc	gag	cgg	cta	ggc	tac	ttc	gca	2304
Ala	Val	Leu	Gly	Asp	Lys	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Phe	Ala	
			755				760					765				
gtg	gac	aca	gac	tcg	aca	cct	gag	aac	att	gtg	ttc	aac	agg	acg	gtt	2352
Val	Asp	Thr	Asp	Ser	Thr	Pro	Glu	Asn	Ile	Val	Phe	Asn	Arg	Thr	Val	
	770					775					780					
acc	ctg	cgt	gat	tcg	tat	ggg	aaa	gct	ggg	cca	aag	tga				2391
Thr	Leu	Arg	Asp	Ser	Tyr	Gly	Lys	Ala	Gly	Pro	Lys					
785					790					795						

<210> 9954

<211> 796

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 9954

Met	Gly	Thr	Gly	Gly	Gly	Glu	Gly	Asp	Lys	Ser	Ala	Val	Leu	Pro	Leu	
1				5					10					15		
Glu	Ala	Leu	Leu	Ala	Leu	Gly	Leu	Asp	Gln	Arg	Thr	Ala	Glu	Asn	Ala	
			20					25					30			
Leu	Val	Asn	Ser	Lys	Val	Thr	Ala	Asn	Leu	Ala	Ala	Val	Ile	Ala	Glu	
		35					40					45				
Ala	Gly	Ile	Ser	Gly	Cys	Asp	Lys	Thr	Val	Gly	Asn	Leu	Leu	Tyr	Thr	
	50				55					60						
Val	Ala	Thr	Lys	Tyr	Pro	Thr	Asn	Ala	Leu	Val	His	Arg	Pro	Val	Leu	
65					70					75					80	
Ile	Asp	Tyr	Ile	Val	Ser	Thr	Lys	Ile	Lys	Asn	Pro	Ala	Gln	Leu	Asp	
				85					90					95		
Ala	Ala	Leu	Ser	Phe	Leu	Thr	Asn	Thr	Gly	Pro	Asp	Ser	Leu	Asp	Thr	
			100					105					110			

PF59083SeqList PF59083.txt

Gly	Lys	Phe	Glu	Glu	Ala	Cys	Gly	Val	Gly	Val	Val	Ser	Ile	Glu
		115					120				125			
Glu	Ile	Lys	Ser	Thr	Val	Asn	Glu	Val	Leu	Lys	His	Asn	Met	Glu
	130					135					140			Ala
Ile	Leu	Glu	Gln	Arg	Tyr	His	Ile	Asn	Val	Gly	Asn	Leu	Cys	Gly
	145				150					155				Gln
Val	Arg	Lys	Arg	His	Pro	Trp	Gly	Asp	Ala	Lys	Ala	Thr	Lys	Asp
				165					170					175
Ile	Asp	Lys	Lys	Leu	Ala	Glu	Ile	Leu	Gly	Pro	Lys	Thr	Asp	Ala
			180					185					190	Asp
Asn	Val	Lys	Pro	Val	Lys	Lys	Lys	Lys	Glu	Lys	Ala	Ala	Lys	Val
		195					200					205		Glu
Glu	Lys	Lys	Ala	Ala	Val	Val	Thr	Ala	Ala	Pro	Pro	Ser	Glu	Glu
	210					215					220			Glu
Leu	Asn	Pro	Tyr	Ser	Ile	Phe	Pro	Gln	Pro	Glu	Glu	Asn	Phe	Lys
	225				230					235				240
His	Thr	Glu	Ile	Phe	Tyr	Ser	Asp	Gly	Asn	Ile	Trp	Arg	Ala	His
				245					250					255
Ser	Lys	Glu	Ile	Leu	Glu	Lys	His	Leu	Lys	Ala	Thr	Gly	Gly	Lys
			260					265					270	Val
Met	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly
		275					280					285		His
Ala	Lys	Ala	Met	Phe	Ile	Asp	Phe	Gly	Leu	Ala	Lys	Glu	Arg	Asn
	290					295					300			Gly
His	Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys
	305				310					315				320
Glu	Tyr	Ile	Asp	His	Ile	Gln	Glu	Ile	Val	His	Trp	Met	Gly	Trp
				325					330					335
Pro	Tyr	Lys	Val	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Gln	Ala	Leu	Tyr
			340					345					350	Glu
His	Ala	Val	Glu	Leu	Ile	Arg	Lys	Gly	Leu	Ala	Tyr	Val	Asp	His
		355					360					365		Gln
Thr	Ala	Glu	Glu	Ile	Lys	Glu	Tyr	Arg	Glu	Lys	Lys	Met	Asn	Ser
	370					375					380			Pro
Trp	Arg	Asp	Arg	Pro	Ile	Glu	Glu	Ser	Leu	Lys	Leu	Phe	Glu	Asp
	385				390					395				400
Arg	Arg	Gly	Leu	Ile	Ala	Glu	Gly	Ala	Ala	Thr	Leu	Arg	Met	Lys
				405					410					415
Asp	Met	Gln	Asn	Asp	Asn	Lys	Asn	Met	Ser	Asp	Leu	Ile	Ala	Tyr
			420					425					430	Arg
Ile	Lys	Phe	Thr	Pro	His	Pro	His	Ala	Gly	Asp	Lys	Trp	Cys	Ile
		435					440					445		Tyr
Pro	Ser	Tyr	Asp	Tyr	Ala	His	Cys	Met	Val	Asp	Ser	Leu	Glu	Asn
	450					455					460			Ile
Thr	His	Ser	Leu	Cys	Thr	Leu	Glu	Phe	Asp	Ile	Arg	Arg	Pro	Ser
	465				470					475				480
Tyr	Trp	Leu	Leu	Val	Ala	Leu	Gly	Leu	Tyr	Gln	Pro	Tyr	Val	Trp
				485					490					495
Tyr	Ser	Arg	Leu	Asn	Ile	Ser	Asn	Thr	Val	Met	Ser	Lys	Arg	Lys
			500					505					510	Leu
Asn	Arg	Leu	Val	Thr	Glu	Lys	Trp	Val	Asp	Gly	Trp	Asp	Asp	Pro
		515					520					525		Arg
Leu	Leu	Thr	Leu	Ala	Gly	Leu	Arg	Arg	Arg	Gly	Val	Ser	Ser	Thr
	530					535					540			Ala
Ile	Asn	Ser	Phe	Ile	Cys	Gly	Ile	Gly	Ile	Thr	Arg	Ser	Asp	Asn
	545				550					555				560
Leu	Ile	Arg	Val	Asp	Arg	Leu	Glu	Tyr	His	Ile	Arg	Glu	Glu	Leu
				565					570					575
Lys	Thr	Ala	Ser	Arg	Ala	Met	Val	Val	Leu	Asn	Pro	Leu	Lys	Val
			580					585					590	Val
Ile	Thr	Asn	Leu	Glu	Asp	Glu	Lys	Val	Ile	Asp	Leu	Asp	Gly	Lys
		595					600					605		Met
Trp	Pro	Asp	Ala	Pro	Ala	Asp	Asp	Ala	Ser	Ser	Tyr	Tyr	Lys	Val
	610					615					620			Pro
Phe	Ser	Arg	Ile	Val	Tyr	Ile	Glu	Lys	Thr	Asp	Phe	Arg	Leu	Lys
	625				630					635				640
Ser	Lys	Asp	Tyr	Tyr	Gly	Leu	Ala	Pro	Gly	Lys	Ser	Ala	Leu	Leu
				645					650					655
Tyr	Ala	Phe	Pro	Ile	Lys	Cys	Thr	Glu	Val	Val	Tyr	Gly	Asp	Asn
														Pro

PF59083SeqList PF59083.txt

```

        660          665          670
Asp Asp Ile Ile Glu Ile Arg Ala Glu Tyr Asp Pro Ser Lys Thr Thr
      675
Lys Pro Lys Gly Val Leu His Trp Val Ala Gln Pro Ala Pro Gly Val
      690
Glu Pro Leu Lys Val Glu Val Arg Leu Phe Asp Lys Leu Phe Leu Ser
      705
Glu Asn Pro Ala Glu Leu Glu Asp Trp Leu Gly Asp Leu Asn Pro Asn
      725
Ser Lys Glu Val Ile Lys Gly Ala Tyr Ala Val Pro Ser Leu Ala Thr
      740
Ala Val Leu Gly Asp Lys Phe Gln Phe Glu Arg Leu Gly Tyr Phe Ala
      755
Val Asp Thr Asp Ser Thr Pro Glu Asn Ile Val Phe Asn Arg Thr Val
      770
Thr Leu Arg Asp Ser Tyr Gly Lys Ala Gly Pro Lys
      785          795

```

<210> 9955

<211> 2400

<212> DNA

<213> Candida albicans SC5314

<220>

<221> CDS

<222> (1)..(2400)

<223> transl_table=12

<400> 9955

```

atg tca aca aaa act gat att tct act gaa gaa ttg gtt tcc tta ttc      48
Met Ser Thr Lys Thr Asp Ile Ser Thr Glu Glu Leu Val Ser Leu Phe
  1          5          10          15
agt aaa gct gga ttt gaa gaa aaa aag tct gca gag ata gtc aag aat      96
Ser Lys Ala Gly Phe Glu Glu Lys Lys Ser Ala Glu Ile Val Lys Asn
          20          25          30
aaa aaa gtt gcc tcc gct tta tat aat att tta ggc tcc aac ttc ccc      144
Lys Lys Val Ala Ser Ala Leu Tyr Asn Ile Leu Gly Ser Asn Phe Pro
          35          40          45
aaa act gat gat aaa aaa tta tct ttg tta cat caa ttg gct ata cat      192
Lys Thr Asp Asp Lys Lys Leu Ser Leu Leu His Gln Leu Ala Ile His
          50          55          60
gaa agt aaa aat gga aaa gta cca aat cat gac ttt atc att gat gga      240
Glu Ser Lys Asn Gly Lys Val Pro Asn His Asp Phe Ile Ile Asp Gly
  65          70          75          80
att caa aaa ggg gac ttg aaa act gct ttg caa gta act gaa ggt atc      288
Ile Gln Lys Gly Asp Leu Lys Thr Ala Leu Gln Val Thr Glu Gly Ile
          85          90          95
aag tat tta caa aac aat gca aca gtt gat aag gaa aaa ttt gat gaa      336
Lys Tyr Leu Gln Asn Asn Ala Thr Val Asp Lys Glu Lys Phe Asp Glu
          100          105          110
gcc agt ggt gta ggt att gag att act cct gaa gaa gcc aag gta gaa      384
Ala Ser Gly Val Gly Ile Glu Ile Thr Pro Glu Glu Ala Lys Val Glu
          115          120          125
att tca aag tac ctt gac tct att aaa act gat ttg gag agt aaa aga      432
Ile Ser Lys Tyr Leu Asp Ser Ile Lys Thr Asp Leu Glu Ser Lys Arg
          130          135          140
tat tca atc tta cct aaa gtt cta ggt gaa gtg aaa acc cag cca tct      480
Tyr Ser Ile Leu Pro Lys Val Leu Gly Glu Val Lys Thr Gln Pro Ser
          145          150          155          160
ttg aaa tgg gca cca cct aac tta ttc aaa cca att tta gat gaa gag      528
Leu Lys Trp Ala Pro Pro Asn Leu Phe Lys Pro Ile Leu Asp Glu Glu
          165          170          175
ttt ttg gcc aga ttg ggt cca aaa gat gaa aga gat gtt aaa aag aag      576
Phe Leu Ala Arg Leu Gly Pro Lys Asp Glu Arg Asp Val Lys Lys Lys
          180          185          190
gaa aaa aaa gcc aag aca cca gct aat gca gct gcc acc aaa aag caa      624
Glu Lys Lys Ala Lys Thr Pro Ala Asn Ala Ala Ala Thr Lys Lys Gln
          195          200          205
gat act ggt tct gaa cct gaa cgt tct atg ttt tct gaa ggg ttc ctt      672

```

PF59083SeqList PF59083.txt

Asp	Thr	Gly	Ser	Glu	Pro	Glu	Arg	Ser	Met	Phe	Ser	Glu	Gly	Phe	Leu	
210	210					215					220					
ggg	gat	ttg	cat	aaa	cca	ggt	gaa	gaa	cct	caa	atg	tac	cct	gaa	ttg	720
Gly	Asp	Leu	His	Lys	Pro	Gly	Glu	Glu	Pro	Gln	Met	Tyr	Pro	Glu	Leu	
225					230					235					240	
tta	gaa	gag	cat	aaa	aag	ttt	att	tgt	gat	aaa	gtc	tac	acc	cgt	ttc	768
Leu	Glu	Glu	His	Lys	Lys	Phe	Ile	Cys	Asp	Lys	Val	Tyr	Thr	Arg	Phe	
				245					250					255		
cca	cct	gaa	cca	aat	gga	ttt	ttg	cac	att	ggt	cac	tct	aag	gcc	att	816
Pro	Pro	Glu	Pro	Asn	Gly	Phe	Leu	His	Ile	Gly	His	Ser	Lys	Ala	Ile	
				260					265					270		
atg	gtt	aat	ttt	ggg	tac	gct	caa	ttc	aac	aag	ggt	aat	tgt	tac	ttg	864
Met	Val	Asn	Phe	Gly	Tyr	Ala	Gln	Phe	Asn	Lys	Gly	Asn	Cys	Tyr	Leu	
				275			280						285			
agg	ttt	gac	gat	aca	aac	cct	gaa	gct	gaa	gag	gaa	gtc	tat	ttc	aat	912
Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Glu	Glu	Val	Tyr	Phe	Asn	
	290					295					300					
tcc	atc	aaa	gaa	atg	gtt	tct	tgg	ttg	ggt	tat	aag	cca	tgg	aag	atc	960
Ser	Ile	Lys	Glu	Met	Val	Ser	Trp	Leu	Gly	Tyr	Lys	Pro	Trp	Lys	Ile	
305					310					315					320	
acc	tat	tct	tcc	gac	tat	ttc	gat	gaa	ttg	tac	gag	ttg	gct	att	aag	1008
Thr	Tyr	Ser	Ser	Asp	Tyr	Phe	Asp	Glu	Leu	Tyr	Glu	Leu	Ala	Ile	Lys	
				325					330					335		
ttg	att	aaa	tca	gac	aag	gca	tat	ata	tgt	cat	tgt	act	cca	gaa	gaa	1056
Leu	Ile	Lys	Ser	Asp	Lys	Ala	Tyr	Ile	Cys	His	Cys	Thr	Pro	Glu	Glu	
				340					345					350		
gtg	aag	gct	tct	cgt	ggg	ttg	aaa	gaa	gat	ggt	aca	ttg	gga	gga	gaa	1104
Val	Lys	Ala	Ser	Arg	Gly	Leu	Lys	Glu	Asp	Gly	Thr	Leu	Gly	Gly	Glu	
				355			360						365			
aga	gtc	gct	tgt	aaa	cac	aga	ttt	caa	act	gtt	gaa	cat	aac	ttg	cgt	1152
Arg	Val	Ala	Cys	Lys	His	Arg	Phe	Gln	Thr	Val	Glu	His	Asn	Leu	Arg	
	370					375					380					
gag	ttt	gaa	aac	atg	aaa	aat	ggg	aaa	tac	aac	gtt	ggt	gaa	gcc	aca	1200
Glu	Phe	Glu	Asn	Met	Lys	Asn	Gly	Lys	Tyr	Asn	Val	Gly	Glu	Ala	Thr	
385					390					395					400	
tta	aga	atg	aaa	caa	gat	ttg	aat	tct	cca	tca	cct	caa	atg	tgg	gat	1248
Leu	Arg	Met	Lys	Gln	Asp	Leu	Asn	Ser	Pro	Ser	Pro	Gln	Met	Trp	Asp	
				405					410					415		
ttg	gtt	gcc	tac	cgt	gtt	ttg	aac	aca	cca	cat	cac	cga	act	ggt	gat	1296
Leu	Val	Ala	Tyr	Arg	Val	Leu	Asn	Thr	Pro	His	His	Arg	Thr	Gly	Asp	
				420					425					430		
aaa	tgg	aag	att	tac	cca	acc	tat	gat	ttt	acg	cat	tgt	ttg	gtt	gat	1344
Lys	Trp	Lys	Ile	Tyr	Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys	Leu	Val	Asp	
				435			440						445			
tct	ttt	gaa	aac	att	acc	cat	tca	ttg	tgt	acc	acc	gaa	ttt	gtc	ttg	1392
Ser	Phe	Glu	Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Thr	Glu	Phe	Val	Leu	
	450					455					460					
tct	aga	gaa	tcg	tat	gag	tgg	ttg	tgt	gat	gca	tta	cat	gtt	tat	aga	1440
Ser	Arg	Glu	Ser	Tyr	Glu	Trp	Leu	Cys	Asp	Ala	Leu	His	Val	Tyr	Arg	
465					470					475					480	
cca	gca	caa	cgt	gaa	tac	ggt	aga	ttg	aac	tta	act	ggt	acc	atc	atg	1488
Pro	Ala	Gln	Arg	Glu	Tyr	Gly	Arg	Leu	Asn	Leu	Thr	Gly	Thr	Ile	Met	
				485					490					495		
tcc	aag	aga	aag	att	gct	aaa	ttg	gtc	aat	gaa	ggt	tat	gtc	aga	gga	1536
Ser	Lys	Arg	Lys	Ile	Ala	Lys	Leu	Val	Asn	Glu	Gly	Tyr	Val	Arg	Gly	
				500				505						510		
tgg	gat	gac	cca	aga	tta	tac	aca	tta	gaa	ggt	atc	aaa	aga	aga	ggt	1584
Trp	Asp	Asp	Pro	Arg	Leu	Tyr	Thr	Leu	Glu	Gly	Ile	Lys	Arg	Arg	Gly	
				515			520						525			
gtc	cct	cca	ggt	gcc	att	ttg	tct	ttc	ata	aac	acc	ttg	gga	gtt	aca	1632
Val	Pro	Pro	Gly	Ala	Ile	Leu	Ser	Phe	Ile	Asn	Thr	Leu	Gly	Val	Thr	
						535					540					
acc	tcg	aca	aca	aat	atc	caa	acg	gtg	aga	ttt	gaa	agt	gcc	gtg	cgt	1680
Thr	Ser	Thr	Thr	Asn	Ile	Gln	Thr	Val	Arg	Phe	Glu	Ser	Ala	Val	Arg	
545					550					555					560	
aac	tac	ctt	gat	caa	aca	act	cca	aga	ttg	atg	atg	gtt	ttg	cac	cca	1728
Asn	Tyr	Leu	Asp	Gln	Thr	Thr	Pro	Arg	Leu	Met	Met	Val	Leu	His	Pro	
				565					570					575		
att	gag	gtt	gtt	att	gat	aat	ttg	gat	gaa	agc	ttt	agt	ttg	gac	gtt	1776

PF59083SeqList PF59083.txt

Ile	Glu	Val	Val	Ile	Asp	Asn	Leu	Asp	Glu	Ser	Phe	Ser	Leu	Asp	Val		
			580					585					590				
gaa	ata	cca	tac	aag	cca	ggt	aaa	gat	gaa	aag	tct	atg	gga	tac	cgt		1824
Glu	Ile	Pro	Tyr	Lys	Pro	Gly	Lys	Asp	Glu	Lys	Ser	Met	Gly	Tyr	Arg		
		595				600						605					
aaa	ctt	aca	ttt	tcc	aaa	cat	att	tac	att	gat	gaa	aat	gat	ggt	aga		1872
Lys	Leu	Thr	Phe	Ser	Lys	His	Ile	Tyr	Ile	Asp	Glu	Asn	Asp	Val	Arg		
	610					615					620						
gct	gaa	cct	gcc	gat	aaa	gag	ttt	tat	aga	ttg	gct	ccg	ggc	caa	cca		1920
Ala	Glu	Pro	Ala	Asp	Lys	Glu	Phe	Tyr	Arg	Leu	Ala	Pro	Gly	Gln	Pro		
	625				630					635					640		
ggt	ggt	ttg	atg	aga	ggt	cct	ttc	aat	atc	agt	ttc	aaa	tca	att	gaa		1968
Val	Gly	Leu	Met	Arg	Val	Pro	Phe	Asn	Ile	Ser	Phe	Lys	Ser	Ile	Glu		
				645				650						655			
gaa	aaa	gat	gga	aag	aaa	atc	gtc	cat	ggt	aac	tat	gac	gaa	ggt	gta		2016
Glu	Lys	Asp	Gly	Lys	Lys	Ile	Val	His	Val	Asn	Tyr	Asp	Glu	Gly	Val		
			660					665					670				
aaa	gct	aaa	cca	aaa	acc	tac	atc	caa	tggt	att	cct	aaa	gac	act	gct		2064
Lys	Ala	Lys	Pro	Lys	Thr	Tyr	Ile	Gln	Trp	Ile	Pro	Lys	Asp	Thr	Ala		
		675				680						685					
ggt	cat	att	aaa	gaa	ggt	aga	atc	tac	aat	caa	ttg	ttc	aaa	agt	gaa		2112
Val	His	Ile	Lys	Glu	Val	Arg	Ile	Tyr	Asn	Gln	Leu	Phe	Lys	Ser	Glu		
	690					695					700						
aac	cct	tct	gca	cat	cct	gaa	ggt	tat	ttg	aag	gac	att	aat	cct	gat		2160
Asn	Pro	Ser	Ala	His	Pro	Glu	Gly	Tyr	Leu	Lys	Asp	Ile	Asn	Pro	Asp		
	705				710					715					720		
agt	gaa	gaa	ggt	ttg	cgt	aat	gca	ggt	ggt	gaa	gaa	aat	ctt	aaa	gac		2208
Ser	Glu	Glu	Val	Leu	Arg	Asn	Ala	Val	Val	Glu	Glu	Asn	Leu	Lys	Asp		
				725				730						735			
att	gtg	gca	aaa	tct	cca	atg	aac	att	gaa	att	cca	gga	agt	gca	ttc		2256
Ile	Val	Ala	Lys	Ser	Pro	Met	Asn	Ile	Glu	Ile	Pro	Gly	Ser	Ala	Phe		
			740					745					750				
aac	att	aaa	gaa	aac	aaa	ggt	aat	aat	act	gtc	aga	ttc	caa	gca	tta		2304
Asn	Ile	Lys	Glu	Asn	Lys	Gly	Asn	Asn	Thr	Val	Arg	Phe	Gln	Ala	Leu		
		755				760						765					
aga	gaa	ggt	tac	ttt	tgc	ttg	gac	aaa	gat	tcc	aaa	gaa	gat	ggt	ttg		2352
Arg	Glu	Gly	Tyr	Phe	Cys	Leu	Asp	Lys	Asp	Ser	Lys	Glu	Asp	Gly	Leu		
	770				775					780							
att	ctt	aat	aga	att	gtc	agc	ttg	aaa	gaa	gat	gct	gct	aaa	aaa			2397
Ile	Leu	Asn	Arg	Ile	Val	Ser	Leu	Lys	Glu	Asp	Ala	Ala	Lys	Lys			
	785				790					795							
tga																	2400

<210> 9956

<211> 799

<212> PRT

<213> Candida albicans SC5314

<400> 9956

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

PF59083SeqList PF59083.txt

Tyr	Ser	Ile	Leu	Pro	Lys	Val	Leu	Gly	Glu	Val	Lys	Thr	Gln	Pro	Ser
145					150					155					160
Leu	Lys	Trp	Ala	Pro	Pro	Asn	Leu	Phe	Lys	Pro	Ile	Leu	Asp	Glu	Glu
				165					170					175	
Phe	Leu	Ala	Arg	Leu	Gly	Pro	Lys	Asp	Glu	Arg	Asp	Val	Lys	Lys	
			180					185					190		
Glu	Lys	Lys	Ala	Lys	Thr	Pro	Ala	Asn	Ala	Ala	Ala	Thr	Lys	Lys	Gln
		195					200					205			
Asp	Thr	Gly	Ser	Glu	Pro	Glu	Arg	Ser	Met	Phe	Ser	Glu	Gly	Phe	Leu
	210					215					220				
Gly	Asp	Leu	His	Lys	Pro	Gly	Glu	Glu	Pro	Gln	Met	Tyr	Pro	Glu	Leu
225					230					235					240
Leu	Glu	Glu	His	Lys	Lys	Phe	Ile	Cys	Asp	Lys	Val	Tyr	Thr	Arg	Phe
				245					250					255	
Pro	Pro	Glu	Pro	Asn	Gly	Phe	Leu	His	Ile	Gly	His	Ser	Lys	Ala	Ile
			260					265					270		
Met	Val	Asn	Phe	Gly	Tyr	Ala	Gln	Phe	Asn	Lys	Gly	Asn	Cys	Tyr	Leu
		275				280						285			
Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Glu	Glu	Val	Tyr	Phe	Asn
	290					295					300				
Ser	Ile	Lys	Glu	Met	Val	Ser	Trp	Leu	Gly	Tyr	Lys	Pro	Trp	Lys	Ile
305					310					315					320
Thr	Tyr	Ser	Ser	Asp	Tyr	Phe	Asp	Glu	Leu	Tyr	Glu	Leu	Ala	Ile	Lys
				325					330					335	
Leu	Ile	Lys	Ser	Asp	Lys	Ala	Tyr	Ile	Cys	His	Cys	Thr	Pro	Glu	Glu
			340					345					350		
Val	Lys	Ala	Ser	Arg	Gly	Leu	Lys	Glu	Asp	Gly	Thr	Leu	Gly	Gly	Glu
		355				360						365			
Arg	Val	Ala	Cys	Lys	His	Arg	Phe	Gln	Thr	Val	Glu	His	Asn	Leu	Arg
	370					375					380				
Glu	Phe	Glu	Asn	Met	Lys	Asn	Gly	Lys	Tyr	Asn	Val	Gly	Glu	Ala	Thr
385					390					395					400
Leu	Arg	Met	Lys	Gln	Asp	Leu	Asn	Ser	Pro	Ser	Pro	Gln	Met	Trp	Asp
				405					410					415	
Leu	Val	Ala	Tyr	Arg	Val	Leu	Asn	Thr	Pro	His	His	Arg	Thr	Gly	Asp
			420					425					430		
Lys	Trp	Lys	Ile	Tyr	Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys	Leu	Val	Asp
		435					440					445			
Ser	Phe	Glu	Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Thr	Glu	Phe	Val	Leu
	450					455					460				
Ser	Arg	Glu	Ser	Tyr	Glu	Trp	Leu	Cys	Asp	Ala	Leu	His	Val	Tyr	Arg
465					470					475					480
Pro	Ala	Gln	Arg	Glu	Tyr	Gly	Arg	Leu	Asn	Leu	Thr	Gly	Thr	Ile	Met
				485					490					495	
Ser	Lys	Arg	Lys	Ile	Ala	Lys	Leu	Val	Asn	Glu	Gly	Tyr	Val	Arg	Gly
			500					505					510		
Trp	Asp	Asp	Pro	Arg	Leu	Tyr	Thr	Leu	Glu	Gly	Ile	Lys	Arg	Arg	Gly
		515					520					525			
Val	Pro	Pro	Gly	Ala	Ile	Leu	Ser	Phe	Ile	Asn	Thr	Leu	Gly	Val	Thr
	530					535					540				
Thr	Ser	Thr	Thr	Asn	Ile	Gln	Thr	Val	Arg	Phe	Glu	Ser	Ala	Val	Arg
545					550					555					560
Asn	Tyr	Leu	Asp	Gln	Thr	Thr	Pro	Arg	Leu	Met	Met	Val	Leu	His	Pro
				565					570					575	
Ile	Glu	Val	Val	Ile	Asp	Asn	Leu	Asp	Glu	Ser	Phe	Ser	Leu	Asp	Val
			580					585					590		
Glu	Ile	Pro	Tyr	Lys	Pro	Gly	Lys	Asp	Glu	Lys	Ser	Met	Gly	Tyr	Arg
		595					600					605			
Lys	Leu	Thr	Phe	Ser	Lys	His	Ile	Tyr	Ile	Asp	Glu	Asn	Asp	Val	Arg
	610					615					620				
Ala	Glu	Pro	Ala	Asp	Lys	Glu	Phe	Tyr	Arg	Leu	Ala	Pro	Gly	Gln	Pro
625					630					635					640
Val	Gly	Leu	Met	Arg	Val	Pro	Phe	Asn	Ile	Ser	Phe	Lys	Ser	Ile	Glu
				645					650					655	
Glu	Lys	Asp	Gly	Lys	Lys	Ile	Val	His	Val	Asn	Tyr	Asp	Glu	Gly	Val
			660					665					670		
Lys	Ala	Lys	Pro	Lys	Thr	Tyr	Ile	Gln	Trp	Ile	Pro	Lys	Asp	Thr	Ala
		675					680					685			
Val	His	Ile	Lys	Glu	Val	Arg	Ile	Tyr	Asn	Gln	Leu	Phe	Lys	Ser	Glu

PF59083SeqList PF59083.txt

```

        690                      695                      700
Asn Pro Ser Ala His Pro Glu Gly Tyr Leu Lys Asp Ile Asn Pro Asp
705 Ser Glu Glu Val Leu Arg Asn Ala Val Val Glu Glu Asn Leu Lys Asp
        725
Ile Val Ala Lys Ser Pro Met Asn Ile Glu Ile Pro Gly Ser Ala Phe
        740
Asn Ile Lys Glu Asn Lys Gly Asn Asn Thr Val Arg Phe Gln Ala Leu
        755
Arg Glu Gly Tyr Phe Cys Leu Asp Lys Asp Ser Lys Glu Asp Gly Leu
        770
Ile Leu Asn Arg Ile Val Ser Leu Lys Glu Asp Ala Ala Lys Lys
        785                      790                      795

```

<210> 9957

<211> 2574

<212> DNA

<213> Ustilago maydis 521

<220>

<221> CDS

<222> (1)..(2574)

<400> 9957

```

atg ccg ccc aag gtc gat gtc aac gat cca gag aat gca agg ctt ctc      48
Met Pro Pro Lys Val Asp Val Asn Asp Pro Glu Asn Ala Arg Leu Leu
1      5      10
aag ctc ttc gaa tcg ctc aat ctg acc gga aac aga gcc atc gag acg      96
Lys Leu Phe Glu Ser Leu Asn Leu Thr Gly Asn Arg Ala Ile Glu Thr
        20      25      30
ctc aca aac cca aag cac gtc gct gct atc gag agc gtt atc gca cac      144
Leu Thr Asn Pro Lys His Val Ala Ala Ile Glu Ser Val Ile Ala His
        35      40      45
aac cat ctc act aac aaa cag atc gac ccc aag gcg tcc gca ctc atc      192
Asn His Leu Thr Asn Lys Gln Ile Asp Pro Lys Ala Ser Ala Leu Ile
        50      55      60
ata tct gca tcc acc gcc aaa gat gct tcc aac cag ccc gcc aga gac      240
Ile Ser Ala Ser Thr Ala Lys Asp Ala Ser Asn Gln Pro Ala Arg Asp
        65      70      75      80
tat atc gta tca cgc atc ctc gac gcc agc ctc aca tcg tcc gat caa      288
Tyr Ile Val Ser Arg Ile Leu Asp Ala Ser Leu Thr Ser Ser Asp Gln
        85      90      95
gtt aac gca gca tac aag tac ctc tca tcc ctc aac agc gag cca gac      336
Val Asn Ala Ala Tyr Lys Tyr Leu Ser Ser Leu Asn Ser Glu Pro Asp
        100      105      110
aag gct gct ttt gac aag gaa tgc ggt gtt ggc gtc gtc gta aca cca      384
Lys Ala Ala Phe Asp Lys Glu Cys Gly Val Gly Val Val Val Thr Pro
        115      120      125
caa caa tct cgc aag gcg gta gat gac tac att gca tct cac cga tcc      432
Gln Gln Ser Arg Lys Ala Val Asp Asp Tyr Ile Ala Ser His Arg Ser
        130      135      140
gaa ctc gat ccc gtt gat ggt tgg ccg aaa ctc ggc tcg atc ctc tct      480
Glu Leu Asp Pro Val Asp Gly Trp Pro Lys Leu Gly Ser Ile Leu Ser
        145      150      155      160
ggc gtc aaa gct tcg ccc gac atg cga tgg gcc aac gca gtc gac ctc      528
Gly Val Lys Ala Ser Pro Asp Met Arg Trp Ala Asn Ala Val Asp Leu
        165      170      175
aag gac gcc gta gat gcg gcg ctc cta gct aca tat ggt ccc aaa aag      576
Lys Asp Ala Val Asp Ala Ala Leu Ala Thr Tyr Gly Pro Lys Lys
        180      185      190
cca cct cct ccc aag gaa aag aag aag cca tct gct tcc acc tcg gcc      624
Pro Pro Pro Pro Lys Glu Lys Lys Lys Pro Ser Ala Ser Thr Ser Ala
        195      200      205
cac ccc aaa aag gaa gct gca cca gct ggt ccc gtc gat cca gac gcc      672
His Pro Lys Lys Glu Ala Pro Ala Gly Pro Val Asp Pro Asp Ala
        210      215      220
atg ttc aag gaa ggc ttc ctc gcc agt ctc cac aaa ccc ggc gaa aac      720
Met Phe Lys Glu Gly Phe Leu Ala Ser Leu His Lys Pro Gly Glu Asn
        225      230      235      240

```

PF59083SeqList PF59083.txt

ccc Pro	cag Gln	atc Ile	aag Lys	cca Pro 245	gag Glu	ctc Leu	aaa Lys	caa Gln	cag Gln 250	cac His	ctc Leu	gcc Ala	gct Ala 255	acc Thr 255	aag Lys	768
ggc Gly	atg Met	gtc Val	atg Met 260	acg Thr	cgt Arg	ttc Phe	cca Pro	cca Pro 265	gaa Glu	ccc Pro	aac Asn	ggc Gly	ttt Phe 270	ctc Leu	cac His	816
att Ile	ggc Gly	cac His 275	agc Ser	aag Lys	gcc Ala	atc Ile	gcc Ala 280	gtc Val	aac Asn	ttt Phe	ggc Gly	ttt Phe 285	gcc Ala	cgc Arg	ttc Phe	864
cat His	cgc Arg 290	ggc Gly	ctc Leu	tgt Cys	tac Tyr	ctc Leu 295	cga Arg	tac Tyr	gac Asp	gat Asp	acc Thr 300	aac Asn	ccc Pro	gag Glu	gca Ala	912
gaa Glu 305	gag Glu	gaa Glu	aag Lys	tac Tyr	ttt Phe 310	acc Thr	agc Ser	atc Ile	ctc Leu	gag Glu 315	aca Thr	ggt Val	cga Arg	tgg Trp	ctt Leu 320	960
ggc Gly	ttc Phe	gaa Glu	ccc Pro	ttc Phe 325	aag Lys	gtc Val	acc Thr	tac Tyr	tcg Ser 330	agt Ser	gac Asp	tac Tyr	ttc Phe 335	cag Gln 335	cag Gln	1008
ctc Leu	tac Tyr	cag Gln 340	ctc Leu	gcc Ala	gtc Val	gaa Glu	ctc Leu	att Ile 345	aag Lys	cgt Arg	ggc Gly	aag Lys	gct Ala 350	tac Tyr	gtc Val	1056
gat Asp	cac His 355	tcg Ser	aca Thr	ccc Pro	gaa Glu	gag Glu	atc Ile 360	aag Lys	gag Glu	cag Gln	cgc Arg	ggc Gly 365	ggc Gly	ccc Pro	gag Glu	1104
cgc Arg	ggc Gly 370	cca Pro	cgc Arg	aag Lys	cct Pro	tca Ser 375	cgc Arg	ttc Phe	cgc Arg	gat Asp	cgt Arg 380	ccc Pro	ggt Val	caa Gln	gag Glu	1152
tcg Ser 385	ctt Leu	cag Gln	gac Asp	ttt Phe 390	gag Glu	gac Asp	atg Met	aag Lys	aac Asn	ggc Gly 395	aaa Lys	tac Tyr	gcc Ala	cca Pro	ggc Gly 400	1200
aaa Lys	gtc Val	acg Thr	ctt Leu 405	cgg Arg	atg Met	aag Lys	cag Gln	gac Asp	atc Ile 410	gag Glu	aat Asn	ggc Gly	aac Asn	ccg Pro 415	cag Gln	1248
atg Met	tgg Trp	gat Asp	ctg Leu 420	atc Ile	gcc Ala	tac Tyr	cgt Arg	gtc Val 425	ctc Leu	gaa Glu	gct Ala	tca Ser 430	cac His	cac His	cgc Arg	1296
acc Thr	ggc Gly	aag Lys 435	gac Asp	tgg Trp	tgc Cys	atc Ile	tat Tyr 440	ccc Pro	acc Thr	tac Tyr	gac Asp	ttt Phe 445	acc Thr	cac His	tgt Cys	1344
ctc Leu	gtc Val 450	gat Asp	agc Ser	ttt Phe	gaa Glu	aac Asn 455	atc Ile	agc Ser	cac His	tcg Ser	ctc Leu 460	tgc Cys	acc Thr	acc Thr	gag Glu	1392
ttt Phe 465	atc Ile	ctc Leu	tcg Ser	cgc Arg	gaa Glu 470	tcc Ser	tac Tyr	gag Glu	tgg Trp	ctg Leu 475	tgc Cys	gac Asp	gcg Ala	ctc Leu	gag Glu 480	1440
gtg Val	tac Tyr	aag Lys	cca Pro	cgt Arg 485	cag Gln	tcc Ser	gag Glu	tac Tyr	ggc Gly 490	cgt Arg	ctg Leu	gcg Ala	ctc Leu	cag Gln 495	gga Gly	1488
acc Thr	gtc Val	atg Met	tcg Ser 500	aag Lys	cgc Arg	aag Lys	att Ile	ctc Leu 505	aaa Lys	ctc Leu	gta Val	aag Lys	gag Glu 510	cgc Arg	tac Tyr	1536
atc Ile	gaa Glu 515	gac Asp	tgg Trp	gat Asp	gac Asp	ccg Pro	cgc Arg 520	atg Met	ttt Phe	acc Thr	ctc Leu	atc Ile 525	gct Ala	ctt Leu	agg Arg	1584
cgt Arg	aga Arg 530	ggc Gly	gta Val	cct Pro	ccc Pro	ggc Gly 535	gcg Ala	atc Ile	ctg Leu	tcc Ser	ttt Phe 540	ggt Val	agc Ser	gcg Ala	ctt Leu	1632
ggc Gly 545	gtc Val	acc Thr	aca Thr	gcc Ala	aaa Lys 550	tcc Ser	acc Thr	atc Ile	cag Gln	atc Ile 555	agt Ser	cgg Arg	ttc Phe	gat Asp	caa Gln 560	1680
gct Ala	gtg Val	cga Arg	caa Gln	tac Tyr 565	ctc Leu	gag Glu	ctt Leu	tcg Ser	acg Thr 570	cca Pro	cgt Arg	ttg Leu	atg Met	atg Met 575	gtg Val	1728
ctc Leu	aac Asn	ccg Pro	ctc Leu 580	aag Lys	gtg Val	acc Thr	atc Ile	gag Glu 585	aac Asn	tta Leu	ccc Pro	gac Asp	gac Asp 590	cac His	ttc Phe	1776
cag Gln	gag Glu	atc Ile 595	gaa Glu	aag Lys	cct Pro	ctg Leu	cat His 600	ccc Pro	aag Lys	gcg Ala	ccc Pro	gag Glu 605	atg Met	ggc Gly	acc Thr	1824

PF59083SeqList PF59083.txt

aac	aag	atc	ccc	ttc	acc	cgc	act	gtc	tac	atc	gac	tcg	tcc	gac	ttc	1872
Asn	Lys	Ile	Pro	Phe	Thr	Arg	Thr	Val	Tyr	Ile	Asp	Ser	Ser	Asp	Phe	
	610					615					620					
cgc	acc	gag	gat	agc	aag	gac	tac	ttc	cgt	ctg	gcc	cca	ggc	aag	acg	1920
Arg	Thr	Glu	Asp	Ser	Lys	Asp	Tyr	Phe	Arg	Leu	Ala	Pro	Gly	Lys	Thr	
	625				630					635					640	
gta	ggc	ctg	ttg	cag	gta	ccc	ttc	ccc	atc	aca	tgt	caa	tcg	ttc	aag	1968
Val	Gly	Leu	Leu	Gln	Val	Pro	Phe	Pro	Ile	Thr	Cys	Gln	Ser	Phe	Lys	
				645					650					655		
acc	aac	gac	cag	ggc	gta	ccg	atc	gaa	gtg	att	gcc	acg	tac	ggc	gat	2016
Thr	Asn	Asp	Gln	Gly	Val	Pro	Ile	Glu	Val	Ile	Ala	Thr	Tyr	Gly	Asp	
			660					665					670			
aca	agc	tcg	gcc	aag	ccc	aag	aca	tac	atc	cag	tgg	gta	gca	gag	cac	2064
Thr	Ser	Ser	Ala	Lys	Pro	Lys	Thr	Tyr	Ile	Gln	Trp	Val	Ala	Glu	His	
		675					680					685				
gct	ccc	tcg	caa	agt	cct	gtc	aaa	gtc	gac	gag	aca	cgc	atc	ttc	cac	2112
Ala	Pro	Ser	Gln	Ser	Pro	Val	Lys	Val	Asp	Glu	Thr	Arg	Ile	Phe	His	
	690					695				700						
cag	ctc	ttc	acc	tcg	gac	gat	ccg	gca	gct	gag	gag	aac	ttc	ttg	gac	2160
Gln	Leu	Phe	Thr	Ser	Asp	Asp	Pro	Ala	Ala	Glu	Glu	Asn	Phe	Leu	Asp	
	705				710					715					720	
cac	gtc	aac	ccg	gat	tct	ctc	gaa	atc	gtg	cgc	ggc	gct	atg	gtc	gag	2208
His	Val	Asn	Pro	Asp	Ser	Leu	Glu	Ile	Val	Arg	Gly	Ala	Met	Val	Glu	
				725					730					735		
gtt	ggc	ttt	tgg	gat	gtg	gcc	aag	cgc	agc	gtc	gag	cac	gct	aga	aag	2256
Val	Gly	Phe	Trp	Asp	Val	Ala	Lys	Arg	Ser	Val	Glu	His	Ala	Arg	Lys	
			740					745					750			
gag	gct	gct	cag	cgc	acc	gaa	aga	gcc	gaa	gcc	gat	gcg	gcc	aaa	gcg	2304
Glu	Ala	Ala	Gln	Arg	Thr	Glu	Arg	Ala	Glu	Ala	Asp	Ala	Ala	Lys	Ala	
		755				760						765				
aga	agc	gag	acc	gag	act	agt	gca	acc	gag	ggc	gct	ggc	gca	ggc	gct	2352
Arg	Ser	Glu	Thr	Glu	Thr	Ser	Ala	Thr	Glu	Gly	Ala	Gly	Ala	Gly	Ala	
	770					775					780					
cct	caa	cgt	act	gct	gat	caa	ctg	gtg	ggc	aaa	gag	ttg	gtc	cgc	ttc	2400
Pro	Gln	Arg	Thr	Ala	Asp	Gln	Leu	Val	Gly	Lys	Glu	Leu	Val	Arg	Phe	
	785				790				795						800	
cag	ggc	atg	cgt	acc	gcc	tac	ttt	gcg	ctc	gat	cgc	ttg	agc	ggc	gat	2448
Gln	Gly	Met	Arg	Thr	Ala	Tyr	Phe	Ala	Leu	Asp	Arg	Leu	Ser	Gly	Asp	
				805				810						815		
ttg	ggc	ctc	ttt	ggc	gat	aaa	cag	aag	ggc	aag	att	gtg	ctc	aac		2496
Leu	Gly	Leu	Phe	Gly	Asp	Lys	Gln	Lys	Gly	Gly	Lys	Ile	Val	Leu	Asn	
			820					825				830				
agg	atc	gtc	tcg	ttg	aaa	gag	gat	gca	aag	aag	gac	gat	aag	gca	gtc	2544
Arg	Ile	Val	Ser	Leu	Lys	Glu	Asp	Ala	Lys	Lys	Asp	Asp	Lys	Ala	Val	
		835				840						845				
gcg	tca	ccg	gtg	gcc	aag	aaa	gcc	aag	taa							2574
Ala	Ser	Pro	Val	Ala	Lys	Lys	Ala	Lys								
	850					855										

<210> 9958

<211> 857

<212> PRT

<213> Ustilago maydis 521

<400> 9958

Met	Pro	Pro	Lys	Val	Asp	Val	Asn	Asp	Pro	Glu	Asn	Ala	Arg	Leu	Leu	
1				5					10					15		
Lys	Leu	Phe	Glu	Ser	Leu	Asn	Leu	Thr	Gly	Asn	Arg	Ala	Ile	Glu	Thr	
		20						25					30			
Leu	Thr	Asn	Pro	Lys	His	Val	Ala	Ile	Glu	Ser	Val	Ile	Ala	His		
		35					40					45				
Asn	His	Leu	Thr	Asn	Lys	Gln	Ile	Asp	Pro	Lys	Ala	Ser	Ala	Leu	Ile	
	50				55					60						
Ile	Ser	Ala	Ser	Thr	Ala	Lys	Asp	Ala	Ser	Asn	Gln	Pro	Ala	Arg	Asp	
	65				70					75					80	
Tyr	Ile	Val	Ser	Arg	Ile	Leu	Asp	Ala	Ser	Leu	Thr	Ser	Ser	Asp	Gln	
				85				90						95		
Val	Asn	Ala	Ala	Tyr	Lys	Tyr	Leu	Ser	Leu	Asn	Ser	Glu	Pro	Asp		
			100				105					110				

PF59083SeqList PF59083.txt

Lys	Ala	Ala	Phe	Asp	Lys	Glu	Cys	Gly	Val	Gly	Val	Val	Val	Thr	Pro
		115					120					125			
Gln	Gln	Ser	Arg	Lys	Ala	Val	Asp	Asp	Tyr	Ile	Ala	Ser	His	Arg	Ser
	130					135					140				
Glu	Leu	Asp	Pro	Val	Asp	Gly	Trp	Pro	Lys	Leu	Gly	Ser	Ile	Leu	Ser
145					150					155					160
Gly	Val	Lys	Ala	Ser	Pro	Asp	Met	Arg	Trp	Ala	Asn	Ala	Val	Asp	Leu
				165					170					175	
Lys	Asp	Ala	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Tyr	Gly	Pro	Lys	Lys
			180					185					190		
Pro	Pro	Pro	Pro	Lys	Glu	Lys	Lys	Lys	Pro	Ser	Ala	Ser	Thr	Ser	Ala
		195					200					205			
His	Pro	Lys	Lys	Glu	Ala	Ala	Pro	Ala	Gly	Pro	Val	Asp	Pro	Asp	Ala
	210					215					220				
Met	Phe	Lys	Glu	Gly	Phe	Leu	Ala	Ser	Leu	His	Lys	Pro	Gly	Glu	Asn
225					230					235					240
Pro	Gln	Ile	Lys	Pro	Glu	Leu	Lys	Gln	Gln	His	Leu	Ala	Ala	Thr	Lys
				245					250					255	
Gly	Met	Val	Met	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Phe	Leu	His
			260					265					270		
Ile	Gly	His	Ser	Lys	Ala	Ile	Ala	Val	Asn	Phe	Gly	Phe	Ala	Arg	Phe
		275					280					285			
His	Arg	Gly	Leu	Cys	Tyr	Leu	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	Glu	Ala
	290					295					300				
Glu	Glu	Glu	Lys	Tyr	Phe	Thr	Ser	Ile	Leu	Glu	Thr	Val	Arg	Trp	Leu
305					310					315					320
Gly	Phe	Glu	Pro	Phe	Lys	Val	Thr	Tyr	Ser	Ser	Asp	Tyr	Phe	Gln	Gln
				325					330					335	
Leu	Tyr	Gln	Leu	Ala	Val	Glu	Leu	Ile	Lys	Arg	Gly	Lys	Ala	Tyr	Val
			340					345					350		
Asp	His	Ser	Thr	Pro	Glu	Glu	Ile	Lys	Glu	Gln	Arg	Gly	Gly	Pro	Glu
		355					360					365			
Arg	Gly	Pro	Arg	Lys	Pro	Ser	Arg	Phe	Arg	Asp	Arg	Pro	Val	Gln	Glu
	370					375					380				
Ser	Leu	Gln	Asp	Phe	Glu	Asp	Met	Lys	Asn	Gly	Lys	Tyr	Ala	Pro	Gly
385					390					395					400
Lys	Val	Thr	Leu	Arg	Met	Lys	Gln	Asp	Ile	Glu	Asn	Gly	Asn	Pro	Gln
				405					410					415	
Met	Trp	Asp	Leu	Ile	Ala	Tyr	Arg	Val	Leu	Glu	Ala	Ser	His	His	Arg
			420					425					430		
Thr	Gly	Lys	Asp	Trp	Cys	Ile	Tyr	Pro	Thr	Tyr	Asp	Phe	Thr	His	Cys
		435					440					445			
Leu	Val	Asp	Ser	Phe	Glu	Asn	Ile	Ser	His	Ser	Leu	Cys	Thr	Thr	Glu
	450					455					460				
Phe	Ile	Leu	Ser	Arg	Glu	Ser	Tyr	Glu	Trp	Leu	Cys	Asp	Ala	Leu	Glu
465					470					475					480
Val	Tyr	Lys	Pro	Arg	Gln	Ser	Glu	Tyr	Gly	Arg	Leu	Ala	Leu	Gln	Gly
				485					490					495	
Thr	Val	Met	Ser	Lys	Arg	Lys	Ile	Leu	Lys	Leu	Val	Lys	Glu	Arg	Tyr
			500					505					510		
Ile	Glu	Asp	Trp	Asp	Asp	Pro	Arg	Met	Phe	Thr	Leu	Ile	Ala	Leu	Arg
		515					520					525			
Arg	Arg	Gly	Val	Pro	Pro	Gly	Ala	Ile	Leu	Ser	Phe	Val	Ser	Ala	Leu
	530					535					540				
Gly	Val	Thr	Thr	Ala	Lys	Ser	Thr	Ile	Gln	Ile	Ser	Arg	Phe	Asp	Gln
545					550					555					560
Ala	Val	Arg	Gln	Tyr	Leu	Glu	Leu	Ser	Thr	Pro	Arg	Leu	Met	Met	Val
				565					570					575	
Leu	Asn	Pro	Leu	Lys	Val	Thr	Ile	Glu	Asn	Leu	Pro	Asp	Asp	His	Phe
			580					585					590		
Gln	Glu	Ile	Glu	Lys	Pro	Leu	His	Pro	Lys	Ala	Pro	Glu	Met	Gly	Thr
		595					600					605			
Asn	Lys	Ile	Pro	Phe	Thr	Arg	Thr	Val	Tyr	Ile	Asp	Ser	Ser	Asp	Phe
	610					615					620				
Arg	Thr	Glu	Asp	Ser	Lys	Asp	Tyr	Phe	Arg	Leu	Ala	Pro	Gly	Lys	Thr
625					630					635					640
Val	Gly	Leu	Leu	Gln	Val	Pro	Phe	Pro	Ile	Thr	Cys	Gln	Ser	Phe	Lys
				645					650					655	
Thr	Asn	Asp	Gln	Gly	Val	Pro	Ile	Glu	Val	Ile	Ala	Thr	Tyr	Gly	Asp

PF59083SeqList PF59083.txt

```

        660          665          670
Thr Ser Ser Ala Lys Pro Lys Thr Tyr Ile Gln Trp Val Ala Glu His
        675          680          685
Ala Pro Ser Gln Ser Pro Val Lys Val Asp Glu Thr Arg Ile Phe His
        690          695          700
Gln Leu Phe Thr Ser Asp Pro Ala Ala Glu Glu Asn Phe Leu Asp
705 His Val Asn Pro Asp Ser Leu Glu Ile Val Arg Gly Ala Met Val Glu
        710          715          720
Val Gly Phe Trp Asp Val Ala Lys Arg Ser Val Glu His Ala Arg Lys
        725          730          735
Glu Ala Ala Gln Arg Thr Glu Arg Ala Glu Ala Asp Ala Ala Lys Ala
        740          745          750
Arg Ser Glu Thr Glu Thr Ser Ala Thr Glu Gly Ala Gly Ala Gly Ala
770 Pro Gln Arg Thr Ala Asp Gln Leu Val Gly Lys Glu Leu Val Arg Phe
785 Gln Gly Met Arg Thr Ala Tyr Phe Ala Leu Asp Arg Leu Ser Gly Asp
        790          795          800
Leu Gly Leu Phe Gly Asp Lys Gln Lys Gly Gly Lys Ile Val Leu Asn
        805          810          815
Arg Ile Val Ser Leu Lys Glu Asp Ala Lys Lys Asp Asp Lys Ala Val
        820          825          830
Ala Ser Pro Val Ala Lys Lys Ala Lys
850          855

```

<210> 9959
 <211> 2343
 <212> DNA
 <213> Gallus gallus

<220>
 <221> CDS
 <222> (1)..(2343)

```

<400> 9959
atg gcg gcg atg gcg gcg acg gag gaa gcg gag gcg ctg gat ttg ttc      48
Met Ala Ala Met Ala Ala Thr Glu Glu Ala Glu Ala Leu Asp Leu Phe
1          5          10          15
acc ggc atc ggg ctg acc gag gcc aaa gcg gag acg ctg cgc aac      96
Thr Gly Ile Gly Leu Thr Glu Ala Lys Ala Arg Glu Thr Leu Arg Asn
        20          25          30
gcc gcg ctg agc gcg cag ctc cgc cag gcc gtg ctg cag gcc cgc gcc      144
Ala Ala Leu Ser Ala Gln Leu Arg Gln Ala Val Leu Gln Ala Arg Ala
        35          40          45
gcg ctg ggc tca ggc ctg gat aaa gcc acc ggc gct ctg ctg tac aac      192
Ala Leu Gly Ser Gly Leu Asp Lys Ala Thr Gly Ala Leu Leu Tyr Asn
        50          55          60
gcg gcc gcc cgg ctc cgc gac ccg gac cgc ttg gcc ttc gtg gtg ggg      240
Ala Ala Ala Arg Leu Arg Asp Pro Asp Arg Leu Ala Phe Val Val Gly
        65          70          75
tac atc ggg cgg agg gag atc cgc acc gac caa cag ttg ggc gcc gcc      288
Tyr Ile Gly Arg Arg Glu Ile Arg Thr Asp Gln Gln Leu Gly Ala Ala
        80          85          90
ctg cag tac ctc cgc agt cac ccg ctg gaa ccg gcg gac      336
Leu Gln Tyr Leu Arg Ser His Pro Leu Glu Pro Leu Glu Pro Ala Asp
        100          105          110
ttc gag cgg gcg tgc ggc gtg gga gtg cgg gtc agc ccc gag cag atc      384
Phe Glu Arg Ala Cys Gly Val Gly Val Arg Val Ser Pro Glu Gln Ile
        115          120          125
gag gag gcg gtg gag gcc gtg gtc agc cgg cac cgg gag gag ctg ctg      432
Glu Glu Ala Val Glu Ala Val Val Ser Arg His Arg Glu Glu Leu Leu
        130          135          140
gcg gag cgg tac cac ttc aac acg ggg ctg ctg atg gcg gag gcg cgg      480
Ala Glu Arg Tyr His Phe Asn Thr Gly Leu Leu Met Ala Glu Ala Arg
145          150          155          160
agc cgg ctg cag tgg gcg gat ggg aag agc atc aag aac gag gtg gat      528
Ser Arg Leu Gln Trp Ala Asp Gly Lys Ser Ile Lys Asn Glu Val Asp
        165          170          175

```

PF59083SeqList PF59083.txt

ctg	cag	gtg	ctg	cat	ttg	ctg	gga	cca	aag	aca	gaa	gct	gat	ctg	gaa	576
Leu	Gln	Val	Leu	His	Leu	Leu	Gly	Pro	Lys	Thr	Glu	Ala	Asp	Leu	Glu	
		180						185					190			
aag	aaa	cca	aag	gct	gcc	aag	gcc	cgg	cca	gcc	cca	gtg	gag	aag	cag	624
Lys	Lys	Pro	Lys	Ala	Ala	Lys	Ala	Arg	Pro	Ala	Pro	Val	Glu	Lys	Gln	
		195					200					205				
aag	gca	gcc	gtg	gtg	gag	aat	ggt	gag	gtg	ggc	gca	gag	aca	aag	tca	672
Lys	Ala	Ala	Val	Val	Glu	Asn	Gly	Glu	Val	Gly	Ala	Glu	Thr	Lys	Ser	
	210					215					220					
ctg	ctg	gag	cag	ctg	cga	gga	gaa	gct	ctg	aaa	ttc	cac	aag	ccg	gga	720
Leu	Leu	Glu	Gln	Leu	Arg	Gly	Glu	Ala	Leu	Lys	Phe	His	Lys	Pro	Gly	
225					230					235					240	
gag	aac	tac	aaa	acg	gag	ggc	tac	gtg	gtg	aca	ccc	aac	acc	atg	gct	768
Glu	Asn	Tyr	Lys	Thr	Glu	Gly	Tyr	Val	Val	Thr	Pro	Asn	Thr	Met	Ala	
				245				250						255		
ctg	ctg	aag	cag	cac	ctg	gcg	ctc	acg	ggt	ggg	cag	gtg	cgg	acg	cgg	816
Leu	Leu	Lys	Gln	His	Leu	Ala	Leu	Thr	Gly	Gly	Gln	Val	Arg	Thr	Arg	
		260						265					270			
ttc	cct	cct	gag	ccc	aat	ggc	att	ctg	cac	atc	ggc	cat	gcc	aag	gca	864
Phe	Pro	Pro	Glu	Pro	Asn	Gly	Ile	Leu	His	Ile	Gly	His	Ala	Lys	Ala	
		275					280					285				
atc	aac	ttc	aac	ttt	ggt	tac	gcc	aag	gcc	aac	ggg	ggc	atc	tgc	ttc	912
Ile	Asn	Phe	Asn	Phe	Gly	Tyr	Ala	Lys	Ala	Asn	Gly	Gly	Ile	Cys	Phe	
	290				295						300					
ttg	cgc	tat	gac	gac	acc	aac	cct	gag	aaa	gag	gag	aag	tac	ttc		960
Leu	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	Glu	Lys	Glu	Glu	Lys	Tyr	Phe		
305					310					315				320		
acg	gcc	atc	cgg	gag	atg	gtg	gag	tgg	ctt	ggc	tac	cag	ccc	tac	gct	1008
Thr	Ala	Ile	Arg	Glu	Met	Val	Glu	Trp	Leu	Gly	Tyr	Gln	Pro	Tyr	Ala	
				325					330					335		
gtg	act	cat	gcc	tca	gac	tac	ttt	gac	cag	ctc	tac	acc	tgg	gct	ctg	1056
Val	Thr	His	Ala	Ser	Asp	Tyr	Phe	Asp	Gln	Leu	Tyr	Thr	Trp	Ala	Leu	
			340					345					350			
gag	ctc	atc	cgc	agg	gga	caa	gcc	tac	gtc	tgc	cat	cag	aag	gtt	gag	1104
Glu	Leu	Ile	Arg	Arg	Gly	Gln	Ala	Tyr	Val	Cys	His	Gln	Lys	Val	Glu	
		355					360					365				
gag	atc	aag	ggt	cac	aac	cca	cca	ccg	tca	ccg	tgg	cgg	gac	cgg	ccc	1152
Glu	Ile	Lys	Gly	His	Asn	Pro	Pro	Pro	Ser	Pro	Trp	Arg	Asp	Arg	Pro	
	370				375						380					
gtg	gag	gag	tca	cta	gtg	ctc	gag	gac	atg	cga	aag	ggg	aag	ttt		1200
Val	Glu	Glu	Ser	Leu	Val	Leu	Phe	Glu	Asp	Met	Arg	Lys	Gly	Lys	Phe	
385					390				395					400		
ggg	gag	ggg	gag	gcc	acg	ctg	cgg	atg	aag	ctg	gtg	atg	gag	gat	ggg	1248
Gly	Glu	Gly	Glu	Ala	Thr	Leu	Arg	Met	Lys	Leu	Val	Met	Glu	Asp	Gly	
				405					410					415		
aag	atg	gac	ccc	gtt	gcc	tac	cgc	gtc	aag	ttc	aca	cca	cac	cac	cgc	1296
Lys	Met	Asp	Pro	Val	Ala	Tyr	Arg	Val	Lys	Phe	Thr	Pro	His	His	Arg	
			420					425					430			
acc	ggg	gac	aag	tgg	tgc	atc	tac	ccg	acg	tat	gac	tac	act	cac	tgc	1344
Thr	Gly	Asp	Lys	Trp	Cys	Ile	Tyr	Pro	Thr	Tyr	Asp	Tyr	Thr	His	Cys	
		435					440					445				
ctt	tgc	gac	tcc	atc	gag	cac	atc	acg	cac	tcc	ctc	tgc	acc	aag	gag	1392
Leu	Cys	Asp	Ser	Ile	Glu	His	Ile	Thr	His	Ser	Leu	Cys	Thr	Lys	Glu	
	450					455					460					
ttc	cag	gcc	agg	cgc	tcc	tac	ttc	tgg	ctg	tgc	aac	gcg	ctg	gac		1440
Phe	Gln	Ala	Arg	Arg	Ser	Tyr	Phe	Trp	Leu	Cys	Asn	Ala	Leu	Asp		
465					470				475					480		
gtg	tac	tgc	cct	gtg	cag	tgg	gaa	tac	ggc	cgc	ctc	aac	ctg	ctt	tac	1488
Val	Tyr	Cys	Pro	Val	Gln	Trp	Glu	Tyr	Gly	Arg	Leu	Asn	Leu	Leu	Tyr	
				485					490					495		
acc	gtt	gtc	tcc	aag	aga	aag	atc	atc	cgc	ctg	gtg	gag	act	ggg	gct	1536
Thr	Val	Val	Ser	Lys	Arg	Lys	Ile	Ile	Arg	Leu	Val	Glu	Thr	Gly	Ala	
			500				505					510				
gtg	cgg	gac	tgg	gat	gac	cca	cgg	ctc	ttc	acg	ctg	aca	gcc	ctg	cgc	1584
Val	Arg	Asp	Trp	Asp	Asp	Pro	Arg	Leu	Phe	Thr	Leu	Thr	Ala	Leu	Arg	
		515					520					525				
cgg	cga	ggc	ttc	cct	cct	gag	gcc	atc	aat	aac	ttc	tgt	gca	cgg	gtt	1632
Arg	Arg	Gly	Phe	Pro	Pro	Glu	Ala	Ile	Asn	Asn	Phe	Cys	Ala	Arg	Val	
	530					535					540					

PF59083SeqList PF59083.txt

ggt	gtg	aca	gtg	gcc	cag	gcg	acg	atg	gaa	ccc	cac	ttg	ctg	gag	gcg	1680
Gly	Val	Thr	Val	Ala	Gln	Ala	Thr	Met	Glu	Pro	His	Leu	Leu	Glu	Ala	
545					550					555					560	
tgt	gtg	agg	gat	gta	ctg	aat	gag	cag	gcc	ccc	cgc	gcc	atg	gcc	gtg	1728
Cys	Val	Arg	Asp	Val	Leu	Asn	Glu	Gln	Ala	Pro	Arg	Ala	Met	Ala	Val	
				565					570					575		
ctg	gag	ccc	ctc	aag	gtc	acc	atc	acc	aac	ttc	cca	gcc	ccc	cag	gca	1776
Leu	Glu	Pro	Leu	Lys	Val	Thr	Ile	Thr	Asn	Phe	Pro	Ala	Pro	Gln	Ala	
			580				585					590				
atc	gat	gtc	ctc	gtg	ccc	aac	ttt	cct	gct	gat	gag	agc	cgg	ggc	ttc	1824
Ile	Asp	Val	Leu	Val	Pro	Asn	Phe	Pro	Ala	Asp	Glu	Ser	Arg	Gly	Phe	
		595					600					605				
cac	aaa	gtg	ccc	ttc	cag	tcc	gtc	gtc	tac	atc	gtg	gag	agc	gac	ttc	1872
His	Lys	Val	Pro	Phe	Gln	Ser	Val	Val	Tyr	Ile	Val	Glu	Ser	Asp	Phe	
	610					615					620					
aag	gag	gag	gca	gac	agg	ggc	tac	aag	cg	ctg	gcc	ctc	ggg	cag	cca	1920
Lys	Glu	Glu	Ala	Asp	Arg	Gly	Tyr	Lys	Arg	Leu	Ala	Leu	Gly	Gln	Pro	
625					630					635					640	
gtg	ggg	ctg	cg	cac	acc	ggc	tac	gtc	atc	gcc	gtg	cag	aat	gtc	atc	1968
Val	Gly	Leu	Arg	His	Thr	Gly	Tyr	Val	Ile	Ala	Val	Gln	Asn	Val	Ile	
				645				650						655		
aag	gat	gcc	cgt	ggg	cgt	gtc	att	gag	ctg	gag	gtg	acc	tgc	acc	aag	2016
Lys	Asp	Ala	Arg	Gly	Arg	Val	Ile	Glu	Leu	Glu	Val	Thr	Cys	Thr	Lys	
			660				665						670			
tct	gac	gca	gcg	gag	aag	ccc	aaa	gcc	ttc	atc	cat	tgg	gtg	tca	gag	2064
Ser	Asp	Ala	Ala	Glu	Lys	Pro	Lys	Ala	Phe	Ile	His	Trp	Val	Ser	Glu	
		675					680					685				
ccg	cg	gtg	tgc	gaa	gtg	cg	ctg	tat	gag	cg	ctg	ttt	ttg	cac	aaa	2112
Pro	Arg	Val	Cys	Glu	Val	Arg	Leu	Tyr	Glu	Arg	Leu	Phe	Leu	His	Lys	
	690					695					700					
aac	ccc	gag	gac	cct	tcg	gag	gtg	ccg	ggt	gga	ttc	ctg	agc	gac	ctc	2160
Asn	Pro	Glu	Asp	Pro	Ser	Glu	Val	Pro	Gly	Gly	Phe	Leu	Ser	Asp	Leu	
705					710				715						720	
aac	cct	gac	tcc	cta	cgt	gtg	gtg	gac	gat	gcc	ctg	gtt	gac	agc	tct	2208
Asn	Pro	Asp	Ser	Leu	Arg	Val	Val	Asp	Ala	Leu	Val	Asp	Ser	Ser		
				725				730					735			
gtc	ctc	ggg	gca	cg	ccc	ttt	gat	aag	ttc	cag	ttt	gag	cg	ttg	ggc	2256
Val	Leu	Gly	Ala	Arg	Pro	Phe	Asp	Lys	Phe	Gln	Phe	Glu	Arg	Leu	Gly	
			740				745					750				
tac	ttc	tca	gtg	gat	cct	gac	agc	act	gac	agc	aag	ctg	gtg	ttc	aac	2304
Tyr	Phe	Ser	Val	Asp	Pro	Asp	Ser	Thr	Asp	Ser	Lys	Leu	Val	Phe	Asn	
		755					760					765				
cg	act	gtg	acg	ctg	aag	gag	gac	ccc	ggc	aaa	gcc	tga				2343
Arg	Thr	Val	Thr	Leu	Lys	Glu	Asp	Pro	Gly	Lys	Ala					
	770					775					780					

<210> 9960
 <211> 780
 <212> PRT
 <213> Gallus gallus

<400> 9960
 Met Ala Ala Met Ala Ala Thr Glu Glu Ala Glu Ala Leu Asp Leu Phe
 1 5 10 15
 Thr Gly Ile Gly Leu Thr Glu Ala Lys Ala Arg Glu Thr Leu Arg Asn
 20 25 30
 Ala Ala Leu Ser Ala Gln Leu Arg Gln Ala Val Leu Gln Ala Arg Ala
 35 40 45
 Ala Leu Gly Ser Gly Leu Asp Lys Ala Thr Gly Ala Leu Leu Tyr Asn
 50 55 60
 Ala Ala Ala Arg Leu Arg Asp Pro Asp Arg Leu Ala Phe Val Val Gly
 65 70 75 80
 Tyr Ile Gly Arg Arg Glu Ile Arg Thr Asp Gln Gln Leu Gly Ala Ala
 85 90 95
 Leu Gln Tyr Leu Arg Ser His Pro Leu Glu Pro Leu Glu Pro Ala Asp
 100 105 110
 Phe Glu Arg Ala Cys Gly Val Gly Val Arg Val Ser Pro Glu Gln Ile
 115 120 125
 Glu Glu Ala Val Glu Ala Val Val Ser Arg His Arg Glu Glu Leu Leu
 Seite 10519

PF59083SeqList PF59083.txt

130	135	140													
Ala	Glu	Arg	Tyr	His	Phe	Asn	Thr	Gly	Leu	Leu	Met	Ala	Glu	Ala	Arg
145					150					155					160
Ser	Arg	Leu	Gln	Trp	Ala	Asp	Gly	Lys	Ser	Ile	Lys	Asn	Glu	Val	Asp
				165					170						175
Leu	Gln	Val	Leu	His	Leu	Leu	Gly	Pro	Lys	Thr	Glu	Ala	Asp	Leu	Glu
				180					185						190
Lys	Lys	Pro	Lys	Ala	Ala	Lys	Ala	Arg	Pro	Ala	Pro	Val	Glu	Lys	Gln
		195					200								205
Lys	Ala	Ala	Val	Val	Glu	Asn	Gly	Glu	Val	Gly	Ala	Glu	Thr	Lys	Ser
		210					215								220
Leu	Leu	Glu	Gln	Leu	Arg	Gly	Glu	Ala	Leu	Lys	Phe	His	Lys	Pro	Gly
225					230					235					240
Glu	Asn	Tyr	Lys	Thr	Glu	Gly	Tyr	Val	Val	Thr	Pro	Asn	Thr	Met	Ala
				245					250						255
Leu	Leu	Lys	Gln	His	Leu	Ala	Leu	Thr	Gly	Gly	Gln	Val	Arg	Thr	Arg
				260				265							270
Phe	Pro	Pro	Glu	Pro	Asn	Gly	Ile	Leu	His	Ile	Gly	His	Ala	Lys	Ala
		275					280								285
Ile	Asn	Phe	Asn	Phe	Gly	Tyr	Ala	Lys	Ala	Asn	Gly	Gly	Ile	Cys	Phe
		290				295									300
Leu	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	Glu	Lys	Glu	Glu	Glu	Lys	Tyr	Phe
305					310					315					320
Thr	Ala	Ile	Arg	Glu	Met	Val	Glu	Trp	Leu	Gly	Tyr	Gln	Pro	Tyr	Ala
				325					330						335
Val	Thr	His	Ala	Ser	Asp	Tyr	Phe	Asp	Gln	Leu	Tyr	Thr	Trp	Ala	Leu
			340					345							350
Glu	Leu	Ile	Arg	Arg	Gly	Gln	Ala	Tyr	Val	Cys	His	Gln	Lys	Val	Glu
		355					360								365
Glu	Ile	Lys	Gly	His	Asn	Pro	Pro	Pro	Ser	Pro	Trp	Arg	Asp	Arg	Pro
		370				375									380
Val	Glu	Glu	Ser	Leu	Val	Leu	Phe	Glu	Asp	Met	Arg	Lys	Gly	Lys	Phe
385					390					395					400
Gly	Glu	Gly	Glu	Ala	Thr	Leu	Arg	Met	Lys	Leu	Val	Met	Glu	Asp	Gly
				405					410						415
Lys	Met	Asp	Pro	Val	Ala	Tyr	Arg	Val	Lys	Phe	Thr	Pro	His	His	Arg
			420					425							430
Thr	Gly	Asp	Lys	Trp	Cys	Ile	Tyr	Pro	Thr	Tyr	Asp	Tyr	Thr	His	Cys
		435					440								445
Leu	Cys	Asp	Ser	Ile	Glu	His	Ile	Thr	His	Ser	Leu	Cys	Thr	Lys	Glu
		450				455									460
Phe	Gln	Ala	Arg	Arg	Ser	Ser	Tyr	Phe	Trp	Leu	Cys	Asn	Ala	Leu	Asp
465					470					475					480
Val	Tyr	Cys	Pro	Val	Gln	Trp	Glu	Tyr	Gly	Arg	Leu	Asn	Leu	Leu	Tyr
				485					490						495
Thr	Val	Val	Ser	Lys	Arg	Lys	Ile	Ile	Arg	Leu	Val	Glu	Thr	Gly	Ala
			500					505							510
Val	Arg	Asp	Trp	Asp	Asp	Pro	Arg	Leu	Phe	Thr	Leu	Thr	Ala	Leu	Arg
		515					520								525
Arg	Arg	Gly	Phe	Pro	Pro	Glu	Ala	Ile	Asn	Asn	Phe	Cys	Ala	Arg	Val
		530				535									540
Gly	Val	Thr	Val	Ala	Gln	Ala	Thr	Met	Glu	Pro	His	Leu	Leu	Glu	Ala
545					550					555					560
Cys	Val	Arg	Asp	Val	Leu	Asn	Glu	Gln	Ala	Pro	Arg	Ala	Met	Ala	Val
				565					570						575
Leu	Glu	Pro	Leu	Lys	Val	Thr	Ile	Thr	Asn	Phe	Pro	Ala	Pro	Gln	Ala
				580				585							590
Ile	Asp	Val	Leu	Val	Pro	Asn	Phe	Pro	Ala	Asp	Glu	Ser	Arg	Gly	Phe
		595					600								605
His	Lys	Val	Pro	Phe	Gln	Ser	Val	Val	Tyr	Ile	Val	Glu	Ser	Asp	Phe
		610				615									620
Lys	Glu	Glu	Ala	Asp	Arg	Gly	Tyr	Lys	Arg	Leu	Ala	Leu	Gly	Gln	Pro
625					630					635					640
Val	Gly	Leu	Arg	His	Thr	Gly	Tyr	Val	Ile	Ala	Val	Gln	Asn	Val	Ile
				645					650						655
Lys	Asp	Ala	Arg	Gly	Arg	Val	Ile	Glu	Leu	Glu	Val	Thr	Cys	Thr	Lys
			660					665							670
Ser	Asp	Ala	Glu	Lys	Pro	Lys	Ala	Phe	Ile	His	Trp	Val	Ser	Glu	
		675				680									685

PF59083SeqList PF59083.txt

Pro Arg Val Cys Glu Val Arg Leu Tyr Glu Arg Leu Phe Leu His Lys
 690 695 700
 Asn Pro Glu Asp Pro Ser Glu Val Pro Gly Gly Phe Leu Ser Asp Leu
 705 710 715 720
 Asn Pro Asp Ser Leu Arg Val Val Asp Asp Ala Leu Val Asp Ser Ser
 725 730 735
 Val Leu Gly Ala Arg Pro Phe Asp Lys Phe Gln Phe Glu Arg Leu Gly
 740 745 750
 Tyr Phe Ser Val Asp Pro Asp Ser Thr Asp Ser Lys Leu Val Phe Asn
 755 760 765
 Arg Thr Val Thr Leu Lys Glu Asp Pro Gly Lys Ala
 770 775 780

<210> 9961
 <211> 2391
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (1)..(2391)

<400> 9961
 atg gcg acc gga gaa gcg gcg gcg gcg gcg gcg tcg ccg ccg gag ctg 48
 Met Ala Thr Gly Glu Ala Ala Ala Ala Ala Ala Ser Pro Pro Glu Leu
 1 5 10 15
 gcg tcg ttc ctg gcg atc ggg ctt gac cag cgc acg gcg gag aac gcc 96
 Ala Ser Phe Leu Ala Ile Gly Leu Asp Gln Arg Thr Ala Glu Asn Ala
 20 25 30
 ctc gcc aac cgc aag gtc acc gcc aac ctc acc gcc gtc atc gcc gag 144
 Leu Ala Asn Arg Lys Val Thr Ala Asn Leu Thr Ala Val Ile Ala Glu
 35 40 45
 gct ggt gtt agt ggg tgt gac aaa tct gtg ggg aat ctt ctc tac act 192
 Ala Gly Val Ser Gly Cys Asp Lys Ser Val Gly Asn Leu Leu Tyr Thr
 50 55 60
 gtc gcg acg aag tat ccg gcg aat gcc ctg gtg cat cgt ccc gtt gtc 240
 Val Ala Thr Lys Tyr Pro Ala Asn Ala Leu Val His Arg Pro Val Val
 65 70 75 80
 atc caa tac att gtg tcg tca aag atc aag acc ccc gcg caa tta gat 288
 Ile Gln Tyr Ile Val Ser Ser Lys Ile Lys Thr Pro Ala Gln Leu Asp
 85 90 95
 gct gct ctg tcg ttt ctt tct act ttg ggt cct gat cca ttg gac aca 336
 Ala Ala Leu Ser Phe Leu Ser Thr Leu Gly Pro Asp Pro Leu Asp Thr
 100 105 110
 gca aag ttt gaa gag aca tgt gga gtg ggg gtg gtt gtt tca act gaa 384
 Ala Lys Phe Glu Glu Thr Cys Gly Val Gly Val Val Val Ser Thr Glu
 115 120 125
 gag att cag tca atg gtc act gat atc ctg aag gaa aac atg gaa gcc 432
 Glu Ile Gln Ser Met Val Thr Asp Ile Leu Lys Glu Asn Met Glu Ala
 130 135 140
 ata gtt gaa cag cga tat cat ata aat gtt ggc agc ttg tgc gga cag 480
 Ile Val Glu Gln Arg Tyr His Ile Asn Val Gly Ser Leu Cys Gly Gln
 145 150 155 160
 gtt agg aag tgg cac ccc tgg ggc gat gct aag ttc ata aag gag gaa 528
 Val Arg Lys Trp His Pro Trp Gly Asp Ala Lys Phe Ile Lys Glu Glu
 165 170 175
 att gat aaa agg ctt aca gag att ctt ggt cca aag aca gaa gct gac 576
 Ile Asp Lys Arg Leu Thr Glu Ile Leu Gly Pro Lys Thr Glu Ala Asp
 180 185 190
 aat gta aag cct gtg aaa aag aag gag aag ccc gca aaa gtt gag 624
 Asn Val Lys Pro Val Lys Lys Lys Lys Glu Lys Pro Ala Lys Val Glu
 195 200 205
 gag aaa aaa act gcg gta gct gct cct gct cca cca tct gag gaa gaa 672
 Glu Lys Lys Thr Ala Val Ala Ala Pro Ala Pro Pro Ser Glu Glu Glu
 210 215 220
 ctt aat ccc tac tcc ata ttt cct caa ccg gag gaa aac tta aag gtc 720
 Leu Asn Pro Tyr Ser Ile Phe Pro Gln Pro Glu Glu Asn Leu Lys Val
 225 230 235 240
 cat aca gaa att ttc ttc agc gat gga aat ata tgg aga gca cac aac 768

PF59083SeqList PF59083.txt

His	Thr	Glu	Ile	Phe	Phe	Ser	Asp	Gly	Asn	Ile	Trp	Arg	Ala	His	Asn	
aga	aag	gac	att	245	tta	gag	aaa	cat	ctt	aaa	gca	act	gga	gga	aaa	gtg
Arg	Lys	Asp	Ile	Leu	Glu	Lys	His	Leu	Lys	Ala	Thr	Gly	Gly	Lys	Val	816
atg	acc	cgc	ttt	ccc	cca	gag	cct	aat	ggc	tac	ctt	cat	att	ggt	cat	
Met	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	864
gct	aag	gct	atg	ttt	att	gat	ttt	gga	ctg	gct	aaa	gag	cgc	aac	gga	
Ala	Lys	Ala	Met	Phe	Ile	Asp	Phe	Gly	Leu	Ala	Lys	Glu	Arg	Asn	Gly	912
cat	tgt	tac	ctt	agg	ttt	gat	gat	aca	aac	cct	gag	gcg	gag	aag	aaa	
His	Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys	Lys	960
gaa	tat	ata	gat	cac	att	caa	gaa	att	gtc	cga	tgg	atg	ggc	tgg	gag	
Glu	Tyr	Ile	Asp	His	Ile	Gln	Glu	Ile	Val	Arg	Trp	Met	Gly	Trp	Glu	1008
cct	tat	aaa	ggt	acc	tat	aca	agt	gac	tat	ttc	caa	gaa	tta	tat	gaa	
Pro	Tyr	Lys	Val	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Gln	Glu	Leu	Tyr	Glu	1056
ctt	gct	ggt	tgt	ttg	ata	aag	aag	gga	cta	gct	tat	gtc	gat	cac	cag	
Leu	Ala	Val	Cys	Leu	Ile	Lys	Lys	Gly	Leu	Ala	Tyr	Val	Asp	His	Gln	1104
aca	cca	gaa	gag	ata	aag	gag	tat	aga	gaa	aag	caa	atg	aat	agt	cca	
Thr	Pro	Glu	Glu	Ile	Lys	Glu	Tyr	Arg	Glu	Lys	Gln	Met	Asn	Ser	Pro	1152
tgg	agg	gat	agg	cct	ata	gaa	gag	tca	cta	aaa	ctg	ttt	gaa	gat	atg	
Trp	Arg	Asp	Arg	Pro	Ile	Glu	Glu	Ser	Leu	Lys	Leu	Phe	Glu	Asp	Met	1200
agg	cat	ggg	ttg	ggt	gct	gag	gga	aag	gca	act	ctt	agg	atg	aaa	caa	
Arg	His	Gly	Leu	Val	Ala	Glu	Gly	Lys	Ala	Thr	Leu	Arg	Met	Lys	Gln	1248
gac	atg	cag	aat	gat	aac	aag	aac	atg	gct	gac	tta	ata	gca	tat	aga	
Asp	Met	Gln	Asn	Asp	Asn	Lys	Asn	Met	Ala	Asp	Leu	Ile	Ala	Tyr	Arg	1296
ata	aag	ttt	aca	cct	cat	ccc	cat	gct	ggc	gac	aag	tgg	ttt	atc	tat	
Ile	Lys	Phe	Thr	Pro	His	Pro	His	Ala	Gly	Asp	Lys	Trp	Phe	Ile	Tyr	1344
cca	agc	tat	gac	tat	gct	cat	tgt	ttg	ggt	gac	tct	ctt	gaa	aac	att	
Pro	Ser	Tyr	Asp	Tyr	Ala	His	Cys	Leu	Val	Asp	Ser	Leu	Glu	Asn	Ile	1392
acc	cat	tcg	ttg	tgc	aca	cta	gaa	ttt	gac	ata	cgt	cgt	cct	tca	tac	
Thr	His	Ser	Leu	Cys	Thr	Leu	Glu	Phe	Asp	Ile	Arg	Arg	Pro	Ser	Tyr	1440
tac	tgg	ctg	ctc	gta	tcc	ctg	gac	cag	tac	cag	cca	tat	ggt	tgg	gaa	
Tyr	Trp	Leu	Leu	Val	Ser	Leu	Asp	Gln	Tyr	Gln	Pro	Tyr	Val	Trp	Glu	1488
tat	tca	agg	tta	aac	ata	tca	aac	aat	ggt	atg	tcc	aag	cga	aag	cta	
Tyr	Ser	Arg	Leu	Asn	Ile	Ser	Asn	Val	Met	Ser	Ser	Lys	Arg	Lys	Leu	1536
aat	aaa	ctt	gtg	aca	gag	aag	tgg	gta	gat	ggg	tgg	gat	gat	cct	cgc	
Asn	Lys	Leu	Val	Thr	Glu	Lys	Trp	Val	Asp	Gly	Trp	Asp	Asp	Pro	Arg	1584
ctg	ttg	aca	ctt	gca	gga	cta	cgg	cgg	aga	gga	gta	tca	tca	aca	gca	
Leu	Leu	Thr	Leu	Ala	Gly	Leu	Arg	Arg	Arg	Gly	Val	Ser	Ser	Thr	Ala	1632
att	aac	tcc	ttt	att	cgt	gga	atg	ggc	ata	aca	agg	agt	gac	aac	agt	
Ile	Asn	Ser	Phe	Ile	Arg	Gly	Met	Gly	Ile	Thr	Arg	Ser	Asp	Asn	Ser	1680
ttg	ata	cgc	tta	gaa	cgc	ctt	gag	tat	cat	att	aga	gaa	gag	ctc	aac	
Leu	Ile	Arg	Leu	Glu	Arg	Leu	Glu	Tyr	His	Ile	Arg	Glu	Glu	Leu	Asn	1728
aaa	gta	gct	cct	cgt	gct	atg	ggt	ggt	ttg	cat	ccc	cta	aag	ggt	ggt	
Lys	Val	Ala	Pro	Arg	Ala	Met	Val	Val	Leu	His	Pro	Leu	Lys	Val	Val	1776
ata	aat	aat	tta	gac	tat	gga	aca	ata	ata	gac	ctt	gat	gca	aaa	aag	
Ile	Asn	Asn	Leu	Asp	Tyr	Gly	Thr	Ile	Ile	Asp	Leu	Asp	Ala	Lys	Lys	1824
tgg	ccc	gat	gct	cca	gga	gat	gat	gct	tcg	gcc	tat	tac	aag	ggt	cca	1872

PF59083SeqList PF59083.txt

Trp	Pro	Asp	Ala	Pro	Gly	Asp	Asp	Ala	Ser	Ala	Tyr	Tyr	Lys	Val	Pro	
610						615					620					
tac	tca	aga	act	gtc	tac	atc	gag	cag	tct	gat	ttt	cgt	gta	aag	gat	1920
Phe	Ser	Arg	Thr	Val	Tyr	Ile	Glu	Gln	Ser	Asp	Phe	Arg	Val	Lys	Asp	
625					630					635					640	
tca	aaa	gat	tat	tat	ggg	ctt	gct	cct	ggg	aaa	aca	gta	cta	cta	agg	1968
Ser	Lys	Asp	Tyr	Tyr	Gly	Leu	Ala	Pro	Gly	Lys	Thr	Val	Leu	Leu	Arg	
				645					650					655		
tat	gca	ttc	cca	ata	aaa	tgt	acg	gaa	ggt	atc	tat	ggg	gat	aat	tca	2016
Tyr	Ala	Phe	Pro	Ile	Lys	Cys	Thr	Val	Ile	Tyr	Gly	Asp	Asn	Ser		
			660					665					670			
gat	aat	atc	att	gaa	atc	cga	gct	gag	tat	gac	cct	tcg	aag	gct	aca	2064
Asp	Asn	Ile	Ile	Glu	Ile	Arg	Ala	Glu	Tyr	Asp	Pro	Ser	Lys	Ala	Thr	
		675				680						685				
aaa	cca	aag	ggg	gtg	ttg	cac	tgg	gtt	gcc	gaa	cct	tct	cca	ggg	gtt	2112
Lys	Pro	Lys	Gly	Val	Leu	His	Trp	Val	Ala	Glu	Pro	Ser	Pro	Gly	Val	
	690					695					700					
aac	ccg	ctc	aaa	gtg	gaa	atc	aga	ttg	ttc	gag	aaa	tta	ttt	ctt	tca	2160
Asn	Pro	Leu	Lys	Val	Glu	Ile	Arg	Leu	Phe	Glu	Lys	Leu	Phe	Leu	Ser	
705				710						715					720	
gag	aat	cct	gtg	gag	ctt	gag	gat	tgg	ctg	ggg	gat	ctc	aac	cca	cga	2208
Glu	Asn	Pro	Val	Glu	Leu	Glu	Asp	Trp	Leu	Gly	Asp	Leu	Asn	Pro	Arg	
			725					730						735		
tca	aag	gaa	gtg	ata	aag	ggg	gcc	tat	gcc	gtg	cct	tcg	ctt	gca	act	2256
Ser	Lys	Glu	Val	Ile	Lys	Gly	Ala	Tyr	Ala	Val	Pro	Ser	Leu	Ala	Thr	
			740					745					750			
gca	gcg	ctg	ggg	gac	aaa	ttt	cag	ttt	gaa	cgc	ctc	ggg	tac	ttt	gct	2304
Ala	Ala	Leu	Gly	Asp	Lys	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Phe	Ala	
		755				760						765				
gtg	gat	tcc	gac	tcg	acg	gct	gag	gaa	ctt	gtg	ttc	aac	aga	acc	gtt	2352
Val	Asp	Ser	Asp	Ser	Thr	Ala	Glu	Glu	Leu	Val	Phe	Asn	Arg	Thr	Val	
	770				775						780					
act	cta	cgg	gat	tcc	tat	gga	aaa	gct	gga	ccc	aag	tga				2391
Thr	Leu	Arg	Asp	Ser	Tyr	Gly	Lys	Ala	Gly	Pro	Lys					
785					790					795						

<210> 9962
 <211> 796
 <212> PRT
 <213> Oryza sativa

<400> 9962

Met	Ala	Thr	Gly	Glu	Ala	Ala	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Glu	Leu
1				5				10						15	
Ala	Ser	Phe	Leu	Ala	Ile	Gly	Leu	Asp	Gln	Arg	Thr	Ala	Glu	Asn	Ala
		20						25					30		
Leu	Ala	Asn	Arg	Lys	Val	Thr	Ala	Asn	Leu	Thr	Ala	Val	Ile	Ala	Glu
		35					40					45			
Ala	Gly	Val	Ser	Gly	Cys	Asp	Lys	Ser	Val	Gly	Asn	Leu	Leu	Tyr	Thr
	50					55					60				
Val	Ala	Thr	Lys	Tyr	Pro	Ala	Asn	Ala	Leu	Val	His	Arg	Pro	Val	Val
65					70					75					80
Ile	Gln	Tyr	Ile	Val	Ser	Ser	Lys	Ile	Lys	Thr	Pro	Ala	Gln	Leu	Asp
			85						90					95	
Ala	Ala	Leu	Ser	Phe	Leu	Ser	Thr	Leu	Gly	Pro	Asp	Pro	Leu	Asp	Thr
			100					105					110		
Ala	Lys	Phe	Glu	Glu	Thr	Cys	Gly	Val	Gly	Val	Val	Val	Ser	Thr	Glu
		115					120					125			
Glu	Ile	Gln	Ser	Met	Val	Thr	Asp	Ile	Leu	Lys	Glu	Asn	Met	Glu	Ala
	130					135					140				
Ile	Val	Glu	Gln	Arg	Tyr	His	Ile	Asn	Val	Gly	Ser	Leu	Cys	Gly	Gln
145					150					155					160
Val	Arg	Lys	Trp	His	Pro	Trp	Gly	Asp	Ala	Lys	Phe	Ile	Lys	Glu	Glu
			165						170					175	
Ile	Asp	Lys	Arg	Leu	Thr	Glu	Ile	Leu	Gly	Pro	Lys	Thr	Glu	Ala	Asp
			180					185					190		
Asn	Val	Lys	Pro	Val	Lys	Lys	Lys	Lys	Glu	Lys	Pro	Ala	Lys	Val	Glu
		195					200					205			
Glu	Lys	Lys	Thr	Ala	Val	Ala	Ala	Pro	Ala	Pro	Pro	Ser	Glu	Glu	Glu

PF59083SeqList PF59083.txt

210	215	220
Leu Asn Pro Tyr Ser Ile	Phe Pro Gln Pro Glu Glu Asn Leu Lys Val	
225	230	235
His Thr Glu Ile Phe Phe	Ser Asp Gly Asn Ile Trp Arg Ala His Asn	
	245	250
Arg Lys Asp Ile Leu Glu Lys His Leu Lys Ala Thr Gly Gly Lys Val		
	260	265
Met Thr Arg Phe Pro Pro Glu Pro Asn Gly Tyr Leu His Ile Gly His		
	275	280
Ala Lys Ala Met Phe Ile Asp Phe Gly Leu Ala Lys Glu Arg Asn Gly		
	290	295
His Cys Tyr Leu Arg Phe Asp Asp Thr Asn Pro Glu Ala Glu Lys Lys		
305	310	315
Glu Tyr Ile Asp His Ile Gln Glu Ile Val Arg Trp Met Gly Trp Glu		
	325	330
Pro Tyr Lys Val Thr Tyr Thr Ser Asp Tyr Phe Gln Glu Leu Tyr Glu		
	340	345
Leu Ala Val Cys Leu Ile Lys Lys Gly Leu Ala Tyr Val Asp His Gln		
	355	360
Thr Pro Glu Glu Ile Lys Glu Tyr Arg Glu Lys Gln Met Asn Ser Pro		
	370	375
Trp Arg Asp Arg Pro Ile Glu Glu Ser Leu Lys Leu Phe Glu Asp Met		
385	390	395
Arg His Gly Leu Val Ala Glu Gly Lys Ala Thr Leu Arg Met Lys Gln		
	405	410
Asp Met Gln Asn Asp Asn Lys Asn Met Ala Asp Leu Ile Ala Tyr Arg		
	420	425
Ile Lys Phe Thr Pro His Pro His Ala Gly Asp Lys Trp Phe Ile Tyr		
	435	440
Pro Ser Tyr Asp Tyr Ala His Cys Leu Val Asp Ser Leu Glu Asn Ile		
	450	455
Thr His Ser Leu Cys Thr Leu Glu Phe Asp Ile Arg Arg Pro Ser Tyr		
465	470	475
Tyr Trp Leu Leu Val Ser Leu Asp Gln Tyr Gln Pro Tyr Val Trp Glu		
	485	490
Tyr Ser Arg Leu Asn Ile Ser Asn Asn Val Met Ser Lys Arg Lys Leu		
	500	505
Asn Lys Leu Val Thr Glu Lys Trp Val Asp Gly Trp Asp Asp Pro Arg		
	515	520
Leu Leu Thr Leu Ala Gly Leu Arg Arg Arg Gly Val Ser Ser Thr Ala		
	530	535
Ile Asn Ser Phe Ile Arg Gly Met Gly Ile Thr Arg Ser Asp Asn Ser		
545	550	555
Leu Ile Arg Leu Glu Arg Leu Glu Tyr His Ile Arg Glu Glu Leu Asn		
	565	570
Lys Val Ala Pro Arg Ala Met Val Val Leu His Pro Leu Lys Val Val		
	580	585
Ile Asn Asn Leu Asp Tyr Gly Thr Ile Ile Asp Leu Asp Ala Lys Lys		
	595	600
Trp Pro Asp Ala Pro Gly Asp Ala Ser Ala Tyr Tyr Lys Val Pro		
	610	615
Phe Ser Arg Thr Val Tyr Ile Glu Gln Ser Asp Phe Arg Val Lys Asp		
625	630	635
Ser Lys Asp Tyr Tyr Gly Leu Ala Pro Gly Lys Thr Val Leu Leu Arg		
	645	650
Tyr Ala Phe Pro Ile Lys Cys Thr Glu Val Ile Tyr Gly Asp Asn Ser		
	660	665
Asp Asn Ile Ile Glu Ile Arg Ala Glu Tyr Asp Pro Ser Lys Ala Thr		
	675	680
Lys Pro Lys Gly Val Leu His Trp Val Ala Glu Pro Ser Pro Gly Val		
	690	695
Asn Pro Leu Lys Val Glu Ile Arg Leu Phe Glu Lys Leu Phe Leu Ser		
705	710	715
Glu Asn Pro Val Glu Leu Glu Asp Trp Leu Gly Asp Leu Asn Pro Arg		
	725	730
Ser Lys Glu Val Ile Lys Gly Ala Tyr Ala Val Pro Ser Leu Ala Thr		
	740	745
Ala Ala Leu Gly Asp Lys Phe Gln Phe Glu Arg Leu Gly Tyr Phe Ala		
	755	760
		765

PF59083SeqList PF59083.txt

Val Asp Ser Asp Ser Thr Ala Glu Glu Leu Val Phe Asn Arg Thr Val
 770 775 780
 Thr Leu Arg Asp Ser Tyr Gly Lys Ala Gly Pro Lys
 785 790 795

<210> 9963
 <211> 2325
 <212> DNA
 <213> Brachydanio rerio

<220>
 <221> CDS
 <222> (1)..(2325)

<400> 9963
 atg gcg gac gtg gtg tct tct ttc atg tca att ggc ctt agt gag cag 48
 Met Ala Asp Val Val Ser Ser Phe Met Ser Ile Gly Leu Ser Glu Gln
 1 5 10 15
 aaa gct aag gaa acg ttg aag aat gaa aca ctt tca tca aca ctc aag 96
 Lys Ala Lys Glu Thr Leu Lys Asn Glu Thr Leu Ser Ser Thr Leu Lys
 20 25 30
 aaa gcc att gat ctg gct caa gtc cag ctg ggg tct tct gcc att gac 144
 Lys Ala Ile Asp Leu Ala Gln Val Gln Leu Gly Ser Ser Ala Ile Asp
 35 40 45
 aag atc act ggc act ctg ttg tac agt atg gtg aca cga ctt aaa gac 192
 Lys Ile Thr Gly Thr Leu Leu Tyr Ser Met Val Thr Arg Leu Lys Asp
 50 55 60
 acg aac agg cct caa ttt ctg aca aaa tac atc att tca cga aaa atc 240
 Thr Asn Arg Pro Gln Phe Leu Thr Lys Tyr Ile Ile Ser Arg Lys Ile
 65 70 75 80
 aca aca gaa ctg cag ctg tca gcg gct ttg gac gac ttt gtg aaa agc cac 288
 Thr Thr Glu Leu Gln Leu Ser Ala Ala Leu Asp Phe Val Lys Ser His
 85 90 95
 cct cag ggc gat gtg gat cag cac aag ttt gag gtg gcc tgt ggt gtg 336
 Pro Gln Gly Asp Val Asp Gln His Lys Phe Glu Val Ala Cys Gly Val
 100 105 110
 gga atg gtt gtc aca cct gag cag ata gag gac gca gtg gaa ttg att 384
 Gly Met Val Val Thr Pro Glu Gln Ile Glu Asp Ala Val Glu Leu Ile
 115 120 125
 atc agg aaa cac aaa gat cag ctg ttg gca gag aga tat cgc ttc aac 432
 Ile Arg Lys His Lys Asp Gln Leu Leu Ala Glu Arg Tyr Arg Phe Asn
 130 135 140
 atg ggg ata ctc atg ggt gag gcc aga gcc act ctt aaa tgg gct gat 480
 Met Gly Ile Leu Met Gly Glu Ala Arg Ala Thr Leu Lys Trp Ala Asp
 145 150 155 160
 ggg aag att gtc aag aat gaa gtg gat atg cag gtg ttg cac ctt ctc 528
 Gly Lys Ile Val Lys Asn Glu Val Asp Met Gln Val Leu His Leu Leu
 165 170 175
 ggt cca aaa act gag gcg gat ctg gaa aaa aag agc aag gca gtc aaa 576
 Gly Pro Lys Thr Glu Ala Asp Leu Glu Lys Lys Ser Lys Ala Val Lys
 180 185 190
 ccc aaa gca cca gaa aaa gat gtg aag att gag cag gct tct gca gta 624
 Pro Lys Ala Pro Glu Lys Asp Val Lys Ile Glu Gln Ala Ser Ala Val
 195 200 205
 aac ggt gat ggg aac att gag aat aag tca ttg atg gag cag ctg aga 672
 Asn Gly Asp Gly Asn Ile Glu Asn Lys Ser Leu Met Glu Gln Leu Arg
 210 215 220
 gga gaa gct ctt aag ttc cat aag cca ggg gag aat tac aaa acg gag 720
 Gly Glu Ala Leu Lys Phe His Lys Pro Gly Glu Asn Tyr Lys Thr Glu
 225 230 235 240
 ggt tat gtt gta aca cct aac acc atg aac ttg ctg aag aag cac ttg 768
 Gly Tyr Val Val Thr Pro Asn Thr Met Asn Leu Leu Lys Lys His Leu
 245 250 255
 gaa gaa act gga gga cag gtc cgc aca cgt ttc cct cct gag cct aat 816
 Glu Glu Thr Gly Gly Gln Val Arg Thr Arg Phe Pro Pro Glu Pro Asn
 260 265 270
 ggt att ctg cat att ggc cat gcc aaa gca atc aac ttc aat ttt ggt 864
 Gly Ile Leu His Ile Gly His Ala Lys Ala Ile Asn Phe Asn Phe Gly
 275 280 285

PF59083SeqList PF59083.txt

ttc	gcc	aag	gcc	aac	aac	ggc	atc	tgt	ttt	ctg	cgg	tat	gac	gac	aca	912
Phe	Ala	Lys	Ala	Asn	Asn	Gly	Ile	Cys	Phe	Leu	Arg	Tyr	Asp	Asp	Thr	
	290					295					300					
aac	cca	gag	aaa	gag	gag	gaa	aaa	tac	ttc	acc	gcc	atc	aaa	gac	atg	960
Asn	Pro	Glu	Lys	Glu	Glu	Glu	Lys	Tyr	Phe	Thr	Ala	Ile	Lys	Asp	Met	
305					310					315					320	
gtg	gag	tgg	ctt	gga	tat	gaa	cca	tat	gct	gtt	aca	cac	gcc	tct	gat	1008
Val	Glu	Trp	Leu	Gly	Tyr	Glu	Pro	Tyr	Ala	Val	Thr	His	Ala	Ser	Asp	
			325						330					335		
aac	ttc	cag	cgt	ctc	tac	aat	ctt	gct	gtt	gat	ctc	att	cgc	agg	ggt	1056
Asn	Phe	Gln	Arg	Leu	Tyr	Asn	Leu	Ala	Val	Asp	Leu	Ile	Arg	Arg	Gly	
			340					345					350			
cat	gca	tat	gtg	tgc	cac	cag	cgc	gga	gag	gag	ctc	aag	ggt	cac	aac	1104
His	Ala	Tyr	Val	Cys	His	Gln	Arg	Gly	Glu	Glu	Leu	Lys	Gly	His	Asn	
		355					360					365				
gtc	cct	tcc	tct	ccc	tgg	aga	gag	cga	ccc	gtg	gaa	gag	tct	ttg	gtt	1152
Val	Pro	Ser	Ser	Pro	Trp	Arg	Glu	Arg	Pro	Val	Glu	Glu	Ser	Leu	Val	
	370					375					380					
ttg	ttt	gag	cac	atg	agg	aag	gga	atg	ttt	gca	gaa	ggg	gaa	gcc	act	1200
Leu	Phe	Glu	His	Met	Arg	Lys	Gly	Met	Phe	Ala	Glu	Gly	Glu	Ala	Thr	
385					390					395					400	
ctc	aga	atg	aag	atg	gtc	atg	gaa	gat	ggc	aaa	atg	gac	ccg	gtg	gca	1248
Leu	Arg	Met	Lys	Met	Val	Met	Glu	Asp	Gly	Lys	Met	Asp	Pro	Val	Ala	
			405						410					415		
tat	cgg	atc	aaa	tac	acg	cca	cat	cac	agg	aca	gga	gac	act	tgg	tgc	1296
Tyr	Arg	Ile	Lys	Tyr	Thr	Pro	His	His	Arg	Thr	Gly	Asp	Thr	Trp	Cys	
			420					425					430			
ata	tac	ccc	aca	tac	gat	tac	acg	cac	tgt	ctg	tgc	gac	tcc	att	gag	1344
Ile	Tyr	Pro	Thr	Tyr	Asp	Tyr	Thr	His	Cys	Leu	Cys	Asp	Ser	Ile	Glu	
		435				440						445				
aac	atc	aca	cac	tct	ctg	tgc	acc	aaa	gag	ttt	cag	gcc	aga	cga	tca	1392
Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Lys	Glu	Phe	Gln	Ala	Arg	Arg	Ser	
	450					455					460					
tca	tat	ttc	tgg	ttg	tgc	aat	gct	ctg	gat	gtg	tat	tgc	ccg	gtg	cag	1440
Ser	Tyr	Phe	Trp	Leu	Cys	Asn	Ala	Leu	Asp	Val	Tyr	Cys	Pro	Val	Gln	
465					470					475					480	
tgg	gaa	tat	ggc	cga	ctg	aac	ctc	act	tat	act	gtc	gtt	tcc	aag	aga	1488
Trp	Glu	Tyr	Gly	Arg	Leu	Asn	Leu	Thr	Tyr	Thr	Val	Val	Ser	Lys	Arg	
			485						490					495		
aag	atc	atc	aaa	gtg	gaa	aca	gga	gtt	agg	gat	tgg	gat	tgg	gat	gat	1536
Lys	Ile	Ile	Lys	Leu	Val	Glu	Thr	Gly	Val	Val	Arg	Asp	Trp	Asp	Asp	
			500					505					510			
cct	agg	ctt	ttt	acc	ctc	aca	gct	ctc	agg	aga	cgt	ggg	ttc	cct	cca	1584
Pro	Arg	Leu	Phe	Thr	Leu	Thr	Ala	Leu	Arg	Arg	Arg	Gly	Phe	Pro	Pro	
		515					520					525				
caa	gcc	atc	aac	aat	ttc	tgt	gcc	cgg	gtg	ggt	gta	act	gtt	gct	cag	1632
Gln	Ala	Ile	Asn	Asn	Phe	Cys	Ala	Arg	Val	Gly	Val	Thr	Val	Ala	Gln	
	530					535					540					
act	aca	atg	gag	cca	cac	ctg	ctg	gag	gag	tgt	ggt	cgg	gag	gtc	cta	1680
Thr	Thr	Met	Glu	Pro	His	Leu	Leu	Glu	Ala	Cys	Val	Arg	Glu	Val	Leu	
545					550					555					560	
aat	gac	act	gct	cct	cgt	gcc	atg	gcc	ata	ctc	gag	cct	ctc	aag	gtc	1728
Asn	Asp	Thr	Ala	Pro	Arg	Ala	Met	Ala	Ile	Leu	Glu	Pro	Leu	Lys	Val	
			565						570					575		
aca	atc	atc	aac	ctg	cca	act	aat	gca	cag	aag	gag	ctt	aga	gtc	cca	1776
Thr	Ile	Ile	Asn	Leu	Pro	Thr	Asn	Ala	Gln	Lys	Glu	Leu	Arg	Val	Pro	
			580					585					590			
gac	ttc	cca	gcc	aat	gaa	gca	agg	ggc	agc	cat	gtg	gtt	ccc	ttc	tca	1824
Asp	Phe	Pro	Ala	Asn	Glu	Ala	Arg	Gly	Ser	His	Val	Val	Pro	Phe	Ser	
		595					600					605				
aag	acc	atc	ttt	att	gag	cag	agc	gac	ttc	aga	gag	gtg	atg	gag	aag	1872
Lys	Thr	Ile	Phe	Ile	Glu	Gln	Ser	Asp	Phe	Arg	Glu	Val	Met	Glu	Lys	
	610					615					620					
ggt	tat	aag	cgc	ctg	act	cca	gat	cag	tca	gtg	ggc	ttg	aga	tat	gca	1920
Gly	Tyr	Lys	Arg	Leu	Thr	Pro	Asp	Gln	Ser	Val	Gly	Leu	Arg	Tyr	Ala	
625					630					635					640	
gga	tac	gtc	atc	tct	gta	cag	cgt	gtc	atc	aag	gat	gac	cgt	ggt	aaa	1968
Gly	Tyr	Val	Ile	Ser	Val	Gln	Arg	Val	Ile	Lys	Asp	Asp	Arg	Gly	Lys	
				645					650					655		

PF59083SeqList PF59083.txt

gta	tgt	gag	ctc	gag	gtg	acc	tgc	gtc	agc	tcc	gac	act	gca	gag	aaa	2016
Val	Cys	Glu	Leu	Glu	Val	Thr	Cys	Val	Ser	Ser	Asp	Thr	Ala	Glu	Lys	
		660						665					670			
ccc	aaa	gcg	ttt	att	cat	tgg	gtg	agc	gag	cca	ctg	ctg	tgt	gaa	gtg	2064
Pro	Lys	Ala	Phe	Ile	His	Trp	Val	Ser	Glu	Pro	Leu	Leu	Cys	Glu	Val	
		675						680					685			
cgc	ctc	tat	gaa	aga	ctg	ttt	ctt	cat	aaa	aac	cca	gag	gac	ccg	gcg	2112
Arg	Leu	Tyr	Glu	Arg	Leu	Phe	Leu	His	Lys	Asn	Pro	Glu	Asp	Pro	Ala	
		690						695					700			
gaa	gtt	cct	gct	gga	ttc	ctg	agt	gac	att	aac	cca	aat	tcc	tta	aca	2160
Glu	Val	Pro	Ala	Gly	Phe	Leu	Ser	Asp	Ile	Asn	Pro	Asn	Ser	Leu	Thr	
															720	
705																
gtt	atc	gaa	agt	gcc	tta	gtg	gac	cgc	tct	gtg	ggc	aaa	gcc	aaa	gtg	2208
Val	Ile	Glu	Ser	Ala	Leu	Val	Asp	Arg	Ser	Val	Gly	Lys	Ala	Lys	Val	
ttt	gac	aag	ttc	cag	ttt	gag	aga	gtg	ggc	tac	ttt	tca	gtg	gat	gct	2256
Phe	Asp	Lys	Phe	Gln	Phe	Glu	Arg	Val	Gly	Tyr	Phe	Ser	Val	Asp	Ala	
gac	agc	aca	ccc	gaa	aag	ctg	gtg	ttc	aac	agg	act	gtt	aca	ctc	aag	2304
Asp	Ser	Thr	Pro	Glu	Lys	Leu	Val	Phe	Asn	Arg	Thr	Val	Thr	Leu	Lys	
gag	gat	cca	gga	aag	ata	tga										2325
Glu	Asp	Pro	Gly	Lys	Ile											

<210> 9964

<211> 774

<212> PRT

<213> Brachydanio rerio

<400> 9964

Met	Ala	Asp	Val	Val	Ser	Ser	Phe	Met	Ser	Ile	Gly	Leu	Ser	Glu	Gln
1				5					10					15	
Lys	Ala	Lys	Glu	Thr	Leu	Lys	Asn	Glu	Thr	Leu	Ser	Ser	Thr	Leu	Lys
			20					25					30		
Lys	Ala	Ile	Asp	Leu	Ala	Gln	Val	Gln	Leu	Gly	Ser	Ser	Ala	Ile	Asp
		35					40					45			
Lys	Ile	Thr	Gly	Thr	Leu	Leu	Tyr	Ser	Met	Val	Thr	Arg	Leu	Lys	Asp
		50				55					60				
Thr	Asn	Arg	Pro	Gln	Phe	Leu	Thr	Lys	Tyr	Ile	Ile	Ser	Arg	Lys	Ile
65					70					75					80
Thr	Thr	Glu	Leu	Gln	Leu	Ser	Ala	Ala	Leu	Asp	Phe	Val	Lys	Ser	His
				85					90					95	
Pro	Gln	Gly	Asp	Val	Asp	Gln	His	Lys	Phe	Glu	Val	Ala	Cys	Gly	Val
			100					105					110		
Gly	Met	Val	Val	Thr	Pro	Glu	Gln	Ile	Glu	Asp	Ala	Val	Glu	Leu	Ile
		115					120					125			
Ile	Arg	Lys	His	Lys	Asp	Gln	Leu	Leu	Ala	Glu	Arg	Tyr	Arg	Phe	Asn
	130					135					140				
Met	Gly	Ile	Leu	Met	Gly	Glu	Ala	Arg	Ala	Thr	Leu	Lys	Trp	Ala	Asp
145					150				155						160
Gly	Lys	Ile	Val	Lys	Asn	Glu	Val	Asp	Met	Gln	Val	Leu	His	Leu	Leu
				165					170					175	
Gly	Pro	Lys	Thr	Glu	Ala	Asp	Leu	Glu	Lys	Lys	Ser	Lys	Ala	Val	Lys
			180					185					190		
Pro	Lys	Ala	Pro	Glu	Lys	Asp	Val	Lys	Ile	Glu	Gln	Ala	Ser	Ala	Val
		195					200					205			
Asn	Gly	Asp	Gly	Asn	Ile	Glu	Asn	Lys	Ser	Leu	Met	Glu	Gln	Leu	Arg
	210					215					220				
Gly	Glu	Ala	Leu	Lys	Phe	His	Lys	Pro	Gly	Glu	Asn	Tyr	Lys	Thr	Glu
225					230					235					240
Gly	Tyr	Val	Val	Thr	Pro	Asn	Thr	Met	Asn	Leu	Leu	Lys	Lys	His	Leu
				245					250					255	
Glu	Glu	Thr	Gly	Gln	Val	Arg	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Pro	Asn
			260				265					270			
Gly	Ile	Leu	His	Ile	Gly	His	Ala	Lys	Ala	Ile	Asn	Phe	Asn	Phe	Gly
		275					280					285			
Phe	Ala	Lys	Ala	Asn	Asn	Gly	Ile	Cys	Phe	Leu	Arg	Tyr	Asp	Asp	Thr
						295					300				

PF59083SeqList PF59083.txt

```

Asn Pro Glu Lys Glu Glu Glu Lys Tyr Phe Thr Ala Ile Lys Asp Met
305 310 315 320
Val Glu Trp Leu Gly Tyr Glu Pro Tyr Ala Val Thr His Ala Ser Asp
325 330 335
Asn Phe Gln Arg Leu Tyr Asn Leu Ala Val Asp Leu Ile Arg Arg Gly
340 345 350
His Ala Tyr Val Cys His Gln Arg Gly Glu Glu Leu Lys Gly His Asn
355 360 365
Val Pro Ser Ser Pro Trp Arg Glu Arg Pro Val Glu Glu Ser Leu Val
370 375 380
Leu Phe Glu His Met Arg Lys Gly Met Phe Ala Glu Gly Glu Ala Thr
385 390 395 400
Leu Arg Met Lys Met Val Met Glu Asp Gly Lys Met Asp Pro Val Ala
405 410 415
Tyr Arg Ile Lys Tyr Thr Pro His His Arg Thr Gly Asp Thr Trp Cys
420 425 430
Ile Tyr Pro Thr Tyr Asp Tyr Thr His Cys Leu Cys Asp Ser Ile Glu
435 440 445
Asn Ile Thr His Ser Leu Cys Thr Lys Glu Phe Gln Ala Arg Arg Ser
450 455 460
Ser Tyr Phe Trp Leu Cys Asn Ala Leu Asp Val Tyr Cys Pro Val Gln
465 470 475 480
Trp Glu Tyr Gly Arg Leu Asn Leu Thr Tyr Thr Val Val Ser Lys Arg
485 490 495
Lys Ile Ile Lys Leu Val Glu Thr Gly Val Val Arg Asp Trp Asp Asp
500 505 510
Pro Arg Leu Phe Thr Leu Thr Ala Leu Arg Arg Arg Gly Phe Pro Pro
515 520 525
Gln Ala Ile Asn Asn Phe Cys Ala Arg Val Gly Val Thr Val Ala Gln
530 535 540
Thr Thr Met Glu Pro His Leu Leu Glu Ala Cys Val Arg Glu Val Leu
545 550 555 560
Asn Asp Thr Ala Pro Arg Ala Met Ala Ile Leu Glu Pro Leu Lys Val
565 570 575
Thr Ile Ile Asn Leu Pro Thr Asn Ala Gln Lys Glu Leu Arg Val Pro
580 585 590
Asp Phe Pro Ala Asn Glu Ala Arg Gly Ser His Val Val Pro Phe Ser
595 600 605
Lys Thr Ile Phe Ile Glu Gln Ser Asp Phe Arg Glu Val Met Glu Lys
610 615 620
Gly Tyr Lys Arg Leu Thr Pro Asp Gln Ser Val Gly Leu Arg Tyr Ala
625 630 635 640
Gly Tyr Val Ile Ser Val Gln Arg Val Ile Lys Asp Asp Arg Gly Lys
645 650 655
Val Cys Glu Leu Glu Val Thr Cys Val Ser Ser Asp Thr Ala Glu Lys
660 665 670
Pro Lys Ala Phe Ile His Trp Val Ser Glu Pro Leu Leu Cys Glu Val
675 680 685
Arg Leu Tyr Glu Arg Leu Phe Leu His Lys Asn Pro Glu Asp Pro Ala
690 695 700
Glu Val Pro Ala Gly Phe Leu Ser Asp Ile Asn Pro Asn Ser Leu Thr
705 710 715 720
Val Ile Glu Ser Ala Leu Val Asp Arg Ser Val Gly Lys Ala Lys Val
725 730 735
Phe Asp Lys Phe Gln Phe Glu Arg Val Gly Tyr Phe Ser Val Asp Ala
740 745 750
Asp Ser Thr Pro Glu Lys Leu Val Phe Asn Arg Thr Val Thr Leu Lys
755 760 765
Glu Asp Pro Gly Lys Ile
770

```

<210> 9965

<211> 2319

<212> DNA

<213> Xenopus laevis

<220>

<221> CDS

<222> (1)..(2319)

PF59083SeqList PF59083.txt

```

<400> 9965
atg gct gct gag tcg ctg tcc ctc ttc aca gcc atc ggt ctt agt gag      48
Met Ala Ala Glu Ser 5 Leu Ser Leu Phe Thr 10 Ala Ile Gly Leu Ser 15 Glu
1
cag aag gct cgg gaa acc tta aag aat gag gcg ctt agc ttg ttg ctt      96
Gln Lys Ala Arg Glu Thr Leu Lys Asn Glu Ala Leu Ser Leu Leu Leu
20
cgg gac gcg att gta cag gcc cag aaa aca ttg ggt cca tct gtc gac      144
Arg Asp Ala Ile Val Gln Ala Gln Lys Thr Leu Gly Pro Ser Val Asp
35
aag gtg acc gga act ctc ctg tac aat gtg gca act cgc ctt aaa gat      192
Lys Val Thr Gly Thr Leu Leu Tyr Asn Val Ala Thr Arg Leu Lys Asp
50
acg aag cgg ttg ggc ttt ctg gtt gaa tac ata gcc agc aag aag att      240
Thr Lys Arg Leu Gly Phe 70 Leu Val Glu Tyr Ile Ala Ser Lys Lys Ile
65
acc aca gac ctg cag tta aat gct gcc ctg gac tat gtc aaa gct cat      288
Thr Thr Asp Leu Gln Leu Asn Ala Ala Leu Asp Tyr Val Lys Ala His
85
cca ctg gat cct att gac acc ggt cat ttt gag aaa gat tgt ggc gtg      336
Pro Leu Asp Pro Ile Asp Thr Gly His Phe Glu Lys Asp Cys Gly Val
100
ggg gtg act gtt acc cca gaa cag ata gaa gaa gct gtg gaa gct gtg      384
Gly Val Thr Val Thr Pro Glu Gln Ile Glu Glu Ala Val Glu Ala Val
115
att cag aaa ttc aga gca cag ttg ttg gcc gaa cgc tat cgc ttt aac      432
Ile Gln Lys Phe Arg Ala Gln Leu Leu Ala Glu Arg Tyr Arg Phe Asn
130
atg ggc ttg tta atg ggg gaa gcc agg aac cag ctg aag tgg gca gat      480
Met Gly Leu Leu Met Gly Glu Ala Arg Asn Gln Leu Lys Trp Ala Asp
145
ggg aag att atc aag aat gag gta gat atg cag gtt ttg cac tta ctt      528
Gly Lys Ile Ile Lys Asn Glu Val Asp Met Gln Val Leu His Leu Leu
165
ggc cca aag act gaa gct gat cta gaa aag aaa cca aag gtg aca aag      576
Gly Pro Lys Thr Glu Ala Asp Leu Glu Lys Lys Pro Lys Val Thr Lys
180
cca aaa gct aca gaa cca gag aag aaa gga gat gcc act gtg aat ggt      624
Pro Lys Ala Thr Glu Pro Glu Lys Lys Gly Asp Ala Thr Val Asn Gly
195
gac gtg aaa ctg gag tcc gta tct ctg atg gag cag ctt agg gga gag      672
Asp Val Lys Leu Glu Ser Val Ser Leu Met Glu Gln Leu Arg Gly Glu
210
gcc ctt aaa ttc cac aaa ccc ggt gag aat tac aag act gag ggg tac      720
Ala Leu Lys Phe His Lys Pro Gly Glu Asn Tyr Lys Thr Glu Gly Tyr
225
gtg gtt aca ccg aaa acc atg gag ctg ctg aag aaa cat ctt gaa atc      768
Val Val Thr Pro Lys Thr Met Glu Leu Leu Lys Lys His Leu Glu Ile
245
aca gga gga cag atc aga act cgg ttc cct cca gag cca aat ggc att      816
Thr Gly Gly Gln Ile Arg Thr Arg Phe Pro Pro Glu Pro Asn Gly Ile
260
ttg cac att ggt cac gcc aag gcc atc aac ttt aac ttt gga tat gca      864
Leu His Ile Gly His Ala Lys Ala Ile Asn Phe Asn Phe Gly Tyr Ala
275
aag gca aat gga ggc atc tgc ttt ctg cgc tat gat gac acc aac cca      912
Lys Ala Asn Gly Gly Ile Cys Phe Leu Arg Tyr Asp Asp Thr Asn Pro
290
gag aag gag gaa gaa aag ttt act gcc att aag gat atg gta gaa      960
Glu Lys Glu Glu Glu Lys Tyr Phe Thr Ala Ile Lys Asp Met Val Glu
305
tggt ctt ggt tac aag ccc tat gct gtg act cac gcc tcc gac aac ttt      1008
Trp Leu Gly Tyr Lys Pro Tyr Ala Val Thr His Ala Ser Asp Asn Phe
325
aac cag ctg tat gag tgg gcg gtg gaa ctc att aga aga ggt caa gct      1056
Asn Gln Leu Tyr Glu Trp Ala Val Glu Leu Ile Arg Arg Gly Gln Ala
340
tat gtt tgc cat cag aaa gtt gaa gaa att aaa ggt cac aac cca cca      1104

```

PF59083SeqList PF59083.txt																
Tyr	Val	Cys	His	Gln	Lys	Val	Glu	Glu	Ile	Lys	Gly	His	Asn	Pro	Pro	
cct	tcc	cca	tgg	aga	gat	cgt	cca	ggt	gaa	gaa	tcc	ctt	ctg	ctc	ttt	1152
Pro	Ser	Pro	Trp	Arg	Asp	Arg	Pro	Val	Glu	Glu	Ser	Leu	Leu	Leu	Phe	
gaa	ggt	atg	aaa	aag	gga	gaa	ttt	gca	gag	gga	gaa	gcg	aca	ctg	cga	1200
Glu	Gly	Met	Lys	Lys	Gly	Lys	Phe	Ala	Glu	Gly	Glu	Ala	Thr	Leu	Arg	
385					390					395					400	
atg	aag	ctt	ata	atg	gaa	gat	ggg	aaa	atg	gat	cct	gtg	gca	tat	cgg	1248
Met	Lys	Leu	Ile	Met	Glu	Asp	Gly	Lys	Met	Asp	Pro	Val	Ala	Tyr	Arg	
				405					410					415		
atc	aag	tac	aca	cca	cat	cac	cga	act	ggg	gac	aaa	tgg	tgt	ata	tat	1296
Ile	Lys	Tyr	Thr	Pro	His	His	Arg	Thr	Gly	Asp	Lys	Trp	Cys	Ile	Tyr	
			420					425					430			
cca	acc	tat	gac	tac	act	cac	tgt	ctc	tgc	gat	tct	att	gaa	cat	ata	1344
Pro	Thr	Tyr	Asp	Tyr	Thr	His	Cys	Leu	Cys	Asp	Ser	Ile	Glu	His	Ile	
			435				440					445				
act	cac	tct	ctg	tgt	acc	aag	gag	ttt	cag	gct	agg	cga	tcg	tca	tat	1392
Thr	His	Ser	Leu	Cys	Thr	Lys	Glu	Phe	Gln	Ala	Arg	Arg	Ser	Ser	Tyr	
						455					460					
ttc	tgg	cta	tgt	aac	acc	tta	gat	gtc	tac	tgc	cct	gtg	cag	tgg	gaa	1440
Phe	Trp	Leu	Cys	Asn	Thr	Leu	Asp	Val	Tyr	Cys	Pro	Val	Gln	Trp	Glu	
465					470					475					480	
tat	gga	cga	tta	aac	ctg	cac	tac	act	gtc	gta	tca	aag	cgg	aaa	atc	1488
Tyr	Gly	Arg	Leu	Asn	Leu	His	Tyr	Thr	Val	Val	Ser	Lys	Arg	Lys	Ile	
				485					490					495		
atc	aaa	ctg	gtc	gaa	act	gga	gct	gtc	agg	gac	tgg	gat	gac	cct	cgt	1536
Ile	Lys	Leu	Val	Glu	Thr	Gly	Ala	Val	Arg	Asp	Trp	Asp	Asp	Pro	Arg	
			500					505					510			
ctc	ttc	acg	ctg	aca	gct	tta	cgc	aga	gga	ttc	cca	cca	gaa	gcc		1584
Leu	Phe	Thr	Leu	Thr	Ala	Leu	Arg	Arg	Gly	Phe	Pro	Pro	Glu	Ala		
			515				520				525					
att	aat	aac	ttc	tgt	gca	agg	ggt	ggg	gtg	act	ggt	gct	cag	act	aca	1632
Ile	Asn	Asn	Phe	Cys	Ala	Arg	Val	Gly	Val	Thr	Val	Ala	Gln	Thr	Thr	
						535					540					
atg	gag	cca	cac	ttg	ctg	gag	tcg	tgc	gtc	aga	gat	gta	ctc	aat	gag	1680
Met	Glu	Pro	His	Leu	Leu	Glu	Ser	Cys	Val	Arg	Asp	Val	Leu	Asn	Glu	
545					550					555					560	
aca	gcc	cca	aga	ata	atg	gca	gtg	ctg	gaa	ccc	ctg	aaa	gta	acc	ata	1728
Thr	Ala	Pro	Arg	Ile	Met	Ala	Val	Leu	Glu	Pro	Leu	Lys	Val	Thr	Ile	
				565					570					575		
aca	aat	ctc	cct	gct	gag	aaa	gcc	atc	gat	gtc	tct	ggt	cca	aat	ttc	1776
Thr	Asn	Leu	Pro	Ala	Glu	Lys	Ala	Ile	Asp	Val	Ser	Val	Pro	Asn	Phe	
			580					585					590			
cca	gcg	gat	gaa	tcc	aaa	ggc	ttt	cat	ggt	ggt	ccc	ttc	tcc	tcc	acc	1824
Pro	Ala	Asp	Glu	Ser	Lys	Gly	Phe	His	Val	Val	Pro	Phe	Ser	Ser	Thr	
			595				600					605				
att	tac	att	gag	cag	tcg	gat	ttc	aga	gag	gta	atg	gag	aag	gga	tat	1872
Ile	Tyr	Ile	Glu	Gln	Ser	Asp	Phe	Arg	Glu	Val	Met	Glu	Lys	Gly	Tyr	
						615					620					
aag	cgc	cta	acc	cca	gat	cag	ccg	gta	ggc	ctc	aga	cac	gct	ggc	tat	1920
Lys	Arg	Leu	Thr	Pro	Asp	Gln	Pro	Val	Gly	Leu	Arg	His	Ala	Gly	Tyr	
625					630					635					640	
ggt	atc	tcc	ttg	caa	aat	att	gtg	aag	gat	caa	agc	ggc	aac	gtg	att	1968
Val	Ile	Ser	Leu	Gln	Asn	Ile	Val	Lys	Asp	Gln	Ser	Gly	Asn	Val	Ile	
				645					650					655		
gaa	ctg	gaa	ggt	acg	tgc	aca	aag	aca	gac	gtc	gct	gaa	aag	cca	aaa	2016
Glu	Leu	Glu	Val	Thr	Cys	Thr	Lys	Thr	Asp	Val	Ala	Glu	Lys	Pro	Lys	
			660					665					670			
gca	ttc	atc	cac	tgg	gtg	tct	gat	cct	ctg	acg	tgt	gaa	gtg	cgt	ctg	2064
Ala	Phe	Ile	His	Trp	Val	Ser	Asp	Pro	Leu	Thr	Cys	Glu	Val	Arg	Leu	
			675				680					685				
tac	gac	agg	ctg	ttc	ctc	cac	aaa	acc	cca	gaa	gat	cca	tct	gaa	ggt	2112
Tyr	Asp	Arg	Leu	Phe	Leu	His	Lys	Thr	Pro	Glu	Asp	Pro	Ser	Glu	Val	
						695					700					
cct	ggt	ggt	ttc	tta	act	gat	ctg	aat	acg	aac	tcc	ttg	acg	aca	atc	2160
Pro	Gly	Gly	Phe	Leu	Thr	Asp	Leu	Asn	Thr	Asn	Ser	Leu	Thr	Thr	Ile	
705					710					715					720	
ccc	agt	gct	tta	gtg	gaa	cgg	tct	gtg	aag	aat	gcc	aaa	gcc	ctg	gac	2208

PF59083SeqList PF59083.txt

Pro	Ser	Ala	Leu	Val	Glu	Arg	Ser	Val	Lys	Asn	Ala	Lys	Ala	Leu	Asp	
				725					730					735		
aag	ttc	cag	ttt	gag	aga	ctt	ggt	tat	ttt	tca	gtg	gat	cca	gac	act	2256
Lys	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Phe	Ser	Val	Asp	Pro	Asp	Thr	
			740					745					750			
act	ccg	gaa	aag	att	gtc	ttc	aac	agg	act	ggt	acc	ctg	aag	gaa	gat	2304
Thr	Pro	Glu	Lys	Ile	Val	Phe	Asn	Arg	Thr	Val	Thr	Leu	Lys	Glu	Asp	
		755					760					765				
cca	gga	aag	atg	tga												2319
Pro	Gly	Lys	Met													
	770															

<210> 9966

<211> 772

<212> PRT

<213> Xenopus laevis

<400> 9966

Met	Ala	Ala	Glu	Ser	Leu	Ser	Leu	Phe	Thr	Ala	Ile	Gly	Leu	Ser	Glu	
1				5					10					15		
Gln	Lys	Ala	Arg	Glu	Thr	Leu	Lys	Asn	Glu	Ala	Leu	Ser	Leu	Leu	Leu	
			20					25					30			
Arg	Asp	Ala	Ile	Val	Gln	Ala	Gln	Lys	Thr	Leu	Gly	Pro	Ser	Val	Asp	
		35					40					45				
Lys	Val	Thr	Gly	Thr	Leu	Leu	Tyr	Asn	Val	Ala	Thr	Arg	Leu	Lys	Asp	
	50					55					60					
Thr	Lys	Arg	Leu	Gly	Phe	Leu	Val	Glu	Tyr	Ile	Ala	Ser	Lys	Lys	Ile	
65				70					75						80	
Thr	Thr	Asp	Leu	Gln	Leu	Asn	Ala	Ala	Leu	Asp	Tyr	Val	Lys	Ala	His	
			85					90						95		
Pro	Leu	Asp	Pro	Ile	Asp	Thr	Gly	His	Phe	Glu	Lys	Asp	Cys	Gly	Val	
			100					105					110			
Gly	Val	Thr	Val	Thr	Pro	Glu	Gln	Ile	Glu	Glu	Ala	Val	Glu	Ala	Val	
		115					120					125				
Ile	Gln	Lys	Phe	Arg	Ala	Gln	Leu	Leu	Ala	Glu	Arg	Tyr	Arg	Phe	Asn	
	130					135					140					
Met	Gly	Leu	Leu	Met	Gly	Glu	Ala	Arg	Asn	Gln	Leu	Lys	Trp	Ala	Asp	
145				150					155						160	
Gly	Lys	Ile	Ile	Lys	Asn	Glu	Val	Asp	Met	Gln	Val	Leu	His	Leu	Leu	
			165					170						175		
Gly	Pro	Lys	Thr	Glu	Ala	Asp	Leu	Glu	Lys	Lys	Pro	Lys	Val	Thr	Lys	
			180					185					190			
Pro	Lys	Ala	Thr	Glu	Pro	Glu	Lys	Lys	Gly	Asp	Ala	Thr	Val	Asn	Gly	
		195					200					205				
Asp	Val	Lys	Leu	Glu	Ser	Val	Ser	Leu	Met	Glu	Gln	Leu	Arg	Gly	Glu	
	210					215					220					
Ala	Leu	Lys	Phe	His	Lys	Pro	Gly	Glu	Asn	Tyr	Lys	Thr	Glu	Gly	Tyr	
225					230				235						240	
Val	Val	Thr	Pro	Lys	Thr	Met	Glu	Leu	Leu	Lys	Lys	His	Leu	Glu	Ile	
			245					250						255		
Thr	Gly	Gly	Gln	Ile	Arg	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Ile	
			260					265					270			
Leu	His	Ile	Gly	His	Ala	Lys	Ala	Ile	Asn	Phe	Asn	Phe	Gly	Tyr	Ala	
		275					280					285				
Lys	Ala	Asn	Gly	Gly	Ile	Cys	Phe	Leu	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	
	290					295					300					
Glu	Lys	Glu	Glu	Glu	Lys	Tyr	Phe	Thr	Ala	Ile	Lys	Asp	Met	Val	Glu	
					310					315					320	
Trp	Leu	Gly	Tyr	Lys	Pro	Tyr	Ala	Val	Thr	His	Ala	Ser	Asp	Asn	Phe	
			325					330						335		
Asn	Gln	Leu	Tyr	Glu	Trp	Ala	Val	Glu	Leu	Ile	Arg	Arg	Gly	Gln	Ala	
			340					345					350			
Tyr	Val	Cys	His	Gln	Lys	Val	Glu	Glu	Ile	Lys	Gly	His	Asn	Pro	Pro	
		355					360					365				
Pro	Ser	Pro	Trp	Arg	Asp	Arg	Pro	Val	Glu	Glu	Ser	Leu	Leu	Leu	Phe	
	370					375					380					
Glu	Gly	Met	Lys	Lys	Gly	Lys	Phe	Ala	Glu	Gly	Glu	Ala	Thr	Leu	Arg	
					390					395					400	
Met	Lys	Leu	Ile	Met	Glu	Asp	Gly	Lys	Met	Asp	Pro	Val	Ala	Tyr	Arg	

PF59083SeqList PF59083.txt

405 410 415
 Ile Lys Tyr Thr Pro His His Arg Thr Gly Asp Lys Trp Cys Ile Tyr
 420 425 430
 Pro Thr Tyr Asp Tyr Thr His Cys Leu Cys Asp Ser Ile Glu His Ile
 435 440 445
 Thr His Ser Leu Cys Thr Lys Glu Phe Gln Ala Arg Arg Ser Ser Tyr
 450 455 460
 Phe Trp Leu Cys Asn Thr Leu Asp Val Tyr Cys Pro Val Gln Trp Glu
 465 470 475 480
 Tyr Gly Arg Leu Asn Leu His Tyr Thr Val Val Ser Lys Arg Lys Ile
 485 490 495
 Ile Lys Leu Val Glu Thr Gly Ala Val Arg Asp Trp Asp Asp Pro Arg
 500 505 510
 Leu Phe Thr Leu Thr Ala Leu Arg Arg Arg Gly Phe Pro Pro Glu Ala
 515 520 525
 Ile Asn Asn Phe Cys Ala Arg Val Gly Val Thr Val Ala Gln Thr Thr
 530 535 540
 Met Glu Pro His Leu Leu Glu Ser Cys Val Arg Asp Val Leu Asn Glu
 545 550 555 560
 Thr Ala Pro Arg Ile Met Ala Val Leu Glu Pro Leu Lys Val Thr Ile
 565 570 575
 Thr Asn Leu Pro Ala Glu Lys Ala Ile Asp Val Ser Val Pro Asn Phe
 580 585 590
 Pro Ala Asp Glu Ser Lys Gly Phe His Val Val Pro Phe Ser Ser Thr
 595 600 605
 Ile Tyr Ile Glu Gln Ser Asp Phe Arg Glu Val Met Glu Lys Gly Tyr
 610 615 620
 Lys Arg Leu Thr Pro Asp Gln Pro Val Gly Leu Arg His Ala Gly Tyr
 625 630 635 640
 Val Ile Ser Leu Gln Asn Ile Val Lys Asp Gln Ser Gly Asn Val Ile
 645 650 655
 Glu Leu Glu Val Thr Cys Thr Lys Thr Asp Val Ala Glu Lys Pro Lys
 660 665 670
 Ala Phe Ile His Trp Val Ser Asp Pro Leu Thr Cys Glu Val Arg Leu
 675 680 685
 Tyr Asp Arg Leu Phe Leu His Lys Thr Pro Glu Asp Pro Ser Glu Val
 690 695 700
 Pro Gly Gly Phe Leu Thr Asp Leu Asn Thr Asn Ser Leu Thr Thr Ile
 705 710 715 720
 Pro Ser Ala Leu Val Glu Arg Ser Val Lys Asn Ala Lys Ala Leu Asp
 725 730 735
 Lys Phe Gln Phe Glu Arg Leu Gly Tyr Phe Ser Val Asp Pro Asp Thr
 740 745 750
 Thr Pro Glu Lys Ile Val Phe Asn Arg Thr Val Thr Leu Lys Glu Asp
 755 760 765
 Pro Gly Lys Met
 770

<210> 9967

<211> 2361

<212> DNA

<213> Caenorhabditis elegans

<220>

<221> CDS

<222> (1)..(2361)

<400> 9967

atg gca aca aag gag gag ctt ctc tct ttg ggc ctc tct gat tca aaa	48
Met Ala Thr Lys Glu Glu Leu Leu Ser Leu Gly Leu Ser Asp Ser Lys	
1 5 10 15	
gta gct gaa acg ctg aaa aat gtg aag ctc acc gaa acg atc ggt tca	96
Val Ala Glu Thr Leu Lys Asn Val Lys Leu Thr Glu Thr Ile Gly Ser	
20 25 30	
att gtg aag ctt gcg agc gag tct ggc gag att tcc aag caa aaa gga	144
Ile Val Lys Leu Ala Ser Glu Ser Gly Glu Ile Ser Lys Gln Lys Gly	
35 40 45	
aca ctt ttg tac cag ttg gcg aca aag ttg aag cca caa gtc gct gct	192
Thr Leu Leu Tyr Gln Leu Ala Thr Lys Leu Lys Pro Gln Val Ala Ala	

PF59083SeqList PF59083.txt

50	55	60	
cac act cca cta gtt gtc aag tat att atg aat gac ggg att aag aca			240
His Thr Pro Leu Val Val Lys Tyr Ile Met Asn Asp Gly Ile Lys Thr			
65	70	75	80
gag cca cag ctc tcc gca gcg atc gag tat ctt ctc tcg cac acc gtt			288
Glu Pro Gln Leu Ser Ala Ala Ile Glu Tyr Leu Leu Ser His Thr Val			
85	90	95	
aaa ggt atc caa gtg cct gat ttc gag aaa tca tgc gga gtc ggc gtt			336
Lys Gly Ile Gln Val Pro Asp Phe Glu Lys Ser Cys Gly Val Gly Val			
100	105	110	
gtt gtc aca atc gac gac atc gaa gcg gcc gtt acc aag gtg att ggc			384
Val Val Thr Ile Asp Asp Ile Glu Ala Ala Val Thr Lys Val Ile Gly			
115	120	125	
caa cac cgc gag aaa atc gtc gcc gag cgg tac tcg ttc ccg gcc gga			432
Gln His Arg Glu Lys Ile Val Ala Glu Arg Tyr Ser Phe Pro Ala Gly			
130	135	140	
aag ttg ctc ggc gag cta cga gct ctg ctt cca tgg gct gat ggt gcg			480
Lys Leu Leu Gly Glu Leu Arg Ala Leu Leu Pro Trp Ala Asp Gly Ala			
145	150	155	160
att acg aag aag gag gtg gat ttg aga ttc ttg gag ctg ctc gga ccg			528
Ile Thr Lys Lys Glu Val Asp Leu Arg Phe Leu Glu Leu Leu Gly Pro			
165	170	175	
aag act gcg gag gat ttg gct ccg aag aag aag gag aag aag ccg gaa			576
Lys Thr Ala Glu Asp Leu Ala Pro Lys Lys Lys Glu Lys Lys Pro Glu			
180	185	190	
ggc ccg aaa cct tcc aaa gac gct gcc gct gcc gcc acc gct cca gga			624
Gly Pro Lys Pro Ser Lys Asp Ala Ala Ala Ala Ala Thr Ala Pro Gly			
195	200	205	
acc aaa aat caa aag gaa gct agc ccc gaa gaa ttc gct gat ggc gcc			672
Thr Lys Asn Gln Lys Glu Ala Ser Pro Glu Glu Phe Ala Asp Gly Ala			
210	215	220	
gaa acc atg gac gag ctg ctc cgc acc cgt gcg cat ttc cac aaa gtc			720
Glu Thr Met Asp Glu Leu Leu Arg Thr Arg Ala His Phe His Lys Val			
225	230	235	240
gga gaa aac ttc aag gac ggc tac gtg acc act cca aaa acc gca			768
Gly Glu Asn Phe Lys Gln Asp Gly Tyr Val Thr Thr Pro Lys Thr Ala			
245	250	255	
gag ctt ctc aag gct cac gtg gcg gct gtc gga ggg aag gtg gtg acc			816
Glu Leu Leu Lys Ala His Val Ala Ala Val Gly Gly Lys Val Val Thr			
260	265	270	
cga ttc ccg cct gaa cca aat ggt gtt ctt cat att gga cac gcg aag			864
Arg Phe Pro Pro Glu Pro Asn Gly Val Leu His Ile Gly His Ala Lys			
275	280	285	
gcg att aac atc aat ttt gga tat gct aaa gct atg ggt ggt gtg tgt			912
Ala Ile Asn Ile Asn Phe Gly Tyr Ala Lys Ala Met Gly Gly Val Cys			
290	295	300	
aat ttg aga ttt gac gat aca aat ccg gaa aag gaa gag gaa aag ttc			960
Asn Leu Arg Phe Asp Thr Asn Pro Glu Lys Glu Glu Glu Lys Phe			
305	310	315	320
ttc tct gca att gag gat att gtt cat tgg ctt gga tat gat ccg gct			1008
Phe Ser Ala Ile Glu Asp Ile Val His Trp Leu Gly Tyr Asp Pro Ala			
325	330	335	
aga gtt act cac tct tcg gat aat ttt cag cag ctt tat ctt tgg gct			1056
Arg Val Thr His Ser Ser Asp Asn Phe Gln Gln Leu Tyr Trp Ala			
340	345	350	
gtt aag ctt att cag aaa gga ctc gct ttc gta tgc cat caa aaa gtc			1104
Val Lys Leu Ile Gln Lys Gly Leu Ala Phe Val Cys His Gln Lys Val			
355	360	365	
gaa gaa atg cgc ggt ttc gaa gtt caa ctg agc ccg tgg cgt gag cga			1152
Glu Glu Met Arg Gly Phe Glu Val Gln Leu Ser Pro Trp Arg Glu Arg			
370	375	380	
cca atc gaa gag aac atc caa ctc ttc gaa gac atg aaa aat gga aaa			1200
Pro Ile Glu Glu Asn Ile Gln Leu Phe Glu Asp Met Lys Asn Gly Lys			
385	390	395	400
ttc gac gaa gga gaa gcc aca ctc cgg ctc aag ttg aca ctg gaa gaa			1248
Phe Asp Glu Gly Glu Ala Thr Leu Arg Leu Lys Leu Thr Leu Glu Glu			
405	410	415	
gga aaa gtc gat cca gtc gcc tac cgt atc aaa tat gtt cca cat cat			1296
Gly Lys Val Asp Pro Val Ala Tyr Arg Ile Lys Tyr Val Pro His His			

PF59083SeqList PF59083.txt

			420				425				430						
cga	act	gga	aat	caa	tgg	tgc	atc	tac	ccg	acc	tac	gat	tat	acc	cat		1344
Arg	Thr	Gly	Asn	Gln	Trp	Cys	Ile	Tyr	Pro	Thr	Tyr	Asp	Tyr	Thr	His		
		435					440				445						
tgc	ctt	tgt	gat	tca	att	gaa	aat	atc	act	cat	tct	ctg	tgc	acc	aaa		1392
Cys	Leu	Cys	Asp	Ser	Ile	Glu	Asn	Ile	Thr	His	Ser	Leu	Cys	Thr	Lys		
		450				455					460						
gag	ttc	cag	tcg	aga	aga	agc	tca	tat	tac	tgg	ctc	tgt	aat	gct	cta		1440
Glu	Phe	Gln	Ser	Arg	Arg	Ser	Ser	Tyr	Tyr	Trp	Leu	Cys	Asn	Ala	Leu		
465					470					475					480		
gat	atc	tat	tgt	cct	gtt	caa	tgg	gag	tac	ggt	aga	cta	aat	gtc	aac		1488
Asp	Ile	Tyr	Cys	Pro	Val	Gln	Trp	Glu	Tyr	Gly	Arg	Leu	Asn	Val	Asn		
				485					490					495			
tat	act	gtg	gtc	tcg	aag	cga	aag	att	ctc	aaa	ctt	atc	acc	aca	aaa		1536
Tyr	Thr	Val	Val	Ser	Lys	Arg	Lys	Ile	Leu	Lys	Leu	Ile	Thr	Thr	Lys		
				500				505					510				
acc	gtc	aac	gat	tgg	gat	gat	cca	cgg	ttg	ttc	aca	ctg	aca	gca	ctc		1584
Thr	Val	Asn	Asp	Trp	Asp	Asp	Pro	Arg	Leu	Phe	Thr	Leu	Thr	Ala	Leu		
		515				520					525						
cga	cgg	cgt	ggt	atc	cca	tct	gag	gcg	att	aat	cga	ttc	ggt	gcg	aag		1632
Arg	Arg	Arg	Gly	Ile	Pro	Ser	Glu	Ala	Ile	Asn	Arg	Phe	Val	Ala	Lys		
		530				535					540						
ctc	gga	ttg	aca	atg	tca	cag	atg	gtt	att	gat	cca	cac	ggt	ctt	gac		1680
Leu	Gly	Leu	Thr	Met	Ser	Gln	Met	Val	Ile	Asp	Pro	His	Val	Leu	Asp		
		545			550					555					560		
gca	act	gtt	agg	gat	tat	ttg	aat	att	cac	gcg	cca	aga	aca	atg	gcc		1728
Ala	Thr	Val	Arg	Asp	Tyr	Leu	Asn	Ile	His	Ala	Pro	Arg	Thr	Met	Ala		
				565					570					575			
gtg	ctc	gag	gga	ttg	aag	ctg	aca	atc	gaa	aac	ttt	tcc	gaa	ctc	aat		1776
Val	Leu	Glu	Gly	Leu	Lys	Leu	Thr	Ile	Glu	Asn	Phe	Ser	Glu	Leu	Asn		
				580				585					590				
ctc	cca	tca	tcc	gtc	gac	gtt	cca	gac	ttc	cca	tct	gat	ccg	act	gat		1824
Leu	Pro	Ser	Ser	Val	Asp	Val	Pro	Asp	Phe	Pro	Ser	Asp	Pro	Thr	Asp		
		595				600					605						
cca	cga	aag	cac	tcg	gta	tcc	gtc	gat	cgg	gag	att	ttc	att	gaa	aag		1872
Pro	Arg	Lys	His	Ser	Val	Ser	Val	Asp	Arg	Glu	Ile	Phe	Ile	Glu	Lys		
		610				615					620						
tcc	gac	tat	aag	ccg	gat	gat	tcg	gac	aaa	tcc	ttc	aga	agg	ctg	acg		1920
Ser	Asp	Tyr	Lys	Pro	Asp	Asp	Ser	Asp	Lys	Ser	Phe	Arg	Arg	Leu	Thr		
		625			630					635					640		
ccg	aaa	caa	gcc	gtc	ggc	ctg	aaa	cac	att	gga	ttg	gtg	ctc	cga	ttc		1968
Pro	Lys	Gln	Ala	Val	Gly	Leu	Lys	His	Ile	Gly	Leu	Val	Leu	Arg	Phe		
				645					650					655			
gtg	aaa	gaa	gtc	aaa	gat	gcc	gag	ggt	cac	gtc	aca	gaa	gtt	gtg	gtg		2016
Val	Lys	Glu	Val	Lys	Asp	Ala	Glu	Gly	His	Val	Thr	Glu	Val	Val	Val		
				660				665					670				
aag	gct	gag	aag	ttg	tcg	gag	aag	gat	aag	ccg	aaa	gca	ttt	att	cat		2064
Lys	Ala	Glu	Lys	Leu	Ser	Glu	Lys	Asp	Lys	Pro	Lys	Ala	Phe	Ile	His		
		675				680					685						
tgg	gtt	gca	aag	cct	gtc	tcg	tgt	gaa	gtt	cgg	ctc	tat	gat	aga	cta		2112
Trp	Val	Ala	Lys	Pro	Val	Ser	Cys	Glu	Val	Arg	Leu	Tyr	Asp	Arg	Leu		
		690				695					700						
ttc	aag	agt	aag	aat	cca	gag	gat	gct	caa	cta	gtt	cca	ggt	gga	ttc		2160
Phe	Lys	Ser	Lys	Asn	Pro	Glu	Asp	Ala	Gln	Leu	Val	Pro	Gly	Gly	Phe		
		705			710					715					720		
ctg	tcg	gat	atc	aat	cca	gat	tca	ttg	aca	gtt	gtc	tac	aat	gct	cta		2208
Leu	Ser	Asp	Ile	Asn	Pro	Asp	Ser	Leu	Thr	Val	Val	Tyr	Asn	Ala	Leu		
				725					730					735			
att	gat	cag	tct	att	gca	aaa	tca	aag	gtt	tat	gat	aga	ttc	caa	ttc		2256
Ile	Asp	Gln	Ser	Ile	Ala	Lys	Ser	Lys	Val	Tyr	Asp	Arg	Phe	Gln	Phe		
				740				745					750				
gaa	cgc	atc	gga	ttc	ttc	tgt	gtc	gat	cgt	gat	tcg	acg	tct	tca	acg		2304
Glu	Arg	Ile	Gly	Phe	Phe	Cys	Val	Asp	Arg	Asp	Ser	Thr	Ser	Ser	Thr		
		755				760						765					
ttg	gtc	ttc	aac	cga	act	gtc	atg	ctg	aaa	gac	gga	gga	gct	tct	gga		2352
Leu	Val	Phe	Asn	Arg	Thr	Val	Met	Leu	Lys	Asp	Gly	Gly	Ala	Ser	Gly		
		770				775					780						
aag	aat	tga															2361
Lys	Asn																

785

<210> 9968

<211> 786

<212> PRT

<213> *Caenorhabditis elegans*

<400> 9968

```

Met Ala Thr Lys Glu Glu Leu Leu Ser Leu Gly Leu Ser Asp Ser Lys
1      5      10      15
Val Ala Glu Thr Leu Lys Asn Val Lys Leu Thr Glu Thr Ile Gly Ser
      20      25      30
Ile Val Lys Leu Ala Ser Glu Ser Gly Glu Ile Ser Lys Gln Lys Gly
      35      40      45
Thr Leu Leu Tyr Gln Leu Ala Thr Lys Leu Lys Pro Gln Val Ala Ala
      50      55      60
His Thr Pro Leu Val Val Lys Tyr Ile Met Asn Asp Gly Ile Lys Thr
65      70      75      80
Glu Pro Gln Leu Ser Ala Ala Ile Glu Tyr Leu Leu Ser His Thr Val
      85      90      95
Lys Gly Ile Gln Val Pro Asp Phe Glu Lys Ser Cys Gly Val Gly Val
      100      105      110
Val Val Thr Ile Asp Asp Ile Glu Ala Ala Val Thr Lys Val Ile Gly
      115      120      125
Gln His Arg Glu Lys Ile Val Ala Glu Arg Tyr Ser Phe Pro Ala Gly
      130      135      140
Lys Leu Leu Gly Glu Leu Arg Ala Leu Leu Pro Trp Ala Asp Gly Ala
145      150      155      160
Ile Thr Lys Lys Val Asp Leu Arg Phe Leu Glu Leu Leu Gly Pro
      165      170      175
Lys Thr Ala Glu Asp Leu Ala Pro Lys Lys Lys Glu Lys Lys Pro Glu
      180      185      190
Gly Pro Lys Pro Ser Lys Asp Ala Ala Ala Ala Thr Ala Pro Gly
      195      200      205
Thr Lys Asn Gln Lys Glu Ala Ser Pro Glu Glu Phe Ala Asp Gly Ala
210      215      220
Glu Thr Met Asp Glu Leu Leu Arg Thr Arg Ala His Phe His Lys Val
225      230      235      240
Gly Glu Asn Phe Lys Gln Asp Gly Tyr Val Thr Thr Pro Lys Thr Ala
      245      250      255
Glu Leu Leu Lys Ala His Val Ala Ala Val Gly Gly Lys Val Val Thr
      260      265      270
Arg Phe Pro Pro Glu Pro Asn Gly Val Leu His Ile Gly His Ala Lys
      275      280      285
Ala Ile Asn Ile Asn Phe Gly Tyr Ala Lys Ala Met Gly Gly Val Cys
290      295      300
Asn Leu Arg Phe Asp Asp Thr Asn Pro Glu Lys Glu Glu Glu Lys Phe
305      310      315      320
Phe Ser Ala Ile Glu Asp Ile Val His Trp Leu Gly Tyr Asp Pro Ala
      325      330      335
Arg Val Thr His Ser Ser Asp Asn Phe Gln Gln Leu Tyr Leu Trp Ala
      340      345      350
Val Lys Leu Ile Gln Lys Gly Leu Ala Phe Val Cys His Gln Lys Val
      355      360      365
Glu Glu Met Arg Gly Phe Glu Val Gln Leu Ser Pro Trp Arg Glu Arg
      370      375      380
Pro Ile Glu Glu Asn Ile Gln Leu Phe Glu Asp Met Lys Asn Gly Lys
385      390      395      400
Phe Asp Glu Gly Glu Ala Thr Leu Arg Leu Lys Leu Thr Leu Glu Glu
      405      410      415
Gly Lys Val Asp Pro Val Ala Tyr Arg Ile Lys Tyr Val Pro His His
      420      425      430
Arg Thr Gly Asn Gln Trp Cys Ile Tyr Pro Thr Tyr Asp Tyr Thr His
435      440      445
Cys Leu Cys Asp Ser Ile Glu Asn Ile Thr His Ser Leu Cys Thr Lys
450      455      460
Glu Phe Gln Ser Arg Arg Ser Ser Tyr Tyr Trp Leu Cys Asn Ala Leu
465      470      475      480
Asp Ile Tyr Cys Pro Val Gln Trp Glu Tyr Gly Arg Leu Asn Val Asn

```

PF59083SeqList PF59083.txt

485 490 495
 Tyr Thr Val Val Ser Lys Arg Lys Ile Leu Lys Leu Ile Thr Thr Lys
 500 505 510
 Thr Val Asn Asp Trp Asp Asp Pro Arg Leu Phe Thr Leu Thr Ala Leu
 515 520 525
 Arg Arg Arg Gly Ile Pro Ser Glu Ala Ile Asn Arg Phe Val Ala Lys
 530 535 540
 Leu Gly Leu Thr Met Ser Gln Met Val Ile Asp Pro His Val Leu Asp
 545 550 555 560
 Ala Thr Val Arg Asp Tyr Leu Asn Ile His Ala Pro Arg Thr Met Ala
 565 570 575
 Val Leu Glu Gly Leu Lys Leu Thr Ile Glu Asn Phe Ser Glu Leu Asn
 580 585 590
 Leu Pro Ser Ser Val Asp Val Pro Asp Phe Pro Ser Asp Pro Thr Asp
 595 600 605
 Pro Arg Lys His Ser Val Ser Val Asp Arg Glu Ile Phe Ile Glu Lys
 610 615 620
 Ser Asp Tyr Lys Pro Asp Asp Ser Asp Lys Ser Phe Arg Arg Leu Thr
 625 630 635 640
 Pro Lys Gln Ala Val Gly Leu Lys His Ile Gly Leu Val Leu Arg Phe
 645 650 655
 Val Lys Glu Val Lys Asp Ala Glu Gly His Val Thr Glu Val Val Val
 660 665 670
 Lys Ala Glu Lys Leu Ser Glu Lys Asp Lys Pro Lys Ala Phe Ile His
 675 680 685
 Trp Val Ala Lys Pro Val Ser Cys Glu Val Arg Leu Tyr Asp Arg Leu
 690 695 700
 Phe Lys Ser Lys Asn Pro Glu Asp Ala Gln Leu Val Pro Gly Gly Phe
 705 710 715 720
 Leu Ser Asp Ile Asn Pro Asp Ser Leu Thr Val Val Tyr Asn Ala Leu
 725 730 735
 Ile Asp Gln Ser Ile Ala Lys Ser Lys Val Tyr Asp Arg Phe Gln Phe
 740 745 750
 Glu Arg Ile Gly Phe Phe Cys Val Asp Arg Asp Ser Thr Ser Ser Thr
 755 760 765
 Leu Val Phe Asn Arg Thr Val Met Leu Lys Asp Gly Gly Ala Ser Gly
 770 775 780
 Lys Asn
 785

<210> 9969
 <211> 2385
 <212> DNA
 <213> Lupinus luteus

<220>
 <221> CDS
 <222> (1)..(2385)

<400> 9969
 atg ccg gcg aag gat gac acc tcc tcc gat aag gag aag tct ttg gaa 48
 Met Pro Ala Lys Asp Asp Thr Ser Ser Asp Lys Glu Lys Ser Leu Glu
 1 5 10 15
 ctg ttt ctc aag atc gga tta gac gag cgc act gcc aaa aac acc gtc 96
 Leu Phe Leu Lys Ile Gly Leu Asp Glu Arg Thr Ala Lys Asn Thr Val
 20 25 30
 gct aac aac aaa gtc acc acc aat ctc act tcc gtt atc aac gat gct 144
 Ala Asn Asn Lys Val Thr Thr Asn Leu Thr Ser Val Ile Asn Asp Ala
 35 40 45
 ggt gtt acc gat gga tgc agc cgc act gtt gga aac ctt ctt tac acg 192
 Gly Val Thr Asp Gly Cys Ser Arg Thr Val Gly Asn Leu Leu Tyr Thr
 50 55 60
 gtt gcg acg aag tac cct gca aat gcc ttg cca cat cgc cca aca ttg 240
 Val Ala Thr Lys Tyr Pro Ala Asn Ala Leu Pro His Arg Pro Thr Leu
 65 70 75 80
 ctg caa tat att gtt aat tca aag gtg aaa aca aca gca cag tta gac 288
 Leu Gln Tyr Ile Val Asn Ser Lys Val Lys Thr Thr Ala Gln Leu Asp
 85 90 95
 gcg gca cta tct ttt ctc agt gcc acg ggt tcg gag aat ctt gat ttg 336
 10536

PF59083SeqList PF59083.txt

Ala	Ala	Leu	Ser	Phe	Leu	Ser	Ala	Thr	Gly	Ser	Glu	Asn	Leu	Asp	Leu	
aac	aag	ttt	gaa	gaa	gct	tgt	ggt	ggt	ggt	gtc	gag	ggt	tca	aca	gaa	384
Asn	Lys	Phe	Glu	Glu	Ala	Cys	Gly	Val	Gly	Val	Glu	Val	Ser	Thr	Glu	
		115					120					125				
gat	atc	aaa	cat	gct	ggt	gat	gaa	ggt	ggt	gaa	gag	aat	aag	gct	aca	432
Asp	Ile	Lys	His	Ala	Val	Asp	Glu	Val	Val	Glu	Glu	Asn	Lys	Ala	Thr	
	130					135					140					
att	ttg	gag	cta	cgt	tat	cga	gtg	aac	gtg	ggt	gag	tta	ctt	ggg	cat	480
Ile	Leu	Glu	Leu	Arg	Tyr	Arg	Val	Asn	Val	Gly	Glu	Leu	Leu	Gly	His	
	145				150					155					160	
gtc	cgg	aag	agg	ctc	cca	tgg	gct	gat	gca	aaa	ggt	gtc	aag	caa	cta	528
Val	Arg	Lys	Arg	Leu	Pro	Trp	Ala	Asp	Ala	Lys	Val	Val	Lys	Gln	Leu	
			165						170					175		
ggt	gat	gca	aaa	tta	tat	gag	ata	ctt	ggt	gat	agg	aca	gca	gca	gat	576
Val	Asp	Ala	Lys	Leu	Tyr	Glu	Ile	Leu	Gly	Asp	Arg	Thr	Ala	Ala	Asp	
			180					185						190		
aat	gaa	aag	cct	aaa	aag	aag	aaa	gag	aaa	cct	gct	aaa	gta	gag	gac	624
Asn	Glu	Lys	Pro	Lys	Lys	Lys	Lys	Glu	Lys	Pro	Ala	Lys	Val	Glu	Asp	
		195				200						205				
aag	gca	gct	cct	ggt	gct	act	tcc	gaa	aag	cca	ctt	gaa	gaa	gat	ctg	672
Lys	Ala	Ala	Pro	Val	Ala	Thr	Ser	Glu	Lys	Pro	Leu	Glu	Glu	Asp	Leu	
	210					215					220					
aat	cca	tat	ttg	ata	ttc	cct	aac	ccg	gag	gac	aac	ttt	aag	gtg	cat	720
Asn	Pro	Tyr	Leu	Ile	Phe	Pro	Asn	Pro	Glu	Asp	Asn	Phe	Lys	Val	His	
	225				230					235				240		
act	gaa	gta	cct	ttt	agt	gat	ggt	aat	att	ctg	aga	tgt	tgc	aat	aca	768
Thr	Glu	Val	Pro	Phe	Ser	Asp	Gly	Asn	Ile	Leu	Arg	Cys	Cys	Asn	Thr	
			245					250						255		
aag	gca	ctc	ctt	gaa	aaa	cac	ctg	aaa	gca	aca	ggt	ggc	aaa	ggt	ttg	816
Lys	Ala	Leu	Leu	Glu	Lys	His	Leu	Lys	Ala	Thr	Gly	Gly	Lys	Val	Leu	
		260					265						270			
acc	cgc	ttt	cct	cct	gaa	cca	aat	gga	tat	ttg	cat	att	ggt	cat	gcc	864
Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ala	
		275					280					285				
aag	gca	atg	ttt	ggt	gat	ttt	ggg	ttg	gcg	aaa	gat	aga	aat	gga	ggg	912
Lys	Ala	Met	Phe	Val	Asp	Phe	Gly	Leu	Ala	Lys	Asp	Arg	Asn	Gly	Gly	
	290					295					300					
tgt	tat	ttg	agg	ttt	gat	gat	aca	aat	cct	gaa	gca	gaa	aag	aaa	gag	960
Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys	Lys	Glu	
	305				310					315					320	
tat	att	gat	cac	att	gaa	gaa	att	gtc	cag	tgg	atg	ggc	tgg	gaa	cca	1008
Tyr	Ile	Asp	His	Ile	Glu	Glu	Ile	Val	Gln	Trp	Met	Gly	Trp	Glu	Pro	
			325					330						335		
ttc	aag	att	act	tac	acc	agt	aat	tac	ttc	caa	gaa	ttg	tat	gaa	ttt	1056
Phe	Lys	Ile	Thr	Tyr	Thr	Ser	Asn	Tyr	Phe	Gln	Glu	Leu	Tyr	Glu	Phe	
		340					345						350			
gcc	gtg	gaa	ctt	ata	aga	agg	ggt	cat	gct	tat	ggt	gat	cat	cag	acg	1104
Ala	Val	Glu	Leu	Ile	Arg	Arg	Gly	His	Ala	Tyr	Val	Asp	His	Gln	Thr	
		355					360					365				
gca	gat	gag	ata	aag	gag	tat	agg	gag	aag	aaa	tta	aac	agt	cct	tgg	1152
Ala	Asp	Glu	Ile	Lys	Glu	Tyr	Arg	Glu	Lys	Lys	Leu	Asn	Ser	Pro	Trp	
	370					375					380					
agg	gat	cga	cca	att	tca	gaa	tca	ttg	aaa	ctc	ttt	gag	gat	atg	agg	1200
Arg	Asp	Arg	Pro	Ile	Ser	Glu	Ser	Leu	Lys	Leu	Phe	Glu	Asp	Met	Arg	
	385				390					395				400		
cgt	ggc	ttt	ata	gaa	gaa	gga	aaa	gcg	aca	ctt	aga	atg	aag	caa	gac	1248
Arg	Gly	Phe	Ile	Glu	Glu	Gly	Lys	Ala	Thr	Leu	Arg	Met	Lys	Gln	Asp	
			405					410						415		
atg	cag	agt	gat	aac	tac	aat	atg	tat	gac	ctt	att	gca	tac	cgt	att	1296
Met	Gln	Ser	Asp	Asn	Tyr	Asn	Met	Tyr	Asp	Leu	Ile	Ala	Tyr	Arg	Ile	
		420					425						430			
aag	ttt	act	cca	cac	cct	cat	gct	gga	gac	aaa	tgg	tgt	atc	tat	cca	1344
Lys	Phe	Thr	Pro	His	Pro	His	Ala	Gly	Asp	Lys	Trp	Cys	Ile	Tyr	Pro	
		435					440					445				
agc	tat	gac	tat	gct	cac	tgc	att	gta	gat	tct	att	gag	aat	gtc	acg	1392
Ser	Tyr	Asp	Tyr	Ala	His	Cys	Ile	Val	Asp	Ser	Ile	Glu	Asn	Val	Thr	
	450					455					460					
cat	tca	ctg	tgt	act	ctt	gag	ttt	gag	aca	cgt	gca	tcg	tac	tat		1440

PF59083SeqList PF59083.txt

His 465	Ser	Leu	Cys	Thr	Leu 470	Glu	Phe	Glu	Thr	Arg 475	Arg	Ala	Ser	Tyr	Tyr 480	
tgg	ttg	tta	cat	gcg	ttg	ggc	atc	tac	caa	cca	tat	gta	tgg	gaa	tat	1488
Trp	Leu	Leu	His	Ala 485	Leu	Gly	Ile	Tyr	Gln 490	Pro	Tyr	Val	Trp	Glu 495	Tyr	
tca	agg	ttg	aat	gtc	tca	aac	aca	gtt	atg	tca	aag	cgt	aag	cta	aat	1536
Ser	Arg	Leu	Asn	Val	Ser	Asn	Thr	Val	Met	Ser	Lys	Arg	Lys	Leu	Asn	
			500				505						510			
cgt	ttg	gtg	aca	gag	aag	tgg	gtt	gat	ggg	tgg	gat	gat	cct	cgt	ctg	1584
Arg	Leu	Val	Thr	Glu	Lys	Trp	Val	Asp	Gly	Trp	Asp	Asp	Pro	Arg	Leu	
		515					520					525				
atg	aca	cta	gct	ggc	ttg	cgg	cgt	aga	ggc	atg	act	ccc	act	gca	atc	1632
Met	Thr	Leu	Ala	Gly	Leu	Arg	Arg	Arg	Gly	Met	Thr	Pro	Thr	Ala	Ile	
	530					535					540					
aat	gcc	ttt	gtc	cga	gga	atg	gga	atc	act	aga	agt	gac	ggc	act	ttg	1680
Asn	Ala	Phe	Val	Arg	Gly	Met	Gly	Ile	Thr	Arg	Ser	Asp	Gly	Thr	Leu	
545					550					555					560	
ata	tct	gtg	gaa	cgt	ctt	gag	tat	cat	gtt	agg	gaa	gaa	ttg	aat	aaa	1728
Ile	Ser	Val	Glu	Arg	Leu	Glu	Tyr	His	Val	Arg	Glu	Glu	Leu	Asn	Lys	
				565					570					575		
aca	gct	cct	cgt	gca	atg	gtt	gtc	ctg	cat	cca	ctc	aag	gtt	gtc	att	1776
Thr	Ala	Pro	Arg	Ala	Met	Val	Val	Leu	His	Pro	Leu	Lys	Val	Val	Ile	
			580					585					590			
act	aat	ctt	gaa	gcc	aaa	tca	gca	att	gag	gtt	gat	gca	aag	aaa	tgg	1824
Thr	Asn	Leu	Glu	Ala	Lys	Ser	Ile	Glu	Val	Asp	Ala	Lys	Lys	Trp		
		595					600					605				
cct	gat	gct	caa	gct	gat	gat	gct	tct	gct	ttc	tac	aag	att	cca	ttt	1872
Pro	Asp	Ala	Gln	Ala	Asp	Asp	Ala	Ser	Ala	Phe	Tyr	Lys	Ile	Pro	Phe	
	610				615						620					
tcc	aat	gtt	gta	tat	att	gaa	cgt	tcg	gat	ttc	cgg	atg	caa	gat	tca	1920
Ser	Asn	Val	Val	Tyr	Ile	Glu	Arg	Ser	Asp	Phe	Arg	Met	Gln	Asp	Ser	
625					630					635					640	
aaa	gat	tat	tat	ggc	ctt	gct	cct	ggc	aaa	tct	gtg	ata	ctc	aga	tat	1968
Lys	Asp	Tyr	Tyr	Gly	Leu	Ala	Pro	Gly	Lys	Ser	Val	Ile	Leu	Arg	Tyr	
				645					650					655		
gca	ttt	cct	ata	aag	tgc	act	gaa	gtt	att	cta	gct	gat	gat	aat	gag	2016
Ala	Phe	Pro	Ile	Lys	Cys	Thr	Glu	Val	Ile	Leu	Ala	Asp	Asp	Asn	Glu	
			660					665					670			
acc	att	ctt	gaa	att	cgg	gct	gag	tat	gat	cct	tca	aag	aag	aca	aag	2064
Thr	Ile	Leu	Glu	Ile	Arg	Ala	Glu	Tyr	Asp	Pro	Ser	Lys	Lys	Thr	Lys	
		675					680					685				
cct	aag	ggc	gtg	ctt	cat	tgg	gtt	tct	caa	cct	tct	ccg	gga	gtt	gat	2112
Pro	Lys	Gly	Val	Leu	His	Trp	Val	Ser	Gln	Pro	Ser	Pro	Gly	Val	Asp	
	690					695					700					
cca	tta	aag	gtg	gaa	gtg	agg	ttg	ttt	gag	agg	cta	ttc	cta	tca	gag	2160
Pro	Leu	Lys	Val	Glu	Val	Arg	Leu	Phe	Glu	Arg	Leu	Phe	Leu	Ser	Glu	
705					710					715					720	
aat	cct	gct	gaa	ctt	gac	aac	tgg	ctc	ggg	gac	cta	aac	cct	cat	tcc	2208
Asn	Pro	Ala	Glu	Leu	Asp	Asn	Trp	Leu	Gly	Asp	Leu	Asn	Pro	His	Ser	
				725					730					735		
aaa	gtg	gaa	att	tcg	aat	gca	tat	ggc	gtg	tcc	ttg	ctg	aag	gat	gca	2256
Lys	Val	Glu	Ile	Ser	Asn	Ala	Tyr	Gly	Val	Ser	Leu	Leu	Lys	Asp	Ala	
			740					745					750			
aaa	ctc	ggg	gac	agg	ttc	cag	ttt	gaa	aga	tta	gga	tat	ttt	gca	gtc	2304
Lys	Leu	Gly	Asp	Arg	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Phe	Ala	Val	
		755					760					765				
gac	cag	gac	tct	acc	cca	gaa	aaa	ctt	gta	ttt	aat	cgg	act	gtc	acc	2352
Asp	Gln	Asp	Ser	Thr	Pro	Glu	Lys	Leu	Val	Phe	Asn	Arg	Thr	Val	Thr	
	770					775					780					
ctt	aaa	gac	agc	tat	ggc	ggc	gga	aag	tag							2385
Leu	Lys	Asp	Ser	Tyr	Gly	Lys	Gly	Gly	Lys							
785					790											

<210> 9970

<211> 794

<212> PRT

<213> Lupinus luteus

<400> 9970

PF59083SeqList PF59083.txt

```

Met  Pro  Ala  Lys  Asp  Asp  Thr  Ser  Ser  Asp  Lys  Glu  Lys  Ser  Leu  Glu
1      5      10      15
Leu  Phe  Leu  Lys  Ile  Gly  Leu  Asp  Glu  Arg  Thr  Ala  Lys  Asn  Thr  Val
      20      25      30
Ala  Asn  Asn  Lys  Val  Thr  Thr  Asn  Leu  Thr  Ser  Val  Ile  Asn  Asp  Ala
      35      40      45
Gly  Val  Thr  Asp  Gly  Cys  Ser  Arg  Thr  Val  Gly  Asn  Leu  Leu  Tyr  Thr
      50      55      60
Val  Ala  Thr  Lys  Tyr  Pro  Ala  Asn  Ala  Leu  Pro  His  Arg  Pro  Thr  Leu
65      70      75      80
Leu  Gln  Tyr  Ile  Val  Asn  Ser  Lys  Val  Lys  Thr  Thr  Ala  Gln  Leu  Asp
      85      90      95
Ala  Ala  Leu  Ser  Phe  Leu  Ser  Ala  Thr  Gly  Ser  Glu  Asn  Leu  Asp  Leu
      100     105     110
Asn  Lys  Phe  Glu  Glu  Ala  Cys  Gly  Val  Gly  Val  Glu  Val  Ser  Thr  Glu
      115     120     125
Asp  Ile  Lys  His  Ala  Val  Asp  Glu  Val  Val  Glu  Glu  Asn  Lys  Ala  Thr
      130     135     140
Ile  Leu  Glu  Leu  Arg  Tyr  Arg  Val  Asn  Val  Gly  Glu  Leu  Leu  Gly  His
145     150     155     160
Val  Arg  Lys  Arg  Leu  Pro  Trp  Ala  Asp  Ala  Lys  Val  Val  Lys  Gln  Leu
      165     170     175
Val  Asp  Ala  Lys  Leu  Tyr  Glu  Ile  Leu  Gly  Asp  Arg  Thr  Ala  Ala  Asp
      180     185     190
Asn  Glu  Lys  Pro  Lys  Lys  Lys  Lys  Glu  Lys  Pro  Ala  Lys  Val  Glu  Asp
      195     200     205
Lys  Ala  Ala  Pro  Val  Ala  Thr  Ser  Glu  Lys  Pro  Leu  Glu  Glu  Asp  Leu
      210     215     220
Asn  Pro  Tyr  Leu  Ile  Phe  Pro  Asn  Pro  Glu  Asp  Asn  Phe  Lys  Val  His
225     230     235     240
Thr  Glu  Val  Pro  Phe  Ser  Asp  Gly  Asn  Ile  Leu  Arg  Cys  Cys  Asn  Thr
      245     250     255
Lys  Ala  Leu  Leu  Glu  Lys  His  Leu  Lys  Ala  Thr  Gly  Gly  Lys  Val  Leu
      260     265     270
Thr  Arg  Phe  Pro  Pro  Glu  Pro  Asn  Gly  Tyr  Leu  His  Ile  Gly  His  Ala
      275     280     285
Lys  Ala  Met  Phe  Val  Asp  Phe  Gly  Leu  Ala  Lys  Asp  Arg  Asn  Gly  Gly
      290     295     300
Cys  Tyr  Leu  Arg  Phe  Asp  Thr  Asn  Pro  Glu  Ala  Glu  Lys  Lys  Glu
305     310     315     320
Tyr  Ile  Asp  His  Ile  Glu  Glu  Ile  Val  Gln  Trp  Met  Gly  Trp  Glu  Pro
      325     330     335
Phe  Lys  Ile  Thr  Tyr  Thr  Ser  Asn  Tyr  Phe  Gln  Glu  Leu  Tyr  Glu  Phe
      340     345     350
Ala  Val  Glu  Leu  Ile  Arg  Arg  Gly  His  Ala  Tyr  Val  Asp  His  Gln  Thr
      355     360     365
Ala  Asp  Glu  Ile  Lys  Glu  Tyr  Arg  Glu  Lys  Lys  Leu  Asn  Ser  Pro  Trp
      370     375     380
Arg  Asp  Arg  Pro  Ile  Ser  Glu  Ser  Leu  Lys  Leu  Phe  Glu  Asp  Met  Arg
385     390     395     400
Arg  Gly  Phe  Ile  Glu  Glu  Gly  Lys  Ala  Thr  Leu  Arg  Met  Lys  Gln  Asp
      405     410     415
Met  Gln  Ser  Asp  Asn  Tyr  Asn  Met  Tyr  Asp  Leu  Ile  Ala  Tyr  Arg  Ile
      420     425     430
Lys  Phe  Thr  Pro  His  Pro  His  Ala  Gly  Asp  Lys  Trp  Cys  Ile  Tyr  Pro
      435     440     445
Ser  Tyr  Asp  Tyr  Ala  His  Cys  Ile  Val  Asp  Ser  Ile  Glu  Asn  Val  Thr
      450     455     460
His  Ser  Leu  Cys  Thr  Leu  Glu  Phe  Glu  Thr  Arg  Arg  Ala  Ser  Tyr  Tyr
465     470     475     480
Trp  Leu  Leu  His  Ala  Leu  Gly  Ile  Tyr  Gln  Pro  Tyr  Val  Trp  Glu  Tyr
      485     490     495
Ser  Arg  Leu  Asn  Val  Ser  Asn  Thr  Val  Met  Ser  Lys  Arg  Lys  Leu  Asn
      500     505     510
Arg  Leu  Val  Thr  Glu  Lys  Trp  Val  Asp  Gly  Trp  Asp  Asp  Pro  Arg  Leu
      515     520     525
Met  Thr  Leu  Ala  Gly  Leu  Arg  Arg  Arg  Gly  Met  Thr  Pro  Thr  Ala  Ile
      530     535     540
Asn  Ala  Phe  Val  Arg  Gly  Met  Gly  Ile  Thr  Arg  Ser  Asp  Gly  Thr  Leu

```

PF59083SeqList PF59083.txt

```

545                               550                               555                               560
Ile Ser Val Glu Arg Leu Glu Tyr His Val Arg Glu Glu Leu Asn Lys
                               565                               570                               575
Thr Ala Pro Arg Ala Met Val Val Leu His Pro Leu Lys Val Val Ile
                               580                               585                               590
Thr Asn Leu Glu Ala Lys Ser Ala Ile Glu Val Asp Ala Lys Lys Trp
                               595                               600                               605
Pro Asp Ala Gln Ala Asp Asp Ala Ser Ala Phe Tyr Lys Ile Pro Phe
610                               615                               620
Ser Asn Val Val Tyr Ile Glu Arg Ser Asp Phe Arg Met Gln Asp Ser
625                               630                               635
Lys Asp Tyr Tyr Gly Leu Ala Pro Gly Lys Ser Val Ile Leu Arg Tyr
645                               650                               655
Ala Phe Pro Ile Lys Cys Thr Glu Val Ile Leu Ala Asp Asp Asn Glu
660                               665                               670
Thr Ile Leu Glu Ile Arg Ala Glu Tyr Asp Pro Ser Lys Lys Thr Lys
675                               680                               685
Pro Lys Gly Val Leu His Trp Val Ser Gln Pro Ser Pro Gly Val Asp
690                               695                               700
Pro Leu Lys Val Glu Val Arg Leu Phe Glu Arg Leu Phe Leu Ser Glu
705                               710                               715
Asn Pro Ala Glu Leu Asp Asn Trp Leu Gly Asp Leu Asn Pro His Ser
725                               730                               735
Lys Val Glu Ile Ser Asn Ala Tyr Gly Val Ser Leu Leu Lys Asp Ala
740                               745                               750
Lys Leu Gly Asp Arg Phe Gln Phe Glu Arg Leu Gly Tyr Phe Ala Val
755                               760                               765
Asp Gln Asp Ser Thr Pro Glu Lys Leu Val Phe Asn Arg Thr Val Thr
770                               775                               780
Leu Lys Asp Ser Tyr Gly Lys Gly Gly Lys
785                               790

```

<210> 9971
 <211> 2436
 <212> DNA
 <213> Schizosaccharomyces pombe

<220>
 <221> CDS
 <222> (1)..(2436)

```

<400> 9971
atg gac cag gat tat gag gag tta cgt gcc aag ttt aca aaa ata gga      48
Met Asp Gln Asp Tyr Glu Glu Leu Arg Ala Lys Phe Thr Lys Ile Gly
1                               5                               10                               15
tta aat gaa aca acg gta aaa gat acg tta aaa aat aaa aag ctt tct      96
Leu Asn Glu Thr Thr Val Lys Asp Thr Leu Lys Asn Lys Lys Leu Ser
20                               25                               30
tct tca tta aat aag gtc att gag gaa act aac gtt ggt tct tcg gga      144
Ser Ser Leu Asn Lys Val Ile Glu Thr Asn Val Gly Ser Ser Gly
35                               40                               45
tgt gat aga aca att gga aat ttg cta ttt aca ttg gcc aac gct tct      192
Cys Asp Arg Thr Ile Gly Asn Leu Leu Phe Thr Leu Ala Asn Ala Ser
50                               55                               60
tta aaa caa aaa gac ccg aaa tcc aat gct cat gag gca ttc ata gct      240
Leu Lys Gln Lys Asp Pro Lys Ser Asn Ala His Glu Ala Phe Ile Ala
65                               70                               75                               80
tcc aaa att gta tct gga gac tta aaa aca aac ctc caa gtc aat gcg      288
Ser Lys Ile Val Ser Gly Asp Leu Lys Thr Asn Leu Gln Val Asn Ala
85                               90                               95
gct att acc tat tgc aag gac aaa gac acg atc gac gaa tct gag ttc      336
Ala Ile Thr Tyr Cys Lys Asp Lys Asp Thr Ile Asp Glu Ser Glu Phe
100                               105                               110
gat aaa gaa act ggt gtt ggt gta gtc tta aca cct gaa caa att gaa      384
Asp Lys Glu Thr Gly Val Gly Val Val Leu Thr Pro Glu Gln Ile Glu
115                               120                               125
caa ctc gtc ggt gat tat gtc gct gag aat aag tca aaa att ttg gag      432
Gln Leu Val Gly Asp Tyr Val Ala Glu Asn Lys Ser Lys Ile Leu Glu
130                               135                               140

```

PF59083SeqList PF59083.txt

caa	aga	tac	cag	ctg	tta	aat	cct	tct	gcc	tct	gct	tta	cgt	cag	cat	480
Gln	Arg	Tyr	Gln	Leu	Leu	Asn	Pro	Ser	Ala	Ser	Ala	Leu	Arg	Gln	His	
145				150						155					160	
gct	tta	ttg	aaa	tgg	gct	cct	caa	ctg	gag	gtc	aag	cag	acc	ctt	gat	528
Ala	Leu	Leu	Lys	Trp	Ala	Pro	Gln	Leu	Glu	Val	Lys	Gln	Thr	Leu	Asp	
				165					170						175	
agg	aaa	ttc	ctt	gaa	ctc	ttg	gga	cca	aaa	acc	gaa	caa	gat	gct	gcc	576
Arg	Lys	Phe	Leu	Glu	Leu	Leu	Gly	Pro	Lys	Thr	Glu	Gln	Asp	Ala	Ala	
				180				185					190			
gct	ggt	aaa	aaa	aaa	ggc	gca	aaa	gcc	aag	aat	tcg	aag	cag	aag	act	624
Ala	Gly	Lys	Lys	Lys	Gly	Ala	Lys	Ala	Lys	Asn	Ser	Lys	Gln	Lys	Thr	
		195					200					205				
gtt	gat	tct	ggg	aaa	gct	aag	gaa	caa	aaa	att	gtt	tct	gaa	cag	tct	672
Val	Asp	Ser	Gly	Lys	Ala	Lys	Glu	Gln	Lys	Ile	Val	Ser	Glu	Gln	Ser	
	210					215					220					
aag	aaa	tat	aat	atg	ttt	gag	gaa	ggg	ttt	tta	gca	aag	cta	cat	aaa	720
Lys	Lys	Tyr	Asn	Met	Phe	Glu	Glu	Gly	Phe	Leu	Ala	Lys	Leu	His	Lys	
225				230						235					240	
cca	ggt	ggt	aat	acg	cag	ctg	att	cct	gaa	agg	atg	aag	gag	cac	ctg	768
Pro	Gly	Gly	Asn	Thr	Gln	Leu	Ile	Pro	Glu	Arg	Met	Lys	Glu	His	Leu	
				245				250						255		
cag	gct	act	gga	ggc	ggc	gtt	gta	acc	agg	ttt	cct	ccg	gaa	cca	aat	816
Gln	Ala	Thr	Gly	Gly	Gly	Val	Val	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	
			260				265						270			
ggg	tac	ctc	cat	att	ggc	cat	tcc	aaa	gca	atc	gct	gtt	aat	ttt	ggg	864
Gly	Tyr	Leu	His	Ile	Gly	His	Ser	Lys	Ala	Ile	Ala	Val	Asn	Phe	Gly	
		275					280					285				
ttt	gct	cgc	tat	cat	aac	ggc	gtt	tgt	tat	tta	cgc	ttt	gat	gat	act	912
Phe	Ala	Arg	Tyr	His	Asn	Gly	Val	Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr	
	290					295					300					
aat	ccg	gaa	gct	gaa	gaa	gag	cgt	tac	ttt	gaa	agc	atc	aag	gat	ttg	960
Asn	Pro	Glu	Ala	Glu	Glu	Glu	Arg	Tyr	Phe	Glu	Ser	Ile	Lys	Asp	Leu	
305				310						315					320	
gta	gcc	tgg	ttg	gga	ttc	caa	cct	tat	aag	atc	acc	tat	tcc	agt	gat	1008
Val	Ala	Trp	Leu	Gly	Phe	Gln	Pro	Tyr	Lys	Ile	Thr	Tyr	Ser	Ser	Asp	
				325				330						335		
tac	ttt	gat	aag	tta	tat	gag	tta	gcc	gaa	gag	ctc	att	aag	cgg	gac	1056
Tyr	Phe	Asp	Lys	Leu	Tyr	Glu	Leu	Ala	Glu	Glu	Leu	Ile	Lys	Arg	Asp	
			340				345						350			
aag	gca	tat	gtt	tgt	cat	tgt	acc	gat	gct	gaa	att	aaa	aaa	gct	aga	1104
Lys	Ala	Tyr	Val	Cys	His	Cys	Thr	Asp	Ala	Glu	Ile	Lys	Lys	Ala	Arg	
		355				360						365				
ggt	ggt	gag	gag	cgc	ggt	cct	cgt	tat	gct	tgt	gtt	cat	cgg	gac	cgc	1152
Gly	Gly	Glu	Glu	Arg	Gly	Pro	Arg	Tyr	Ala	Cys	Val	His	Arg	Asp	Arg	
	370					375					380					
ccg	ata	gaa	gaa	tcg	ctt	ctt	gaa	ttt	cgt	aat	atg	cgt	gat	gga	aag	1200
Pro	Ile	Glu	Glu	Ser	Leu	Leu	Glu	Phe	Arg	Asn	Met	Arg	Asp	Gly	Lys	
385				390						395				400		
tat	caa	ccg	aag	gag	gct	att	tta	cgt	atg	aaa	caa	gat	ctc	agt	gat	1248
Tyr	Gln	Pro	Lys	Glu	Ala	Ile	Leu	Arg	Met	Lys	Gln	Asp	Leu	Ser	Asp	
				405				410						415		
gga	aat	cct	caa	atg	tgg	gac	ctt	att	gcc	tac	cgt	gtt	ctt	aat	tct	1296
Gly	Asn	Pro	Gln	Met	Trp	Asp	Leu	Ile	Ala	Tyr	Arg	Val	Leu	Asn	Ser	
			420			425							430			
cct	cat	cct	cgt	act	gga	gac	aag	tgg	aaa	att	tac	cca	act	tat	gat	1344
Pro	His	Pro	Arg	Thr	Gly	Asp	Lys	Trp	Lys	Ile	Tyr	Pro	Thr	Tyr	Asp	
		435				440						445				
ttt	acc	cat	tgt	tta	gtt	gat	tcg	ttc	gag	aac	att	tct	cac	tct	ttg	1392
Phe	Thr	His	Cys	Leu	Val	Asp	Ser	Phe	Glu	Asn	Ile	Ser	His	Ser	Leu	
	450					455					460					
tgt	acg	act	gag	ttt	ata	tta	tct	aga	gta	agt	tat	gag	tgg	tta	tgt	1440
Cys	Thr	Thr	Glu	Phe	Ile	Leu	Ser	Arg	Val	Ser	Tyr	Glu	Trp	Leu	Cys	
465				470						475				480		
aat	gcc	ttg	gaa	gtt	tat	tgt	cct	gct	cag	cgt	gag	tac	ggt	cgt	ttg	1488
Asn	Ala	Leu	Glu	Val	Tyr	Cys	Pro	Ala	Gln	Arg	Glu	Tyr	Gly	Arg	Leu	
				485				490						495		
aac	gtt	gtc	gga	acc	ctc	atg	agc	aaa	cga	aaa	ata	atg	aaa	ttg	gta	1536
Asn	Val	Val	Gly	Thr	Leu	Met	Ser	Lys	Arg	Lys	Ile	Met	Lys	Leu	Val	
			500					505					510			

PF59083SeqList PF59083.txt

aag	gaa	gga	tac	ggt	cat	ggt	tg	aat	gat	cct	agg	cta	tat	acc	ctt	1584
Lys	Glu	Gly	Tyr	Val	His	Gly	Trp	Asn	Asp	Pro	Arg	Leu	Tyr	Thr	Leu	
		515					520					525				
gta	gct	ctt	cgc	cgc	cga	ggt	ggt	cct	cca	ggt	gct	atc	ctt	gag	ttt	1632
Val	Ala	Leu	Arg	Arg	Arg	Gly	Val	Pro	Pro	Gly	Ala	Ile	Leu	Glu	Phe	
		530					535					540				
ggt	agt	gaa	gtc	ggt	gtc	act	act	gcc	gtc	agc	aat	ata	gaa	ggt	gct	1680
Val	Ser	Glu	Val	Gly	Val	Thr	Thr	Ala	Val	Ser	Asn	Ile	Glu	Val	Ala	
		545													560	
cga	ttt	gag	aac	tgt	ggt	cga	aaa	ttt	ctc	gaa	aac	agt	gta	cca	cgt	1728
Arg	Phe	Glu	Asn	Cys	Val	Arg	Lys	Phe	Leu	Glu	Asn	Ser	Val	Pro	Arg	
				565					570						575	
ctt	atg	ttt	ctt	cct	gat	cct	atc	aag	ggt	aca	tta	gaa	aat	cta	gac	1776
Leu	Met	Phe	Leu	Pro	Asp	Pro	Ile	Lys	Val	Thr	Leu	Glu	Asn	Leu	Asp	
			580						585							
gac	tct	tac	aga	gag	caa	att	gag	ata	ccc	ttt	aat	cct	aaa	gat	cct	1824
Asp	Ser	Tyr	Arg	Glu	Gln	Ile	Glu	Ile	Pro	Phe	Asn	Pro	Lys	Asp	Pro	
		595							600							
tct	atg	gga	tct	cgt	tct	gct	ttt	ctt	aca	aag	cat	ata	tac	att	gac	1872
Ser	Met	Gly	Ser	Arg	Ser	Ala	Phe	Leu	Thr	Lys	His	Ile	Tyr	Ile	Asp	
		610														
cgt	tct	gat	ttt	cgt	gag	gaa	gca	tct	tct	gac	ttt	ttc	cgt	ttg	aca	1920
Arg	Ser	Asp	Phe	Arg	Glu	Glu	Ala	Ser	Ser	Asp	Phe	Phe	Arg	Leu	Thr	
		625													640	
tta	ggt	caa	ccg	ggt	ggc	ttg	ttc	cgt	gcc	tct	cat	cct	gta	ggt	gcc	1968
Leu	Gly	Gln	Pro	Val	Gly	Leu	Phe	Arg	Ala	Ser	His	Pro	Val	Val	Ala	
				645					650						655	
aaa	agg	ggt	gta	aaa	aat	gat	gaa	ggg	gaa	cca	ata	gaa	atc	atc	gct	2016
Lys	Arg	Val	Val	Lys	Asn	Asp	Glu	Gly	Glu	Pro	Ile	Glu	Ile	Ile	Ala	
			660						665							
gag	tac	gac	gct	agc	tct	tca	aag	aag	cct	aag	acc	ttt	att	caa	tg	2064
Glu	Tyr	Asp	Ala	Ser	Ser	Ser	Lys	Lys	Pro	Lys	Thr	Phe	Ile	Gln	Trp	
		675							680							
gtg	tct	agg	gac	aaa	gaa	agt	aat	agt	cca	gta	ctt	att	gct	gaa	acc	2112
Val	Ser	Arg	Asp	Lys	Glu	Ser	Asn	Ser	Pro	Val	Leu	Ile	Ala	Glu	Thr	
		690														
cgc	ctc	ttt	aat	aat	ctt	ttc	aaa	tgt	gat	aac	cct	gcc	gcc	cta	aaa	2160
Arg	Leu	Phe	Asn	Asn	Leu	Phe	Lys	Cys	Asp	Asn	Pro	Ala	Ala	Leu	Lys	
		705													720	
gaa	caa	gag	ctc	gct	gca	caa	ttg	aat	cca	gag	agc	gaa	gtc	gta	cta	2208
Glu	Gln	Glu	Leu	Ala	Ala	Gln	Leu	Asn	Pro	Glu	Ser	Glu	Val	Val	Leu	
				725					730						735	
aaa	aat	tcc	att	att	gaa	cct	ggc	att	tat	gat	tta	att	aaa	tcg	gca	2256
Lys	Asn	Ser	Ile	Ile	Glu	Pro	Gly	Ile	Tyr	Asp	Leu	Ile	Lys	Ser	Ala	
			740						745							
cct	tg	cct	aag	act	gat	tca	tcg	gct	ggt	gtc	gac	aaa	gcc	gaa	aat	2304
Pro	Trp	Pro	Lys	Thr	Asp	Ser	Ser	Ala	Gly	Val	Asp	Lys	Ala	Glu	Asn	
		755							760							
cct	gaa	agt	gtc	cgt	ttt	caa	gct	atg	cgg	ggt	gga	tat	ttc	tgt	tta	2352
Pro	Glu	Ser	Val	Arg	Phe	Gln	Ala	Met	Arg	Val	Gly	Tyr	Phe	Cys	Leu	
		770														
gat	gag	gat	act	aag	aaa	cca	aat	cat	ctt	gta	ttg	aat	aga	att	gta	2400
Asp	Glu	Asp	Thr	Lys	Lys	Pro	Asn	His	Leu	Val	Leu	Asn	Arg	Ile	Val	
															800	
tcc	ctc	aga	gaa	gat	tcg	gct	aag	aat	aaa	aat	tag					2436
Ser	Leu	Arg	Glu	Asp	Ser	Ala	Lys	Asn	Lys	Asn						
				805						810						

<210> 9972

<211> 811

<212> PRT

<213> Schizosaccharomyces pombe

<400> 9972

Met	Asp	Gln	Asp	Tyr	Glu	Glu	Leu	Arg	Ala	Lys	Phe	Thr	Lys	Ile	Gly
1				5					10					15	
Leu	Asn	Glu	Thr	Thr	Val	Lys	Asp	Thr	Leu	Lys	Asn	Lys	Lys	Leu	Ser
			20					25					30		
Ser	Ser	Leu	Asn	Lys	Val	Ile	Glu	Glu	Thr	Asn	Val	Gly	Ser	Ser	Gly

PF59083SeqList PF59083.txt

		35				40				45					
Cys	Asp	Arg	Thr	Ile	Gly	Asn	Leu	Leu	Phe	Thr	Leu	Ala	Asn	Ala	Ser
	50					55					60				
Leu	Lys	Gln	Lys	Asp	Pro	Lys	Ser	Asn	Ala	His	Glu	Ala	Phe	Ile	Ala
65					70					75					80
Ser	Lys	Ile	Val	Ser	Gly	Asp	Leu	Lys	Thr	Asn	Leu	Gln	Val	Asn	Ala
				85					90					95	
Ala	Ile	Thr	Tyr	Cys	Lys	Asp	Lys	Asp	Thr	Ile	Asp	Glu	Ser	Glu	Phe
			100					105					110		
Asp	Lys	Glu	Thr	Gly	Val	Gly	Val	Val	Leu	Thr	Pro	Glu	Gln	Ile	Glu
		115					120					125			
Gln	Leu	Val	Gly	Asp	Tyr	Val	Ala	Glu	Asn	Lys	Ser	Lys	Ile	Leu	Glu
	130					135					140				
Gln	Arg	Tyr	Gln	Leu	Leu	Asn	Pro	Ser	Ala	Ser	Ala	Leu	Arg	Gln	His
145					150					155					160
Ala	Leu	Leu	Lys	Trp	Ala	Pro	Gln	Leu	Glu	Val	Lys	Gln	Thr	Leu	Asp
				165					170					175	
Arg	Lys	Phe	Leu	Glu	Leu	Leu	Gly	Pro	Lys	Thr	Glu	Gln	Asp	Ala	Ala
			180					185					190		
Ala	Gly	Lys	Lys	Lys	Gly	Ala	Lys	Ala	Lys	Asn	Ser	Lys	Gln	Lys	Thr
		195					200					205			
Val	Asp	Ser	Gly	Lys	Ala	Lys	Glu	Gln	Lys	Ile	Val	Ser	Glu	Gln	Ser
	210					215					220				
Lys	Lys	Tyr	Asn	Met	Phe	Glu	Glu	Gly	Phe	Leu	Ala	Lys	Leu	His	Lys
225					230					235					240
Pro	Gly	Gly	Asn	Thr	Gln	Leu	Ile	Pro	Glu	Arg	Met	Lys	Glu	His	Leu
			245						250					255	
Gln	Ala	Thr	Gly	Gly	Gly	Val	Val	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn
			260					265					270		
Gly	Tyr	Leu	His	Ile	Gly	His	Ser	Lys	Ala	Ile	Ala	Val	Asn	Phe	Gly
		275					280					285			
Phe	Ala	Arg	Tyr	His	Asn	Gly	Val	Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr
	290					295					300				
Asn	Pro	Glu	Ala	Glu	Glu	Glu	Arg	Tyr	Phe	Glu	Ser	Ile	Lys	Asp	Leu
305					310					315					320
Val	Ala	Trp	Leu	Gly	Phe	Gln	Pro	Tyr	Lys	Ile	Thr	Tyr	Ser	Ser	Asp
			325						330					335	
Tyr	Phe	Asp	Lys	Leu	Tyr	Glu	Leu	Ala	Glu	Glu	Leu	Ile	Lys	Arg	Asp
			340					345					350		
Lys	Ala	Tyr	Val	Cys	His	Cys	Thr	Asp	Ala	Glu	Ile	Lys	Lys	Ala	Arg
		355					360					365			
Gly	Gly	Glu	Glu	Arg	Gly	Pro	Arg	Tyr	Ala	Cys	Val	His	Arg	Asp	Arg
	370					375					380				
Pro	Ile	Glu	Glu	Ser	Leu	Glu	Phe	Arg	Asn	Met	Arg	Asp	Gly	Lys	
385					390				395						
Tyr	Gln	Pro	Lys	Glu	Ala	Ile	Leu	Arg	Met	Lys	Gln	Asp	Leu	Ser	Asp
			405						410					415	
Gly	Asn	Pro	Gln	Met	Trp	Asp	Leu	Ile	Ala	Tyr	Arg	Val	Leu	Asn	Ser
			420					425					430		
Pro	His	Pro	Arg	Thr	Gly	Asp	Lys	Trp	Lys	Ile	Tyr	Pro	Thr	Tyr	Asp
		435					440					445			
Phe	Thr	His	Cys	Leu	Val	Asp	Ser	Phe	Glu	Asn	Ile	Ser	His	Ser	Leu
	450					455					460				
Cys	Thr	Thr	Glu	Phe	Ile	Leu	Ser	Arg	Val	Ser	Tyr	Glu	Trp	Leu	Cys
465					470					475					480
Asn	Ala	Leu	Glu	Val	Tyr	Cys	Pro	Ala	Gln	Arg	Glu	Tyr	Gly	Arg	Leu
			485						490					495	
Asn	Val	Val	Gly	Thr	Leu	Met	Ser	Lys	Arg	Lys	Ile	Met	Lys	Leu	Val
			500					505					510		
Lys	Glu	Gly	Tyr	Val	His	Gly	Trp	Asn	Asp	Pro	Arg	Leu	Tyr	Thr	Leu
		515					520					525			
Val	Ala	Leu	Arg	Arg	Arg	Gly	Val	Pro	Pro	Gly	Ala	Ile	Leu	Glu	Phe
	530					535					540				
Val	Ser	Glu	Val	Gly	Val	Thr	Thr	Ala	Val	Ser	Asn	Ile	Glu	Val	Ala
545					550					555					560
Arg	Phe	Glu	Asn	Cys	Val	Arg	Lys	Phe	Leu	Glu	Asn	Ser	Val	Pro	Arg
			565						570					575	
Leu	Met	Phe	Leu	Pro	Asp	Pro	Ile	Lys	Val	Thr	Leu	Glu	Asn	Leu	Asp
			580					585					590		

PF59083SeqList PF59083.txt

Asp Ser Tyr Arg Glu Gln Ile Glu Ile Pro Phe Asn Pro Lys Asp Pro
 595 600 605
 Ser Met Gly Ser Arg Ser Ala Phe Leu Thr Lys His Ile Tyr Ile Asp
 610 615 620
 Arg Ser Asp Phe Arg Glu Ala Ser Ser Asp Phe Phe Arg Leu Thr
 625 630 635 640
 Leu Gly Gln Pro Val Gly Leu Phe Arg Ala Ser His Pro Val Val Ala
 645 650 655
 Lys Arg Val Val Lys Asn Asp Glu Gly Glu Pro Ile Glu Ile Ile Ala
 660 665 670
 Glu Tyr Asp Ala Ser Ser Ser Lys Lys Pro Lys Thr Phe Ile Gln Trp
 675 680 685
 Val Ser Arg Asp Lys Glu Ser Asn Ser Pro Val Leu Ile Ala Glu Thr
 690 695 700
 Arg Leu Phe Asn Asn Leu Phe Lys Cys Asp Asn Pro Ala Ala Leu Lys
 705 710 715 720
 Glu Gln Glu Leu Ala Ala Gln Leu Asn Pro Glu Ser Glu Val Val Leu
 725 730 735
 Lys Asn Ser Ile Ile Glu Pro Gly Ile Tyr Asp Leu Ile Lys Ser Ala
 740 745 750
 Pro Trp Pro Lys Thr Asp Ser Ser Ala Gly Val Asp Lys Ala Glu Asn
 755 760 765
 Pro Glu Ser Val Arg Phe Gln Ala Met Arg Val Gly Tyr Phe Cys Leu
 770 775 780
 Asp Glu Asp Thr Lys Lys Pro Asn His Leu Val Leu Asn Arg Ile Val
 785 790 795 800
 Ser Leu Arg Glu Asp Ser Ala Lys Asn Lys Asn
 805 810

<210> 9973
 <211> 2175
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(2175)

<400> 9973
 atg gaa ggg atc aag ctc tct ttc cca ccg aag act ccg cca ccg ctt 48
 Met Glu Gly Ile Lys Leu Ser Phe Pro Pro Lys Thr Pro Pro Pro Leu
 1 5 10 15
 tca gta atc gct gct ctc tcc ctc tca tcc tct ccg gta acc atc gac 96
 Ser Val Ile Ala Ala Leu Ser Leu Ser Ser Pro Val Thr Ile Asp
 20 25 30
 tcc tcc tcc tcc gcc gca acc acc gtc cct act ttc gtc ttc tcc gac 144
 Ser Ser Ser Ser Ala Ala Thr Thr Val Pro Thr Phe Val Phe Ser Asp
 35 40 45
 ggg cga aag ctg agt ggg aca tca gtt ctt ctc cgg tac gtt ggt cga 192
 Gly Arg Lys Leu Ser Gly Thr Ser Val Leu Leu Arg Tyr Val Gly Arg
 50 55 60
 tca gcg aag tct ctt cct ggg ttt tac ggc cac gat gct ttc gaa tct 240
 Ser Ala Lys Ser Leu Pro Gly Phe Tyr Gly His Asp Ala Phe Glu Ser
 65 70 75 80
 tca cag att gat gag tgg gta gat tac gct cct gtc ttc tcc tct ggc 288
 Ser Gln Ile Asp Glu Trp Val Asp Tyr Ala Pro Val Phe Ser Ser Gly
 85 90 95
 tca gag ttt gag aat gct tgc act cgc gtc gat aac tac ctt caa agt 336
 Ser Glu Phe Glu Asn Ala Cys Thr Arg Val Asp Asn Tyr Leu Gln Ser
 100 105 110
 ggc acc ttt ctt gtt ggc cat tct ctt tcc att gcc gat gtt gct gtt 384
 Gly Thr Phe Leu Val Gly His Ser Leu Ser Ile Ala Asp Val Ala Val
 115 120 125
 tgg tca gct ctt gct gca tcc gcc cca aga tgg gag agt ttg agg aaa 432
 Trp Ser Ala Leu Ala Ala Ser Ala Pro Arg Trp Glu Ser Leu Arg Lys
 130 135 140
 tct aaa aag tac cac aac ttg gtc aga cgg ttc aac tca aaa tcg ctc 480
 Ser Lys Lys Tyr His Asn Leu Val Arg Arg Phe Asn Ser Lys Ser Leu
 145 150 155 160

PF59083SeqList PF59083.txt																
gag Glu	cac His	gca Ala	gag Glu	cca Pro 165	ctc Leu	aac Asn	aag Lys	cta Leu 170	gct Ala 175	aca Thr	tat Tyr	act Thr	gcg Ala 175	aag Lys 175	aag Lys	528
cct Pro	tca Ser	ggg Gly 180	aag Lys 180	act Thr	gtt Val	tct Ser	gct Ala 185	gca Pro 185	cca Arg	agg Thr	acc Lys	aag Lys 190	gac Asp 190	caa Gln	caa Gln	576
gca Ala	gac Asp	aac Asn 195	gct Ala 195	aac Asn	gac Asp	aaa Lys 200	gga Gly 200	aag Lys	cct Pro	gaa Glu	gtg Val 205	gac Asp 205	ttg Leu	cct Pro	gga Gly	624
gca Ala 210	gaa Glu 210	ctc Leu	gga Gly	aaa Lys	gtc Val 215	aaa Lys 215	ctc Leu	cgg Arg	ttc Phe	gct Ala 220	cca Pro 220	gag Glu	cca Pro	agc Ser	ggc Gly	672
tac Tyr 225	ctc Leu	cac His	atc Ile	ggc Gly	cac His 230	gcc Ala	aag Lys	gcc Ala	gcc Ala	ctt Leu 235	ctc Leu	aac Asn	aag Lys	tac Tyr	ttc Phe 240	720
gcc Ala	gag Glu	cgg Arg	tac Tyr	caa Gln 245	ggg Gly	gaa Glu	gtc Val 250	atc Ile	atc Ile	arg Arg	ttc Phe	gac Asp	gac Asp	acc Thr 255	aac Asn	768
ccc Pro	gcc Ala	aaa Lys 260	gag Glu 260	agc Ser	aac Asn	gag Glu	ttc Phe 265	gtc Val 265	gaa Glu	aac Asn	ctc Leu	gtc Val 270	aaa Lys 270	gac Asp	atc Ile	816
ggg Gly	acc Thr 275	ttg Leu	ggg Gly	atc Ile	aag Lys	tac Tyr 280	gag Glu 280	cgc Arg	gtg Val	acc Thr	tac Tyr	acc Thr 285	tca Ser	gac Asp	tac Tyr	864
ttc Phe 290	ccc Pro	gac Asp	ctg Leu	atg Met	gcc Ala	atg Met 295	gcc Ala	gag Glu	aag Lys	ctc Leu	atg Met 300	caa Gln	gag Glu	ggg Gly	aag Lys	912
gct Ala 305	tac Tyr	gtg Val	gac Asp	gac Asp	acg Thr 310	ccg Pro	agg Arg	gag Glu	cag Gln	atg Met 315	cag Gln	aag Lys	gag Glu	agg Arg	atg Met 320	960
gac Asp	ggg Gly	atc Ile	gat Asp	tcc Ser 325	aaa Lys	tgc Cys	agg Arg	agc Ser	cat His 330	acc Thr	atc Ile	gag Glu	gag Glu	aat Asn 335	ctt Leu	1008
aac Asn	ctc Leu	tgg Trp 340	cga Arg	gag Glu	atg Met	atc Ile	gct Ala 345	gga Gly 345	aac Asn	gtg Val	aga Arg	ggg Gly 350	ttg Leu	cag Gln	tgc Cys	1056
tgc Cys	gta Val	cgc Arg 355	ggg Gly	aag Lys	ctg Leu	gac Asp	atg Met 360	caa Gln	gac Asp	ccc Pro	aac Asn	aaa Lys 365	gcc Ala	atg Met	cga Arg	1104
gac Asp 370	cct Pro	gtt Val	tac Tyr	tac Tyr	cgt Arg	tgc Cys 375	acc Asn	cct Pro	atg Met	tct Ser	cac His 380	cac His	cggt Arg	ata Ile	ggg Gly	1152
aac Asn 385	aag Lys	tac Tyr	aag Lys	ata Ile	tat Tyr 390	cca Pro	acg Thr	tat Tyr	gac Asp	ttt Phe 395	gct Ala	tgc Cys	ccc Pro	ttt Phe	gtg Val 400	1200
gac Asp	tcc Ser	att Ile	gaa Glu	ggg Gly 405	ata Ile	acg Thr	cat His	gcg Ala 410	ctt Leu	cgg Arg	tct Ser	agt Ser	gag Glu	tat Tyr 415	cat His	1248
gac Asp	agg Arg	aat Asn	gct Ala 420	cag Gln	tac Tyr	tat Tyr	aag Lys	gtt Val 425	ctg Leu	gag Glu	gat Asp	atg Met	ggg Gly 430	ttg Leu	agg Arg	1296
aga Arg	gtt Val 435	gag Glu	att Ile	tat Tyr	gag Glu	ttt Phe 440	agt Ser	agg Arg	ttg Leu	aat Asn	ctg Leu	gtt Val 445	tac Tyr	acg Thr	ctt Leu	1344
ctg Leu	agt Ser 450	aag Lys	agg Arg	aag Lys	ctt Leu	cta Leu 455	tgg Trp	ttt Phe	gtt Val	cag Gln	caa Gln 460	ggg Gly	ttg Leu	gtt Val	ggt Gly	1392
ggg Gly 465	tgg Trp	gat Asp	gat Asp	cct Pro	cgc Arg 470	ttc Phe	cct Pro	aca Thr	gtg Val	caa Gln 475	ggc Gly	att Ile	gtt Val	cgt Arg	aga Arg 480	1440
ggg Gly	ttg Leu	aaa Lys	att Ile	gag Glu 485	gct Ala	ctg Leu	att Ile	cag Gln	ttc Phe 490	att Ile	ctc Leu	gag Glu	cag Gln	ggg Gly 495	gct Ala	1488
tca Ser	aag Lys	aat Asn	cta Leu 500	aac Asn	ttg Leu	atg Met	gaa Glu	tgg Trp 505	gac Asp	aag Lys	ctc Leu	tgg Trp 510	act Thr	att Ile	aac Asn	1536
aag Lys	aag Lys	ata Ile 515	atc Ile	gac Asp	cct Pro	gtg Val 520	tgt Cys	cct Pro	aga Arg	cac His	acg Thr	gct Ala 525	gtg Val	atc Ile	gaa Glu	1584

PF59083SeqList PF59083.txt

gag	agg	cgt	gta	ctg	ttg	aca	cta	acc	gat	ggt	cct	gat	gag	ccg	ttt	1632
Glu	Arg	Arg	Val	Leu	Leu	Thr	Leu	Thr	Asp	Gly	Pro	Asp	Glu	Pro	Phe	
	530					535				540						
gtc	cgg	ata	ata	cca	aag	cac	aag	aag	ttc	gaa	ggc	gcc	gga	gag	aag	1680
Val	Arg	Ile	Ile	Pro	Lys	His	Lys	Lys	Phe	Glu	Gly	Ala	Gly	Glu	Lys	
545					550					555					560	
gca	acc	act	ttc	acc	aag	agc	ata	tgg	atc	gag	gga	gct	gat	gcg	agt	1728
Ala	Thr	Thr	Phe	Thr	Lys	Ser	Ile	Trp	Ile	Glu	Gly	Ala	Asp	Ala	Ser	
				565					570						575	
gcc	atc	tct	gtt	aac	gag	gaa	gta	act	ttg	atg	gat	tgg	gga	aac	gcc	1776
Ala	Ile	Ser	Val	Asn	Glu	Glu	Val	Thr	Leu	Met	Asp	Trp	Gly	Asn	Ala	
			580						585						590	
att	gtg	aaa	gaa	atc	aca	aaa	gac	gac	gaa	ggt	cgt	gtc	act	gcg	ttg	1824
Ile	Val	Lys	Glu	Ile	Thr	Lys	Asp	Asp	Glu	Gly	Arg	Val	Thr	Ala	Leu	
		595					600									
tct	ggc	gtt	ctg	aat	ctc	caa	gga	tct	gtg	aag	act	aca	aag	ctg	aag	1872
Ser	Gly	Val	Leu	Asn	Leu	Gln	Gly	Ser	Val	Lys	Thr	Thr	Lys	Leu	Lys	
	610					615										
ctc	aca	tgg	ctt	cca	gag	act	aat	gag	ttg	gtt	aag	ctc	acg	ttg	aca	1920
Leu	Thr	Trp	Leu	Pro	Glu	Thr	Asn	Glu	Leu	Val	Lys	Leu	Thr	Leu	Thr	
625					630					635					640	
gac	ttt	gat	tat	tta	atc	acc	aag	aag	aag	cta	gag	gaa	gac	gat	gag	1968
Asp	Phe	Asp	Tyr	Leu	Ile	Thr	Lys	Lys	Lys	Leu	Glu	Glu	Asp	Asp	Glu	
				645					650						655	
gtt	gct	act	ttt	gtg	aat	cct	tac	acg	aag	aag	gaa	acg	tcg	gca	ctt	2016
Val	Ala	Thr	Phe	Val	Asn	Pro	Tyr	Thr	Lys	Lys	Glu	Thr	Ser	Ala	Leu	
			660						665							
ggt	gat	tcc	aat	atg	agg	aac	ctg	cag	cgt	ggt	gat	gtg	att	cag	ctt	2064
Gly	Asp	Ser	Asn	Met	Arg	Asn	Leu	Gln	Arg	Gly	Asp	Val	Ile	Gln	Leu	
		675					680									
gag	agg	aaa	ggc	tac	tac	aga	tgt	gat	gtg	ccg	ttt	gtc	aag	tct	tca	2112
Glu	Arg	Lys	Gly	Tyr	Tyr	Arg	Cys	Asp	Val	Pro	Phe	Val	Lys	Ser	Ser	
	690					695				700						
aaa	cct	atc	gtc	ttg	ttc	tca	atc	cca	gat	gga	agg	caa	cac	cag	cat	2160
Lys	Pro	Ile	Val	Leu	Phe	Ser	Ile	Pro	Asp	Gly	Arg	Gln	His	Gln	His	
705					710					715					720	
aag	gct	gct	aat	tga												2175
Lys	Ala	Ala	Asn													

<210> 9974
 <211> 724
 <212> PRT
 <213> Brassica napus

<400> 9974
 Met Glu Gly Ile Lys Leu Ser Phe Pro Pro Lys Thr Pro Pro Pro Leu
 1 5 10 15
 Ser Val Ile Ala Leu Ser Leu Ser Ser Pro Val Thr Ile Asp
 20 25 30
 Ser Ser Ser Ser Ala Ala Thr Thr Val Pro Thr Phe Val Phe Ser Asp
 35 40 45
 Gly Arg Lys Leu Ser Gly Thr Ser Val Leu Leu Arg Tyr Val Gly Arg
 50 55 60
 Ser Ala Lys Ser Leu Pro Gly Phe Tyr Gly His Asp Ala Phe Glu Ser
 65 70 75 80
 Ser Gln Ile Asp Glu Trp Val Asp Tyr Ala Pro Val Phe Ser Ser Gly
 85 90 95
 Ser Glu Phe Glu Asn Ala Cys Thr Arg Val Asp Asn Tyr Leu Gln Ser
 100 105 110
 Gly Thr Phe Leu Val Gly His Ser Leu Ser Ile Ala Asp Val Ala Val
 115 120 125
 Trp Ser Ala Leu Ala Ala Ser Ala Pro Arg Trp Glu Ser Leu Arg Lys
 130 135 140
 Ser Lys Lys Tyr His Asn Leu Val Arg Arg Phe Asn Ser Lys Ser Leu
 145 150 155 160
 Glu His Ala Glu Pro Leu Asn Lys Leu Ala Thr Tyr Thr Ala Lys Lys
 165 170 175
 Pro Ser Gly Lys Thr Val Ser Ala Ala Pro Arg Thr Lys Asp Gln Gln
 Seite 10546

PF59083SeqList PF59083.txt

			180					185				190			
Ala	Asp	Asn	Ala	Asn	Asp	Lys	Gly	Lys	Pro	Glu	Val	Asp	Leu	Pro	Gly
		195					200					205			
Ala	Glu	Leu	Gly	Lys	Val	Lys	Leu	Arg	Phe	Ala	Pro	Glu	Pro	Ser	Gly
	210					215					220				
Tyr	Leu	His	Ile	Gly	His	Ala	Lys	Ala	Ala	Leu	Leu	Asn	Lys	Tyr	Phe
225					230					235					240
Ala	Glu	Arg	Tyr	Gln	Gly	Glu	Val	Ile	Ile	Arg	Phe	Asp	Asp	Thr	Asn
				245					250					255	
Pro	Ala	Lys	Glu	Ser	Asn	Glu	Phe	Val	Glu	Asn	Leu	Val	Lys	Asp	Ile
			260					265					270		
Gly	Thr	Leu	Gly	Ile	Lys	Tyr	Glu	Arg	Val	Thr	Tyr	Thr	Ser	Asp	Tyr
		275					280					285			
Phe	Pro	Asp	Leu	Met	Ala	Met	Ala	Glu	Lys	Leu	Met	Gln	Glu	Gly	Lys
	290					295					300				
Ala	Tyr	Val	Asp	Asp	Thr	Pro	Arg	Glu	Gln	Met	Gln	Lys	Glu	Arg	Met
305					310					315					320
Asp	Gly	Ile	Asp	Ser	Lys	Cys	Arg	Ser	His	Thr	Ile	Glu	Glu	Asn	Leu
				325					330					335	
Asn	Leu	Trp	Arg	Glu	Met	Ile	Ala	Gly	Asn	Val	Arg	Gly	Leu	Gln	Cys
			340					345					350		
Cys	Val	Arg	Gly	Lys	Leu	Asp	Met	Gln	Asp	Pro	Asn	Lys	Ala	Met	Arg
		355					360				365				
Asp	Pro	Val	Tyr	Tyr	Arg	Cys	Asn	Pro	Met	Ser	His	His	Arg	Ile	Gly
	370					375					380				
Asn	Lys	Tyr	Lys	Ile	Tyr	Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Phe	Val
385					390					395					400
Asp	Ser	Ile	Glu	Gly	Ile	Thr	His	Ala	Leu	Arg	Ser	Ser	Glu	Tyr	His
				405					410					415	
Asp	Arg	Asn	Ala	Gln	Tyr	Tyr	Lys	Val	Leu	Glu	Asp	Met	Gly	Leu	Arg
			420					425					430		
Arg	Val	Glu	Ile	Tyr	Glu	Phe	Ser	Arg	Leu	Asn	Leu	Val	Tyr	Thr	Leu
		435					440				445				
Leu	Ser	Lys	Arg	Lys	Leu	Leu	Trp	Phe	Val	Gln	Gln	Gly	Leu	Val	Gly
	450					455					460				
Gly	Trp	Asp	Asp	Pro	Arg	Phe	Pro	Thr	Val	Gln	Gly	Ile	Val	Arg	Arg
465					470					475					480
Gly	Leu	Lys	Ile	Glu	Ala	Leu	Ile	Gln	Phe	Ile	Leu	Glu	Gln	Gly	Ala
				485					490					495	
Ser	Lys	Asn	Leu	Asn	Leu	Met	Glu	Trp	Asp	Lys	Leu	Trp	Thr	Ile	Asn
			500					505					510		
Lys	Lys	Ile	Ile	Asp	Pro	Val	Cys	Pro	Arg	His	Thr	Ala	Val	Ile	Glu
		515					520					525			
Glu	Arg	Arg	Val	Leu	Leu	Thr	Leu	Thr	Asp	Gly	Pro	Asp	Glu	Pro	Phe
	530					535					540				
Val	Arg	Ile	Ile	Pro	Lys	His	Lys	Lys	Phe	Glu	Gly	Ala	Gly	Glu	Lys
545					550					555					560
Ala	Thr	Thr	Phe	Thr	Lys	Ser	Ile	Trp	Ile	Glu	Gly	Ala	Asp	Ala	Ser
				565					570					575	
Ala	Ile	Ser	Val	Asn	Glu	Glu	Val	Thr	Leu	Met	Asp	Trp	Gly	Asn	Ala
			580					585					590		
Ile	Val	Lys	Glu	Ile	Thr	Lys	Asp	Asp	Glu	Gly	Arg	Val	Thr	Ala	Leu
		595					600					605			
Ser	Gly	Val	Leu	Asn	Leu	Gln	Gly	Ser	Val	Lys	Thr	Thr	Lys	Leu	Lys
	610					615					620				
Leu	Thr	Trp	Leu	Pro	Glu	Thr	Asn	Glu	Leu	Val	Lys	Leu	Thr	Leu	Thr
625					630					635					640
Asp	Phe	Asp	Tyr	Leu	Ile	Thr	Lys	Lys	Lys	Leu	Glu	Glu	Asp	Asp	Glu
				645					650					655	
Val	Ala	Thr	Phe	Val	Asn	Pro	Tyr	Thr	Lys	Lys	Glu	Thr	Ser	Ala	Leu
			660					665					670		
Gly	Asp	Ser	Asn	Met	Arg	Asn	Leu	Gln	Arg	Gly	Asp	Val	Ile	Gln	Leu
		675					680					685			
Glu	Arg	Lys	Gly	Tyr	Tyr	Arg	Cys	Asp	Val	Pro	Phe	Val	Lys	Ser	Ser
	690					695					700				
Lys	Pro	Ile	Val	Leu	Phe	Ser	Ile	Pro	Asp	Gly	Arg	Gln	His	Gln	His
705					710					715					720
Lys	Ala	Ala	Asn												

PF59083SeqList PF59083.txt

<210> 9975
<211> 2202
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(2202)

```

<400> 9975
atg gac atc aaa acc ttt gcc ttc gcc cca tct tct ccg ccg tta tcg      48
Met Asp Ile Lys Thr Phe Ala Phe Ala Pro Ser Ser Pro Pro Leu Ser
 1      5      10      15
gta atc gcc gcc gcc aag ctc gcc gga atc tct ccc acg att gat acc      96
Val Ile Ala Ala Lys Leu Ala Gly Ile Ser Pro Thr Ile Asp Thr
      20      25      30
gct ctc tct cct gac tca cct ccc tca ttt atc ttc tcc gat ggg cta     144
Ala Leu Ser Pro Asp Ser Pro Pro Ser Phe Ile Phe Ser Asp Gly Leu
      35      40      45
aag ttg cac gga cca tat gct ctt cta cgt tat atc ggg cga gtt gcc     192
Lys Leu His Gly Pro Tyr Ala Leu Leu Arg Tyr Ile Gly Arg Val Ala
      50      55      60
agc ctt cct aat ttc tat ggg caa aat cca ttt gaa tct agc cag att     240
Ser Leu Pro Asn Phe Tyr Gly Gln Asn Pro Phe Glu Ser Ser Gln Ile
      65      70      75
gat gaa tgg ctg gac tat gct cct atc ctc tca tcg ggc cct gct ttt     288
Asp Glu Trp Leu Asp Tyr Ala Pro Ile Leu Ser Ser Gly Pro Ala Phe
      85      90      95
gag aat gca tgc aaa tat ata gat gag tac ctg gag aag cgt act ctt     336
Glu Asn Ala Cys Lys Tyr Ile Asp Glu Tyr Leu Glu Lys Arg Thr Leu
      100      105      110
ttg gtt ggt tat tca ttg tca att gca gac cta gca atc tgg gca ggt     384
Leu Val Gly Tyr Ser Leu Ser Ile Ala Asp Leu Ala Ile Trp Ala Gly
      115      120      125
ctt gca ggt tct gga aag aga tgg gaa agt cta agg aag tca aag aaa     432
Leu Ala Gly Ser Gly Lys Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys
      130      135      140
tat cca aat ctt gca cga tgg ttc aat tca ata gtg gaa gaa cat ggt     480
Tyr Pro Asn Leu Ala Arg Trp Phe Asn Ser Ile Val Glu Glu His Gly
      145      150      155
act gcc tta aat gaa gtc aca tca gta tat gct ggc aaa aaa gga ttg     528
Thr Ala Leu Asn Glu Val Thr Ser Val Tyr Ala Gly Lys Lys Gly Leu
      165      170      175
gga gaa cca aca gcc acc aag tca aaa gaa cag tca gta aac act gat     576
Gly Glu Pro Thr Ala Thr Lys Ser Lys Glu Gln Ser Val Asn Thr Asp
      180      185      190
aaa gtg aag aag gtg aat gga gat gta tct gag aac aac aaa gga gga     624
Lys Val Lys Lys Val Asn Gly Asp Val Ser Glu Asn Asn Lys Gly Gly
      195      200      205
agc aaa cca tca gca gaa ata gat ctt cca gat gct gaa gtt gga aaa     672
Ser Lys Pro Ser Ala Glu Ile Asp Leu Pro Asp Ala Glu Val Gly Lys
      210      215      220
gtt cgc ttg cga ttt gcc cct gaa cca agt ggt tat ctt cat att gga     720
Val Arg Leu Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly
      225      230      235
cac tca aaa gca gct ttg ttg aac aaa tat ttt gct gag cga tac aag     768
His Ser Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Lys
      245      250      255
ggt cag gtt att gtg cgt ttt gat gat acc aat cct gct aaa gaa agc     816
Gly Gln Val Ile Val Arg Phe Asp Asp Thr Asn Pro Ala Lys Glu Ser
      260      265      270
aat gaa ttt gtg gac aac ctt att aaa gat att gat aca ttg ggt atc     864
Asn Glu Phe Val Asp Asn Leu Ile Lys Asp Ile Asp Thr Leu Gly Ile
      275      280      285
aaa tat gaa caa att aca tat acg tca gat tac ttc cct gag ttg atg     912
Lys Tyr Glu Gln Ile Thr Tyr Thr Ser Asp Tyr Phe Pro Glu Leu Met
      290      295      300
gag atg gct gaa aaa tta att cgc cag ggt aaa gca tat gtt gat gac     960

```

PF59083SeqList PF59083.txt

Glu 305	Met	Ala	Glu	Lys	Leu 310	Ile	Arg	Gln	Gly	Lys 315	Ala	Tyr	Val	Asp	Asp 320	
aca	cca	cgt	gaa	caa	atg	caa	aaa	gag	aga	atg	gat	ggc	ata	gat	tct	1008
Thr	Pro	Arg	Glu	Gln 325	Met	Gln	Lys	Glu	Arg 330	Met	Asp	Gly	Ile	Asp 335	Ser	
aaa	tgc	aga	aat	aat	agt	gta	gag	gag	aat	cta	aaa	ttg	ttg	aag	gaa	1056
Lys	Cys	Arg	Asn	Asn	Ser	Val	Glu	Glu	Asn	Leu	Lys	Leu	Trp 350	Lys	Glu	
atg	att	gca	gga	aca	gag	agg	ggc	ttg	cag	tgt	tgt	gtc	cgt	ggc	aag	1104
Met	Ile	Ala 355	Gly	Thr	Glu	Arg	Gly 360	Leu	Gln	Cys	Cys	Val 365	Arg	Gly	Lys	
ttg	gat	atg	cag	gac	cca	aac	aaa	tca	ctt	aga	gat	cct	gtt	tat	tat	1152
Leu	Asp 370	Met	Gln	Asp	Pro	Asn 375	Lys	Ser	Leu	Arg	Asp 380	Pro	Val	Tyr	Tyr	
cgt	tgc	aat	cca	atg	ccc	cat	cat	aga	att	gga	tcc	aag	tat	aaa	gtg	1200
Arg 385	Cys	Asn	Pro	Met	Pro 390	His	His	Arg	Ile	Gly 395	Ser	Lys	Tyr	Lys	Val 400	
tat	cca	act	tat	gat	ttt	gct	tgt	cca	tat	gtt	gat	tct	ata	gaa	gga	1248
Tyr	Pro	Thr	Tyr	Asp 405	Phe	Ala	Cys	Pro	Tyr 410	Val	Asp	Ser	Ile	Glu 415	Gly	
atc	acg	cat	gcc	ctt	cga	tct	agt	gaa	tac	cat	gat	cgc	aat	gcc	cag	1296
Ile	Thr	His	Ala 420	Leu	Arg	Ser	Ser	Glu 425	Tyr	His	Asp	Arg	Asn 430	Ala	Gln	
tat	tac	tgg	att	caa	gag	gac	atg	ggg	ctt	aga	aaa	gtt	ctt	atc	tac	1344
Tyr	Tyr	Trp 435	Ile	Gln	Glu	Asp 440	Met	Gly	Leu	Arg	Lys	Val 445	Leu	Ile	Tyr	
gaa	ttt	agc	cgg	ttg	aat	atg	gtc	tac	act	ctt	ctg	agc	aaa	cga	aag	1392
Glu	Phe 450	Ser	Arg	Leu	Asn	Met 455	Val	Tyr	Thr	Leu	Leu 460	Ser	Lys	Arg	Lys	
ctt	ttg	tgg	ttt	gta	caa	aat	ggg	aaa	gtt	gat	gga	tgg	gat	gat	gca	1440
Leu 465	Leu	Trp	Phe	Val	Gln 470	Asn	Gly	Lys	Val	Asp 475	Gly	Trp	Asp	Asp	Ala 480	
cga	ttt	cct	aca	gtg	caa	gga	att	gtg	cgt	aga	ggg	ttg	aaa	att	gaa	1488
Arg	Phe	Pro	Thr	Val 485	Gln	Gly	Ile	Val	Arg 490	Arg	Gly	Leu	Lys	Ile 495	Glu	
gcc	ctg	ata	cag	ttt	att	gtt	gag	cag	ggg	gcg	tcc	aaa	aat	ctc	aat	1536
Ala	Leu	Ile	Gln	Phe	Ile	Val	Glu	Gln 505	Gly	Ala	Ser	Lys	Asn 510	Leu	Asn	
ctc	atg	gaa	tgg	gac	aag	ctc	tgg	acc	att	aat	aag	aag	att	att	gac	1584
Leu	Met	Glu 515	Trp	Asp	Lys	Leu	Trp 520	Thr	Ile	Asn	Lys	Lys 525	Ile	Ile	Asp	
cct	gtc	tgt	cct	aga	cac	act	gct	gtc	att	gca	gac	aga	cgt	gtg	ttg	1632
Pro	Val 530	Cys	Pro	Arg	His	Thr 535	Ala	Val	Ile	Ala	Asp 540	Arg	Arg	Val	Leu	
ttg	act	ctc	acc	gat	ggg	cct	gag	aaa	cca	ttt	gtc	cgc	atc	ata	cct	1680
Leu 545	Thr	Leu	Thr	Asp	Gly 550	Pro	Glu	Lys	Pro	Phe 555	Val	Arg	Ile	Ile	Pro 560	
cgg	cac	aag	aaa	tat	gaa	gct	gcc	gga	gat	aaa	gct	aca	aca	tat	act	1728
Arg	His	Lys	Lys	Tyr 565	Glu	Ala	Ala	Gly	Asp 570	Lys	Ala	Thr	Thr	Tyr 575	Thr	
aaa	agg	ata	tgg	ctt	gac	ctt	gct	gat	gca	gtg	tct	tta	tca	gca	ggg	1776
Lys	Arg	Ile	Trp 580	Leu	Asp	Leu	Ala	Asp 585	Ala	Val	Ser	Leu	Ser	Ala	Gly	
gag	gaa	gta	aca	ttg	atg	gat	tgg	gga	aat	gcc	ata	gtg	aag	gaa	ata	1824
Glu	Glu	Val 595	Thr	Leu	Met	Asp	Trp 600	Gly	Asn	Ala	Ile	Val 605	Lys	Glu	Ile	
gag	aag	gac	caa	gat	gga	aat	atc	aca	ggg	ttg	agt	ggg	gtt	ttg	cat	1872
Glu	Lys 610	Asp	Gln	Asp	Gly	Asn 615	Ile	Thr	Gly	Leu	Ser 620	Gly	Val	Leu	His	
ctt	gaa	gga	tct	gtg	aag	acc	aca	aaa	ttg	aaa	ctc	act	tgg	cta	cct	1920
Leu 625	Glu	Gly	Ser	Val	Lys 630	Thr	Thr	Lys	Leu	Lys 635	Leu	Thr	Trp	Leu	Pro 640	
gag	ata	gat	gaa	cta	gtt	agc	ctg	aca	tta	gtg	gag	ttt	gat	tat	cta	1968
Glu	Ile	Asp	Glu	Leu 645	Val	Ser	Leu	Thr	Leu 650	Val	Glu	Phe	Asp	Tyr 655	Leu	
att	aca	aag	aaa	aag	ctt	gaa	gaa	ggg	gag	gat	ttc	att	gat	gtg	gtt	2016
Ile	Thr	Lys	Lys	Lys	Leu	Glu	Glu	Gly 665	Glu	Asp	Phe	Ile	Asp 670	Val	Val	
aac	cca	tgt	acc	aaa	aag	gag	act	tta	gct	tat	gga	gac	tcc	aac	atg	2064

PF59083SeqList PF59083.txt

Asn	Pro	Cys	Thr	Lys	Lys	Glu	Thr	Leu	Ala	Tyr	Gly	Asp	Ser	Asn	Met	
		675					680					685				
cga	aat	ctt	cag	cgt	gga	gat	tta	ttg	caa	ctg	gag	aga	aag	gga	tat	2112
Arg	Asn	Leu	Gln	Arg	Gly	Asp	Leu	Leu	Gln	Leu	Glu	Arg	Lys	Gly	Tyr	
	690					695					700					
ttc	agg	tgt	gat	tta	ccc	ttc	att	cgc	ccc	tca	caa	atc	gtg	cta		2160
Phe	Arg	Cys	Asp	Leu	Pro	Phe	Ile	Arg	Pro	Ser	Gln	Pro	Ile	Val	Leu	
705					710					715					720	
tat	gca	atc	cct	gat	ggc	agg	caa	cag	aca	agt	ttg	aag	taa			2202
Tyr	Ala	Ile	Pro	Asp	Gly	Arg	Gln	Gln	Thr	Ser	Leu	Lys				
				725					730							

<210> 9976
 <211> 733
 <212> PRT
 <213> Glycine max

<400> 9976

Met	Asp	Ile	Lys	Thr	Phe	Ala	Phe	Ala	Pro	Ser	Ser	Pro	Pro	Leu	Ser	
1				5					10					15		
Val	Ile	Ala	Ala	Lys	Leu	Ala	Gly	Ile	Ser	Pro	Thr	Ile	Asp	Thr		
			20				25					30				
Ala	Leu	Ser	Pro	Asp	Ser	Pro	Pro	Ser	Phe	Ile	Phe	Ser	Asp	Gly	Leu	
		35				40					45					
Lys	Leu	His	Gly	Pro	Tyr	Ala	Leu	Leu	Arg	Tyr	Ile	Gly	Arg	Val	Ala	
	50					55					60					
Ser	Leu	Pro	Asn	Phe	Tyr	Gly	Gln	Asn	Pro	Phe	Glu	Ser	Ser	Gln	Ile	
65					70					75					80	
Asp	Glu	Trp	Leu	Asp	Tyr	Ala	Pro	Ile	Leu	Ser	Ser	Gly	Pro	Ala	Phe	
				85					90					95		
Glu	Asn	Ala	Cys	Lys	Tyr	Ile	Asp	Glu	Tyr	Leu	Glu	Lys	Arg	Thr	Leu	
			100					105					110			
Leu	Val	Gly	Tyr	Ser	Leu	Ser	Ile	Ala	Asp	Leu	Ala	Ile	Trp	Ala	Gly	
		115					120					125				
Leu	Ala	Gly	Ser	Gly	Lys	Arg	Trp	Glu	Ser	Leu	Arg	Lys	Ser	Lys	Lys	
	130					135					140					
Tyr	Pro	Asn	Leu	Ala	Arg	Trp	Phe	Asn	Ser	Ile	Val	Glu	Glu	His	Gly	
145					150					155					160	
Thr	Ala	Leu	Asn	Glu	Val	Thr	Ser	Val	Tyr	Ala	Gly	Lys	Lys	Gly	Leu	
			165						170					175		
Gly	Glu	Pro	Thr	Ala	Thr	Lys	Ser	Lys	Glu	Gln	Ser	Val	Asn	Thr	Asp	
			180					185					190			
Lys	Val	Lys	Lys	Val	Asn	Gly	Asp	Val	Ser	Glu	Asn	Asn	Lys	Gly	Gly	
		195					200					205				
Ser	Lys	Pro	Ser	Ala	Glu	Ile	Asp	Leu	Pro	Asp	Ala	Glu	Val	Gly	Lys	
	210					215					220					
Val	Arg	Leu	Arg	Phe	Ala	Pro	Glu	Pro	Ser	Gly	Tyr	Leu	His	Ile	Gly	
225					230					235					240	
His	Ser	Lys	Ala	Ala	Leu	Leu	Asn	Lys	Tyr	Phe	Ala	Glu	Arg	Tyr	Lys	
			245						250					255		
Gly	Gln	Val	Ile	Val	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Ala	Lys	Glu	Ser	
			260					265					270			
Asn	Glu	Phe	Val	Asp	Asn	Leu	Ile	Lys	Asp	Ile	Asp	Thr	Leu	Gly	Ile	
		275					280					285				
Lys	Tyr	Glu	Gln	Ile	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Pro	Glu	Leu	Met	
	290					295					300					
Glu	Met	Ala	Glu	Lys	Leu	Ile	Arg	Gln	Gly	Lys	Ala	Tyr	Val	Asp	Asp	
305					310					315					320	
Thr	Pro	Arg	Glu	Gln	Met	Gln	Lys	Glu	Arg	Met	Asp	Gly	Ile	Asp	Ser	
				325					330					335		
Lys	Cys	Arg	Asn	Asn	Ser	Val	Glu	Glu	Asn	Leu	Lys	Leu	Trp	Lys	Glu	
			340					345					350			
Met	Ile	Ala	Gly	Thr	Glu	Arg	Gly	Leu	Gln	Cys	Cys	Val	Arg	Gly	Lys	
		355					360					365				
Leu	Asp	Met	Gln	Asp	Pro	Asn	Lys	Ser	Leu	Arg	Asp	Pro	Val	Tyr	Tyr	
	370					375					380					
Arg	Cys	Asn	Pro	Met	Pro	His	His	Arg	Ile	Gly	Ser	Lys	Tyr	Lys	Val	
385					390					395					400	
Tyr	Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Tyr	Val	Asp	Ser	Ile	Glu	Gly	

PF59083SeqList PF59083.txt

405 410 415
 Ile Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln
 420 425 430
 Tyr Tyr Trp Ile Gln Glu Asp Met Gly Leu Arg Lys Val Leu Ile Tyr
 435 440 445
 Glu Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys
 450 455 460
 Leu Leu Trp Phe Val Gln Asn Gly Lys Val Asp Gly Trp Asp Asp Ala
 465 470 475 480
 Arg Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Ile Glu
 485 490 495
 Ala Leu Ile Gln Phe Ile Val Glu Gln Gly Ala Ser Lys Asn Leu Asn
 500 505 510
 Leu Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp
 515 520 525
 Pro Val Cys Pro Arg His Thr Ala Val Ile Ala Asp Arg Arg Val Leu
 530 535 540
 Leu Thr Leu Thr Asp Gly Pro Glu Lys Pro Phe Val Arg Ile Ile Pro
 545 550 555 560
 Arg His Lys Lys Tyr Glu Ala Ala Gly Asp Lys Ala Thr Thr Tyr Thr
 565 570 575
 Lys Arg Ile Trp Leu Asp Leu Ala Asp Ala Val Ser Leu Ser Ala Gly
 580 585 590
 Glu Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile
 595 600 605
 Glu Lys Asp Gln Asp Gly Asn Ile Thr Gly Leu Ser Gly Val Leu His
 610 615 620
 Leu Glu Gly Ser Val Lys Thr Thr Lys Leu Lys Leu Thr Trp Leu Pro
 625 630 635 640
 Glu Ile Asp Glu Leu Val Ser Leu Thr Leu Val Glu Phe Asp Tyr Leu
 645 650 655
 Ile Thr Lys Lys Lys Leu Glu Glu Gly Glu Asp Phe Ile Asp Val Val
 660 665 670
 Asn Pro Cys Thr Lys Lys Glu Thr Leu Ala Tyr Gly Asp Ser Asn Met
 675 680 685
 Arg Asn Leu Gln Arg Gly Asp Leu Leu Gln Leu Glu Arg Lys Gly Tyr
 690 695 700
 Phe Arg Cys Asp Leu Pro Phe Ile Arg Pro Ser Gln Pro Ile Val Leu
 705 710 715 720
 Tyr Ala Ile Pro Asp Gly Arg Gln Gln Thr Ser Leu Lys
 725 730

<210> 9977
 <211> 2385
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(2385)

<400> 9977
 atg ccg gcg aag gac gac ggc tcc gac aag gag aag tgc ctc gat ctc 48
 Met Pro Ala Lys Asp Asp Gly Ser Asp Lys Glu Lys Cys Leu Asp Leu
 1 5 10 15
 ttt ctc aaa atc ggc tta gac gag cgc acc gct aaa aac acc gtc gca 96
 Phe Leu Lys Ile Gly Leu Asp Glu Arg Thr Ala Lys Asn Thr Val Ala
 20 25 30
 aac aac aaa gtc acc gcc aat ctc act gca gtc atc gac gag gcc ggt 144
 Asn Asn Lys Val Thr Ala Asn Leu Thr Ala Val Ile Asp Glu Ala Gly
 35 40 45
 gct act gat gga tgc agc cga acg gtc gga aat ctt ctt tac acg gtt 192
 Ala Thr Asp Gly Cys Ser Arg Thr Val Gly Asn Leu Leu Tyr Thr Val
 50 55 60
 gca acg aag tac cct gca aat gcc ttg cca cat cgc cca aca tta cta 240
 Ala Thr Lys Tyr Pro Ala Asn Ala Leu Pro His Arg Pro Thr Leu Leu
 65 70 75 80
 cag tac att gtc tcg tta aag gtg aaa aca act gcc cag tta gat gca 288
 Gln Tyr Ile Val Ser Leu Lys Val Lys Thr Thr Ala Gln Leu Asp Ala

PF59083SeqList PF59083.txt

														85															90															95							
gca	tta	tca	ttt	ctt	gct	acc	aca	ggc	tcc	gag	aat	ctt	gat	ttg	aac	336																																			
Ala	Leu	Ser	Phe	Leu	Ala	Thr	Thr	Gly	Ser	Glu	Asn	Leu	Asp	Leu	Asn																																				
																100																	105																	110	
aag	ttt	gaa	gaa	gct	tgt	ggg	gtt	ggg	gtt	gag	gtt	tca	gaa	gaa	gat	384																																			
Lys	Phe	Glu	Glu	Ala	Cys	Gly	Val	Gly	Val	Glu	Val	Ser	Glu	Glu	Asp																																				
																115																	120																	125	
atc	aaa	caa	gct	gtt	aat	gaa	gtt	gtg	gag	gag	aac	aag	gct	aca	att	432																																			
Ile	Lys	Gln	Ala	Val	Asn	Glu	Val	Val	Glu	Glu	Asn	Lys	Ala	Thr	Ile																																				
																130																	135																	140	
ttg	gag	cta	cgt	tat	cga	aat	gtg	ggg	gag	ttg	ctg	ggg	cat	ctg		480																																			
Leu	Glu	Leu	Arg	Tyr	Arg	Thr	Asn	Val	Gly	Glu	Leu	Leu	Gly	His	Leu																																				
																145																	150																	155	
cgc	aag	agg	ctg	cca	tgg	ggg	gat	gca	aaa	gtt	gcc	aag	caa	ctt	gtt	528																																			
Arg	Lys	Arg	Leu	Pro	Trp	Gly	Asp	Ala	Lys	Val	Ala	Lys	Gln	Leu	Val																																				
																165																	170																	175	
gat	gca	aaa	cta	tat	gaa	cta	ctt	ggg	gat	cgg	aca	gca	gca	gat	gat	576																																			
Asp	Ala	Lys	Leu	Tyr	Glu	Leu	Leu	Gly	Asp	Arg	Thr	Ala	Ala	Asp	Asp																																				
																180																	185																	190	
gaa	aag	cct	tct	aga	aag	aag	aag	gag	aaa	cct	gca	aaa	gta	gag	gat	624																																			
Glu	Lys	Pro	Ser	Arg	Lys	Lys	Lys	Glu	Lys	Pro	Ala	Lys	Val	Glu	Asp																																				
																195																	200																	205	
aag	gca	gct	cct	gtt	tct	acc	cct	gaa	aag	tca	cct	gaa	gaa	gac	gtt	672																																			
Lys	Ala	Ala	Pro	Val	Ser	Thr	Pro	Glu	Lys	Ser	Pro	Glu	Glu	Asp	Val																																				
																210																	215																	220	
aat	cca	ttt	tta	ata	ttc	cct	aat	cca	gag	gaa	aat	ttc	aag	gtg	cat	720																																			
Asn	Pro	Phe	Leu	Ile	Phe	Pro	Asn	Pro	Glu	Glu	Asn	Phe	Lys	Val	His																																				
																225																	230																	235	
act	gaa	gtg	cct	ttt	agt	gat	ggg	agt	att	ttg	aga	tgt	tgc	aat	aca	768																																			
Thr	Glu	Val	Pro	Phe	Ser	Asp	Gly	Ser	Ile	Leu	Arg	Cys	Cys	Asn	Thr																																				
																245																	250																	255	
aga	gat	ctg	ctt	gac	aaa	cac	tta	aaa	gca	aca	ggg	gga	aaa	gtc	ttg	816																																			
Arg	Asp	Leu	Leu	Asp	Lys	His	Leu	Lys	Ala	Thr	Gly	Gly	Lys	Val	Leu																																				
																260																	265																	270	
acc	cgg	ttt	cca	ccc	gaa	cct	aat	gga	tat	ttg	cat	att	ggc	cat	gca	864																																			
Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ala																																				
																275																	280																	285	
aaa	gca	atg	ttt	att	gat	ttt	ggg	ttg	gcg	aaa	gac	agg	gat	gga	ggg	912																																			
Lys	Ala	Met	Phe	Ile	Asp	Phe	Gly	Leu	Ala	Lys	Asp	Arg	Asp	Gly	Gly																																				
																290																	295																	300	
tgc	tat	ctg	agg	tat	gat	gat	aca	aat	cct	gaa	gca	gaa	aag	aaa	gag	960																																			
Cys	Tyr	Leu	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys	Lys	Glu																																				
																305																	310																	315	
tat	att	gat	cat	att	gaa	gaa	att	gtc	cag	tgg	atg	ggg	tgg	aaa	cca	1008																																			
Tyr	Ile	Asp	His	Ile	Glu	Glu	Ile	Val	Gln	Trp	Met	Gly	Trp	Lys	Pro																																				
																325																	330																	335	
ttt	aag	att	act	tac	aca	agt	gat	tac	ttc	caa	gaa	ttg	tac	gaa	tta	1056																																			
Phe	Lys	Ile	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Gln	Glu	Leu	Tyr	Glu	Leu																																				
																340																	345																	350	
gca	gtg	gag	ctc	ata	aaa	aag	ggg	cat	gct	tat	gtt	gat	cat	cag	aca	1104																																			
Ala	Val	Glu	Leu	Ile	Lys	Lys	Gly	His	Ala	Tyr	Val	Asp	His	Gln	Thr																																				
																355																	360																	365	
cct	gat	gag	ata	aag	gag	tat	agg	gag	aag	aaa	ctg	aac	agt	cct	tgg	1152																																			
Pro	Asp	Glu	Ile	Lys	Glu	Tyr	Arg	Glu	Lys	Lys	Leu	Asn	Ser	Pro	Trp																																				
																370																	375																	380	
aga	gac	aga	cca	att	tca	gag	tca	ttg	aaa	ctc	ttt	gag	gat	atg	aaa	1200																																			
Arg	Asp	Arg	Pro	Ile	Ser	Glu	Ser	Leu	Lys	Leu	Phe	Glu	Asp	Met	Lys																																				
																385																	390																	395	
aat	ggc	agt	atc	gaa	gaa	gga	aaa	gcc	aca	ctt	aga	atg	aag	caa	gac	1248																																			
Asn	Gly	Ser	Ile	Glu	Glu	Gly	Lys	Ala	Thr	Leu	Arg	Met	Lys	Gln	Asp																																				
																405																	410																	415	
atg	cag	agt	gat	aac	tac	aat	atg	tat	gac	ctt	att	gca	tat	aga	att	1296																																			
Met	Gln	Ser	Asp	Asn	Tyr	Asn	Met	Tyr	Asp	Leu	Ile	Ala	Tyr	Arg	Ile																																				
																420																	425																	430	
aag	ttt	acc	cca	cac	cct	cat	gct	gga	gac	aaa	tgg	tgt	atc	tat	cca	1344																																			
Lys	Phe	Thr	Pro	His	Pro	His	Ala	Gly	Asp	Lys	Trp	Cys	Ile	Tyr	Pro																																				
																435																	440																	445	
agt	tat	gat	tat	gca	cac	tgc	att	gtg	gat	tct	cta	gag	aat	atc	aca	1392																																			
Ser	Tyr	Asp	Tyr	Ala	His	Cys	Ile	Val	Asp	Ser	Leu	Glu	Asn	Ile	Thr																																				

PF59083SeqList PF59083.txt

450	cat tca ctg tgt aca ctt	455	gaa ttt gag aca cgt	460	cgt gca tca tac tat	1440
His Ser Leu Cys Thr Leu	470	Glu Phe Glu Thr Arg	475	Arg Arg Ala Ser Tyr Tyr	480	
465	tgg ttg ttg cat gcg tta	470	ggc att tac caa cct	475	tat gtg tgg gag tat	1488
Trp Leu Leu His Ala	485	Gly Ile Tyr Gln Pro	490	Tyr Val Trp Glu Tyr	495	
tca agg ttg aat gtc tct	500	aac aca gtt atg tca	505	aag cgt aag cta aat	510	1536
Ser Arg Leu Asn Val Ser	500	Asn Thr Val Met Ser	510	Lys Arg Lys Leu Asn	515	
cgt cta gtt aca gag aag	515	tgg gtt gat ggg tgg	520	gat gat cct cgt ttg	525	1584
Arg Leu Val Thr Glu Lys	520	Trp Val Asp Gly Trp	525	Asp Asp Pro Arg Leu	530	
atg aca cta gct ggt ttg	530	cgg cgt aga ggc atg	535	acc cca act gca atc	540	1632
Met Thr Leu Ala Gly Leu	535	Arg Arg Arg Gly Met	540	Thr Pro Thr Ala Ile	545	
aat gct ttt gtc cga gga	545	att gga ata act aga	550	agt gat ggc act ttg	555	1680
Asn Ala Phe Val Arg Gly	550	Ile Gly Ile Thr Arg	555	Ser Asp Gly Thr Leu	560	
545	att tct gtg gaa cgc ctt	555	agg gaa gaa ttg aac	565	aaa aaa	1728
Ile Ser Val Glu Arg Leu	565	Glu Tyr His Val Arg	570	Glu Glu Leu Asn Lys	575	
aca gca cct cgt gca atg	580	gtt gtc cta cat cca	585	ctc aag gtt gtc att	590	1776
Thr Ala Pro Arg Ala Met	580	Val Val Leu His Pro	590	Leu Lys Val Val Ile	595	
act aat ctt gaa gcc aac	595	tca gca att gag gtt	600	gat gca aag aaa tgg	605	1824
Thr Asn Leu Glu Ala Asn	600	Ser Ala Ile Glu Val	605	Asp Ala Lys Lys Trp	610	
cct gat gct caa gct gat	610	gat gct tct gct ttc	615	tac aag att cca ttt	620	1872
Pro Asp Ala Gln Ala Asp	615	Asp Ala Ser Ala Phe	620	Tyr Lys Ile Pro Phe	625	
tcc aat gtt gta tat att	625	gaa cat tcg gac ttc	630	cgg atg caa gat tca	635	1920
Ser Asn Val Val Tyr Ile	630	Glu His Ser Asp Phe	635	Arg Met Gln Asp Ser	640	
625	aaa gat tat tat ggc ctt	645	gtg ata ctc aga tat	650	tat tat	1968
Lys Asp Tyr Tyr Gly Leu	645	Ala Pro Gly Lys Ser	650	Val Ile Leu Arg Tyr	655	
gca ttt cct ata aag tgc	660	act gaa gtt att cta	665	gct gat gat aat gag	670	2016
Ala Phe Pro Ile Lys Cys	660	Thr Glu Val Ile Leu	670	Ala Asp Asp Asn Glu	675	
act att ctt gaa att cga	675	gcc gag tat gat cct	680	tca aag aag acc aag	685	2064
Thr Ile Leu Glu Ile Arg	680	Ala Glu Tyr Asp Pro	685	Ser Lys Lys Thr Lys	690	
cct aag ggg gtt ctc cat	690	tgg gtt gct caa cct	695	tct cct gga gtt gat	700	2112
Pro Lys Gly Val Leu His	695	Trp Val Ala Gln Pro	700	Ser Pro Gly Val Asp	705	
cca ttg aag gtg gaa gtc	705	aga ttg ttt gag agg	710	cta ttc cta tca gag	715	2160
Pro Leu Lys Val Glu Val	710	Arg Leu Phe Glu Arg	715	Leu Phe Leu Ser Glu	720	
aat ccc gct gaa ctt gac	725	aac tgg ctt ggc gat	730	ttg aac cca aat tcc	735	2208
Asn Pro Ala Glu Leu Asp	725	Asn Trp Leu Gly Asp	730	Leu Asn Pro Asn Ser	735	
aaa gtg ata att ccc gat	740	gca tat ggt gtg tct	745	tcc ata cag aat gca	750	2256
Lys Val Ile Ile Pro Asp	740	Ala Tyr Gly Val Ser	745	Ser Ile Gln Asn Ala	755	
aaa gtt ggg gac aat ttc	755	caa ttt gaa aga tta	760	ggc tat ttt gtg gtt	765	2304
Lys Val Gly Asp Asn Phe	760	Gln Phe Glu Arg Leu	765	Gly Tyr Phe Val Val	770	
gac cgg gac tcg aca tca	770	gaa aaa ctt gtt ttt	775	aat agg act gtc acc	780	2352
Asp Arg Asp Ser Thr Ser	775	Glu Lys Leu Val Phe	780	Asn Arg Thr Val Thr	785	
tta aag ggc agc tat agc	785	aaa ggt gga aag tag	790	Lys Gly Gly Lys	795	2385
Leu Lys Gly Ser Tyr Ser	790	Lys Gly Gly Lys	795		800	

<210> 9978
 <211> 794
 <212> PRT
 <213> Glycine max

PF59083SeqList PF59083.txt

<400> 9978

```

Met Pro Ala Lys Asp Asp Gly Ser Asp Lys Glu Lys Cys Leu Asp Leu
1      5      10      15
Phe Leu Lys Ile Gly Leu Asp Glu Arg Thr Ala Lys Asn Thr Val Ala
      20      25      30
Asn Asn Lys Val Thr Ala Asn Leu Thr Ala Val Ile Asp Glu Ala Gly
      35      40      45
Ala Thr Asp Gly Cys Ser Arg Thr Val Gly Asn Leu Leu Tyr Thr Val
      50      55      60
Ala Thr Lys Tyr Pro Ala Asn Ala Leu Pro His Arg Pro Thr Leu Leu
65      70      75      80
Gln Tyr Ile Val Ser Leu Lys Val Lys Thr Thr Ala Gln Leu Asp Ala
      85      90      95
Ala Leu Ser Phe Leu Ala Thr Thr Gly Ser Glu Asn Leu Asp Leu Asn
      100      105      110
Lys Phe Glu Glu Ala Cys Gly Val Gly Val Glu Val Ser Glu Glu Asp
      115      120      125
Ile Lys Gln Ala Val Asn Glu Val Val Glu Glu Asn Lys Ala Thr Ile
130      135      140
Leu Glu Leu Arg Tyr Arg Thr Asn Val Gly Glu Leu Leu Gly His Leu
145      150      155      160
Arg Lys Arg Leu Pro Trp Gly Asp Ala Lys Val Ala Lys Gln Leu Val
      165      170      175
Asp Ala Lys Leu Tyr Glu Leu Leu Gly Asp Arg Thr Ala Ala Asp Asp
      180      185      190
Glu Lys Pro Ser Arg Lys Lys Lys Glu Lys Pro Ala Lys Val Glu Asp
      195      200      205
Lys Ala Ala Pro Val Ser Thr Pro Glu Lys Ser Pro Glu Glu Asp Val
210      215      220
Asn Pro Phe Leu Ile Phe Pro Asn Pro Glu Glu Asn Phe Lys Val His
225      230      235      240
Thr Glu Val Pro Phe Ser Asp Gly Ser Ile Leu Arg Cys Cys Asn Thr
      245      250      255
Arg Asp Leu Leu Asp Lys His Leu Lys Ala Thr Gly Gly Lys Val Leu
      260      265      270
Thr Arg Phe Pro Pro Glu Pro Asn Gly Tyr Leu His Ile Gly His Ala
      275      280      285
Lys Ala Met Phe Ile Asp Phe Gly Leu Ala Lys Asp Arg Asp Gly Gly
290      295      300
Cys Tyr Leu Arg Tyr Asp Asp Thr Asn Pro Glu Ala Glu Lys Lys Glu
305      310      315      320
Tyr Ile Asp His Ile Glu Glu Ile Val Gln Trp Met Gly Trp Lys Pro
      325      330      335
Phe Lys Ile Thr Tyr Thr Ser Asp Tyr Phe Gln Glu Leu Tyr Glu Leu
      340      345      350
Ala Val Glu Leu Ile Lys Lys Gly His Ala Tyr Val Asp His Gln Thr
      355      360      365
Pro Asp Glu Ile Lys Glu Tyr Arg Glu Lys Lys Leu Asn Ser Pro Trp
370      375      380
Arg Asp Arg Pro Ile Ser Glu Ser Leu Lys Leu Phe Glu Asp Met Lys
385      390      395      400
Asn Gly Ser Ile Glu Glu Gly Lys Ala Thr Leu Arg Met Lys Gln Asp
      405      410      415
Met Gln Ser Asp Asn Tyr Asn Met Tyr Asp Leu Ile Ala Tyr Arg Ile
      420      425      430
Lys Phe Thr Pro His Pro His Ala Gly Asp Lys Trp Cys Ile Tyr Pro
      435      440      445
Ser Tyr Asp Tyr Ala His Cys Ile Val Asp Ser Leu Glu Asn Ile Thr
450      455      460
His Ser Leu Cys Thr Leu Glu Phe Glu Thr Arg Arg Ala Ser Tyr Tyr
465      470      475      480
Trp Leu Leu His Ala Leu Gly Ile Tyr Gln Pro Tyr Val Trp Glu Tyr
      485      490      495
Ser Arg Leu Asn Val Ser Asn Thr Val Met Ser Lys Arg Lys Leu Asn
      500      505      510
Arg Leu Val Thr Glu Lys Trp Val Asp Gly Trp Asp Asp Pro Arg Leu
515      520      525
Met Thr Leu Ala Gly Leu Arg Arg Arg Gly Met Thr Pro Thr Ala Ile

```

PF59083SeqList PF59083.txt

530	Asn	Ala	Phe	Val	Arg	Gly	Ile	Gly	Ile	Thr	Arg	Ser	Asp	Gly	Thr	Leu
545	Ile	Ser	Val	Glu	Arg	Leu	Glu	Tyr	His	Val	Arg	Glu	Glu	Leu	Asn	Lys
	Thr	Ala	Pro	Arg	Ala	Met	Val	Val	Leu	His	Pro	Leu	Lys	Val	Val	Ile
	Thr	Asn	Leu	Glu	Ala	Asn	Ser	Ala	Ile	Glu	Val	Asp	Ala	Lys	Lys	Trp
	Pro	Asp	Ala	Gln	Ala	Asp	Asp	Ala	Ser	Ala	Phe	Tyr	Lys	Ile	Pro	Phe
	Ser	Asn	Val	Val	Tyr	Ile	Glu	His	Ser	Asp	Phe	Arg	Met	Gln	Asp	Ser
625	Lys	Asp	Tyr	Tyr	Gly	Leu	Ala	Pro	Gly	Lys	Ser	Val	Ile	Leu	Arg	Tyr
	Ala	Phe	Pro	Ile	Lys	Cys	Thr	Glu	Val	Ile	Leu	Ala	Asp	Asp	Asn	Glu
	Thr	Ile	Leu	Glu	Ile	Arg	Ala	Glu	Tyr	Asp	Pro	Ser	Lys	Lys	Thr	Lys
	Pro	Lys	Gly	Val	Leu	His	Trp	Val	Ala	Gln	Pro	Ser	Pro	Gly	Val	Asp
	Pro	Leu	Lys	Val	Glu	Val	Arg	Leu	Phe	Glu	Arg	Leu	Phe	Leu	Ser	Glu
705	Asn	Pro	Ala	Glu	Leu	Asp	Asn	Trp	Leu	Gly	Asp	Leu	Asn	Pro	Asn	Ser
	Lys	Val	Ile	Ile	Pro	Asp	Ala	Tyr	Gly	Val	Ser	Ser	Ile	Gln	Asn	Ala
	Lys	Val	Gly	Asp	Asn	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Phe	Val	Val
	Asp	Arg	Asp	Ser	Thr	Ser	Glu	Lys	Leu	Val	Phe	Asn	Arg	Thr	Val	Thr
	Leu	Lys	Gly	Ser	Tyr	Ser	Lys	Gly	Gly	Lys						
785																

<210> 9979
 <211> 2199
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(2199)

<400> 9979	
atg gat atc aaa acc ttt gcc ttc gcc cca tct tct ccg ccg tta tcg	48
Met Asp Ile Lys Thr Phe Ala Phe Ala Pro Ser Ser Pro Pro Leu Ser	
1 5 10 15	
gta atc gcc gcc gcc aag ctc gcc gga atc tct ccc acg att gat acc	96
Val Ile Ala Ala Ala Lys Leu Ala Gly Ile Ser Pro Thr Ile Asp Thr	
20 25 30	
gct ctc tct cct gac tca cct ccc tca ttt atc ttc tcc gat ggg cta	144
Ala Leu Ser Pro Asp Ser Pro Pro Ser Phe Ile Phe Ser Asp Gly Leu	
35 40 45	
aag ttg cac gga cca tat gct ctt cta cgt tat atc ggg cga gtt gcc	192
Lys Leu His Gly Pro Tyr Ala Leu Leu Arg Tyr Ile Gly Arg Val Ala	
50 55 60	
agc ctt cct aat ttc tat ggg caa aat cca ttt gaa tct agc cag att	240
Ser Leu Pro Asn Phe Tyr Gly Gln Asn Pro Phe Glu Ser Ser Gln Ile	
65 70 75 80	
gat gaa tgg ctg gac tat gct cct atc ctc tca tcg ggc cct gct ttt	288
Asp Glu Trp Leu Asp Tyr Ala Pro Ile Leu Ser Ser Gly Pro Ala Phe	
85 90 95	
gag aat gca tgc aaa tat ata gat gag tac ctg gag aag cgt act ttt	336
Glu Asn Ala Cys Lys Tyr Ile Asp Glu Tyr Leu Glu Lys Arg Thr Phe	
100 105 110	
ttg gtt ggt tat tca ttg tca att gca gac cta gca atc tgg gca ggt	384
Leu Val Gly Tyr Ser Leu Ser Ile Ala Asp Leu Ala Ile Trp Ala Gly	
115 120 125	
ctt gca ggt tct gga aag aga tgg gaa agt cta agg aag tca aag aaa	432

PF59083SeqList PF59083.txt															
Leu	Ala	Gly	Ser	Gly	Lys	Arg	Trp	Glu	Ser	Leu	Arg	Lys	Ser	Lys	Lys
130	130					135				140	140				
tat	cca	aat	ctt	gca	cga	tgg	ttc	aat	tca	ata	gtg	gaa	gaa	cat	ggt
Tyr	Pro	Asn	Leu	Ala	Arg	Trp	Phe	Asn	Ser	Ile	Val	Glu	Glu	His	Gly
145					150					155					160
act	gcc	tta	aat	gaa	gtc	aca	tca	gta	tat	gct	ggc	aaa	aaa	gga	ttg
Thr	Ala	Leu	Asn	Glu	Val	Thr	Ser	Val	Tyr	Ala	Gly	Lys	Lys	Gly	Leu
				165					170					175	
ggt	gaa	cca	aca	gca	acc	aag	tca	aaa	gaa	cag	tca	gta	aac	act	gat
Gly	Glu	Pro	Thr	Ala	Thr	Lys	Ser	Lys	Glu	Gln	Ser	Val	Asn	Thr	Asp
			180					185					190		
aaa	gtg	aag	aag	gtg	aat	gga	gat	gtg	tct	gag	aac	aac	aaa	gga	gga
Lys	Val	Lys	Lys	Val	Asn	Gly	Asp	Val	Ser	Glu	Asn	Asn	Lys	Gly	Gly
		195				200				205					
agc	aaa	cca	tca	gca	gaa	ata	gat	ctt	cca	gat	gct	gaa	gtt	gga	aaa
Ser	Lys	Pro	Ser	Ala	Glu	Ile	Asp	Leu	Pro	Asp	Ala	Glu	Val	Gly	Lys
	210					215				220					
gtt	cgc	ttg	cga	ttt	gcc	cct	gaa	cca	agt	ggt	tat	ctt	cat	att	gga
Val	Arg	Leu	Arg	Phe	Ala	Pro	Glu	Pro	Ser	Gly	Tyr	Leu	His	Ile	Gly
225					230					235					240
cac	tca	aaa	gca	gct	ttg	ttg	aac	aaa	tat	ttt	gct	gag	cga	tac	cag
His	Ser	Lys	Ala	Ala	Leu	Leu	Asn	Lys	Tyr	Phe	Ala	Glu	Arg	Tyr	Gln
			245						250					255	
ggt	cag	gtt	att	gtg	cgt	ttt	gat	gat	acc	aat	cct	gct	aaa	gaa	agc
Gly	Gln	Val	Ile	Val	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Ala	Lys	Glu	Ser
			260				265						270		
aat	gaa	ttt	gtg	gac	aac	ctg	att	aaa	gat	att	gat	aca	ttg	ggc	atc
Asn	Glu	Phe	Val	Asp	Asn	Leu	Ile	Lys	Asp	Ile	Asp	Thr	Leu	Gly	Ile
		275				280						285			
aaa	tat	gaa	caa	att	aca	tat	aca	tca	gat	tac	ttc	cct	gag	ttg	atg
Lys	Tyr	Glu	Gln	Ile	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Pro	Glu	Leu	Met
	290					295				300					
gaa	atg	gct	gaa	aaa	tta	att	cgc	gag	ggt	aaa	aca	tat	gtt	gat	gac
Glu	Met	Ala	Glu	Lys	Leu	Ile	Arg	Glu	Gly	Lys	Thr	Tyr	Val	Asp	Asp
305					310					315					320
act	cca	cgt	gaa	caa	atg	caa	aaa	gag	aga	atg	gat	ggc	ata	gaa	tct
Thr	Pro	Arg	Glu	Gln	Met	Gln	Lys	Glu	Arg	Met	Asp	Gly	Ile	Glu	Ser
				325				330						335	
aaa	tgc	aga	aat	aat	ata	gta	gag	gag	aat	cta	aaa	ctg	tgg	aag	gaa
Lys	Cys	Arg	Asn	Asn	Ile	Val	Glu	Glu	Asn	Leu	Lys	Leu	Trp	Lys	Glu
			340				345						350		
atg	att	gca	gga	aca	gag	agg	gga	ttg	cag	tgt	tgt	gtc	cgt	ggc	aag
Met	Ile	Ala	Gly	Thr	Glu	Arg	Gly	Leu	Gln	Cys	Cys	Val	Arg	Gly	Lys
		355				360						365			
ttg	gat	atg	cag	gac	cca	aac	aaa	tca	ctt	aga	gat	cct	gta	tat	tat
Leu	Asp	Met	Gln	Asp	Pro	Asn	Lys	Ser	Leu	Arg	Asp	Pro	Val	Tyr	Tyr
	370				375						380				
cgt	tgc	aat	cca	atg	ccc	cat	cat	aga	att	gga	tcc	aag	tat	aaa	gtg
Arg	Cys	Asn	Pro	Met	Pro	His	His	Arg	Ile	Gly	Ser	Lys	Tyr	Lys	Val
385					390					395					400
tat	cca	act	tat	gat	ttt	gct	tgt	cca	tat	gtt	gat	gct	ata	gaa	gga
Tyr	Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Tyr	Val	Asp	Ala	Ile	Glu	Gly
				405				410						415	
atc	acg	cat	gcc	ctt	cga	tct	agt	gaa	tac	cat	gat	cgc	aat	gcc	cag
Ile	Thr	His	Ala	Leu	Arg	Ser	Ser	Glu	Tyr	His	Asp	Arg	Asn	Ala	Gln
			420					425					430		
tat	tac	tgg	att	caa	gag	gac	atg	ggt	ctt	aga	aaa	gtt	ctt	atc	tac
Tyr	Tyr	Trp	Ile	Gln	Glu	Asp	Met	Gly	Leu	Arg	Lys	Val	Leu	Ile	Tyr
		435				440						445			
gaa	ttt	agc	cgg	ttg	aat	atg	gtc	tac	act	ctt	ctg	agc	aaa	cga	aag
Glu	Phe	Ser	Arg	Leu	Asn	Met	Val	Tyr	Thr	Leu	Leu	Ser	Lys	Arg	Lys
	450				455					460					
ctt	ttg	tgg	ttt	gta	caa	aat	ggg	aaa	gtt	gat	gga	tgg	gat	gat	gca
Leu	Leu	Trp	Phe	Val	Gln	Asn	Gly	Lys	Val	Asp	Gly	Trp	Asp	Asp	Ala
465					470					475					480
cga	ttt	cct	aca	gtg	caa	gga	att	gtg	cgt	aga	ggt	ttg	aaa	att	gaa
Arg	Phe	Pro	Thr	Val	Gln	Gly	Ile	Val	Arg	Arg	Gly	Leu	Lys	Ile	Glu
			485					490						495	
gcc	ctg	ata	cag	ttt	att	gtt	gag	cag	ggg	gcg	tcc	aaa	aat	ctc	aat

PF59083SeqList PF59083.txt

Ala	Leu	Ile	Gln	Phe	Ile	Val	Glu	Gln	Gly	Ala	Ser	Lys	Asn	Leu	Asn	
			500					505					510			
ctc	atg	gaa	tgg	gac	aag	ctc	tgg	acc	att	aat	aag	aag	att	att	gac	1584
Leu	Met	Glu	Trp	Asp	Lys	Leu	Trp	Thr	Ile	Asn	Lys	Lys	Ile	Ile	Asp	
		515					520					525				
cct	gtc	tgt	cct	aga	cac	act	gct	gtc	att	gca	gac	aga	cgt	gtg	ttg	1632
Pro	Val	Cys	Pro	Arg	His	Thr	Ala	Val	Ile	Ala	Asp	Arg	Arg	Val	Leu	
	530					535					540					
ttg	act	ctc	acc	gat	ggg	cct	gag	aaa	cca	ttt	gtc	cgc	atc	ata	cct	1680
Leu	Thr	Leu	Thr	Asp	Gly	Pro	Glu	Lys	Pro	Phe	Val	Arg	Ile	Ile	Pro	
545					550					555					560	
cgg	cac	aag	aaa	tat	gaa	gct	gcc	gga	gat	aaa	gct	aca	aca	tat	act	1728
Arg	His	Lys	Lys	Tyr	Glu	Ala	Ala	Gly	Asp	Lys	Ala	Thr	Thr	Tyr	Thr	
				565					570					575		
aaa	agg	ata	tgg	ctt	gac	cat	gct	gat	gca	gtg	tct	tta	tca	gca	ggg	1776
Lys	Arg	Ile	Trp	Leu	Asp	His	Ala	Asp	Ala	Val	Ser	Leu	Ser	Ala	Gly	
			580					585					590			
gag	gaa	gta	aca	ttg	atg	gat	tgg	gga	aat	gcc	ata	gtg	aag	gaa	ata	1824
Glu	Glu	Val	Thr	Leu	Met	Asp	Trp	Gly	Asn	Ala	Ile	Val	Lys	Glu	Ile	
		595					600					605				
gag	aag	gac	caa	gat	gga	aat	atc	aca	ggg	ttg	agc	ggg	gct	ttg	cat	1872
Glu	Lys	Asp	Gln	Asp	Gly	Asn	Ile	Thr	Gly	Leu	Ser	Gly	Ala	Leu	His	
	610				615						620					
ctt	gaa	gga	tct	gtg	aag	acc	aca	aaa	ttg	aaa	ctc	act	tgg	cta	cct	1920
Leu	Glu	Gly	Ser	Val	Lys	Thr	Thr	Lys	Leu	Lys	Leu	Thr	Trp	Leu	Pro	
625					630					635					640	
gag	ata	gat	gaa	cta	gtt	tgc	ctg	aca	tta	gtg	gag	ttt	gat	tat	cta	1968
Glu	Ile	Asp	Glu	Leu	Val	Cys	Leu	Thr	Leu	Val	Glu	Phe	Asp	Tyr	Leu	
				645					650					655		
att	aca	aag	aaa	aag	ctt	gaa	gag	gag	gat	ttc	att	gat	gtg	ctt	aac	2016
Ile	Thr	Lys	Lys	Lys	Leu	Glu	Glu	Glu	Asp	Phe	Ile	Asp	Val	Leu	Asn	
			660					665					670			
cca	tgt	acc	aaa	aag	gag	act	tta	gct	tat	gga	gac	tcc	aac	atg	cga	2064
Pro	Cys	Thr	Lys	Lys	Glu	Thr	Leu	Ala	Tyr	Gly	Asp	Ser	Asn	Met	Arg	
		675					680					685				
aat	ctt	cag	cgt	gga	gat	tta	ttg	caa	ctg	gag	aga	aag	gga	tat	ttc	2112
Asn	Leu	Gln	Arg	Gly	Asp	Leu	Leu	Gln	Leu	Glu	Arg	Lys	Gly	Tyr	Phe	
	690				695					700						
agg	tgt	gat	tta	ccc	ttc	att	cgc	ccc	tca	caa	cca	atc	gtg	cta	tat	2160
Arg	Cys	Asp	Leu	Pro	Phe	Ile	Arg	Pro	Ser	Gln	Pro	Ile	Val	Leu	Tyr	
705					710					715					720	
gca	atc	cct	gat	ggc	agg	caa	cag	aca	agt	ttg	aag	taa				2199
Ala	Ile	Pro	Asp	Gly	Arg	Gln	Gln	Thr	Ser	Leu	Lys					
				725					730							

<210> 9980
 <211> 732
 <212> PRT
 <213> Glycine max

<400> 9980
 Met Asp Ile Lys Thr Phe Ala Phe Ala Pro Ser Ser Pro Pro Leu Ser
 1 5 10 15
 Val Ile Ala Ala Lys Leu Ala Gly Ile Ser Pro Thr Ile Asp Thr
 20 25 30
 Ala Leu Ser Pro Asp Ser Pro Pro Ser Phe Ile Phe Ser Asp Gly Leu
 35 40 45
 Lys Leu His Gly Pro Tyr Ala Leu Leu Arg Tyr Ile Gly Arg Val Ala
 50 55 60
 Ser Leu Pro Asn Phe Tyr Gly Gln Asn Pro Phe Glu Ser Ser Gln Ile
 65 70 75 80
 Asp Glu Trp Leu Asp Tyr Ala Pro Ile Leu Ser Ser Gly Pro Ala Phe
 85 90 95
 Glu Asn Ala Cys Lys Tyr Ile Asp Glu Tyr Leu Glu Lys Arg Thr Phe
 100 105 110
 Leu Val Gly Tyr Ser Leu Ser Ile Ala Asp Leu Ala Ile Trp Ala Gly
 115 120 125
 Leu Ala Gly Ser Gly Lys Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys
 130 135 140

PF59083SeqList PF59083.txt

Tyr	Pro	Asn	Leu	Ala	Arg	Trp	Phe	Asn	Ser	Ile	Val	Glu	Glu	His	Gly
145					150					155					160
Thr	Ala	Leu	Asn	Glu	Val	Thr	Ser	Val	Tyr	Ala	Gly	Lys	Lys	Gly	Leu
				165					170					175	
Gly	Glu	Pro	Thr	Ala	Thr	Lys	Ser	Lys	Glu	Gln	Ser	Val	Asn	Thr	Asp
			180					185					190		
Lys	Val	Lys	Lys	Val	Asn	Gly	Asp	Val	Ser	Glu	Asn	Asn	Lys	Gly	Gly
		195					200					205			
Ser	Lys	Pro	Ser	Ala	Glu	Ile	Asp	Leu	Pro	Asp	Ala	Glu	Val	Gly	Lys
	210					215					220				
Val	Arg	Leu	Arg	Phe	Ala	Pro	Glu	Pro	Ser	Gly	Tyr	Leu	His	Ile	Gly
225					230					235					240
His	Ser	Lys	Ala	Ala	Leu	Leu	Asn	Lys	Tyr	Phe	Ala	Glu	Arg	Tyr	Gln
				245					250					255	
Gly	Gln	Val	Ile	Val	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Ala	Lys	Glu	Ser
			260					265					270		
Asn	Glu	Phe	Val	Asp	Asn	Leu	Ile	Lys	Asp	Ile	Asp	Thr	Leu	Gly	Ile
		275					280					285			
Lys	Tyr	Glu	Gln	Ile	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Pro	Glu	Leu	Met
	290					295					300				
Glu	Met	Ala	Glu	Lys	Leu	Ile	Arg	Glu	Gly	Lys	Thr	Tyr	Val	Asp	Asp
305					310					315					320
Thr	Pro	Arg	Glu	Gln	Met	Gln	Lys	Glu	Arg	Met	Asp	Gly	Ile	Glu	Ser
				325					330					335	
Lys	Cys	Arg	Asn	Asn	Ile	Val	Glu	Glu	Asn	Leu	Lys	Leu	Trp	Lys	Glu
			340					345					350		
Met	Ile	Ala	Gly	Thr	Glu	Arg	Gly	Leu	Gln	Cys	Cys	Val	Arg	Gly	Lys
		355					360					365			
Leu	Asp	Met	Gln	Asp	Pro	Asn	Lys	Ser	Leu	Arg	Asp	Pro	Val	Tyr	Tyr
	370					375					380				
Arg	Cys	Asn	Pro	Met	Pro	His	His	Arg	Ile	Gly	Ser	Lys	Tyr	Lys	Val
385					390					395					400
Tyr	Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Tyr	Val	Asp	Ala	Ile	Glu	Gly
				405					410					415	
Ile	Thr	His	Ala	Leu	Arg	Ser	Ser	Glu	Tyr	His	Asp	Arg	Asn	Ala	Gln
			420					425					430		
Tyr	Tyr	Trp	Ile	Gln	Glu	Asp	Met	Gly	Leu	Arg	Lys	Val	Leu	Ile	Tyr
		435					440					445			
Glu	Phe	Ser	Arg	Leu	Asn	Met	Val	Tyr	Thr	Leu	Leu	Ser	Lys	Arg	Lys
	450					455					460				
Leu	Leu	Trp	Phe	Val	Gln	Asn	Gly	Lys	Val	Asp	Gly	Trp	Asp	Asp	Ala
465					470					475					480
Arg	Phe	Pro	Thr	Val	Gln	Gly	Ile	Val	Arg	Arg	Gly	Leu	Lys	Ile	Glu
				485					490					495	
Ala	Leu	Ile	Gln	Phe	Ile	Val	Glu	Gln	Gly	Ala	Ser	Lys	Asn	Leu	Asn
			500					505					510		
Leu	Met	Glu	Trp	Asp	Lys	Leu	Trp	Thr	Ile	Asn	Lys	Lys	Ile	Ile	Asp
		515					520					525			
Pro	Val	Cys	Pro	Arg	His	Thr	Ala	Val	Ile	Ala	Asp	Arg	Arg	Val	Leu
	530					535					540				
Leu	Thr	Leu	Thr	Asp	Gly	Pro	Glu	Lys	Pro	Phe	Val	Arg	Ile	Ile	Pro
545					550					555					560
Arg	His	Lys	Lys	Tyr	Glu	Ala	Ala	Gly	Asp	Lys	Ala	Thr	Thr	Tyr	Thr
				565					570					575	
Lys	Arg	Ile	Trp	Leu	Asp	His	Ala	Asp	Ala	Val	Ser	Leu	Ser	Ala	Gly
			580					585					590		
Glu	Glu	Val	Thr	Leu	Met	Asp	Trp	Gly	Asn	Ala	Ile	Val	Lys	Glu	Ile
		595					600					605			
Glu	Lys	Asp	Gln	Asp	Gly	Asn	Ile	Thr	Gly	Leu	Ser	Gly	Ala	Leu	His
	610					615					620				
Leu	Glu	Gly	Ser	Val	Lys	Thr	Thr	Lys	Leu	Lys	Leu	Thr	Trp	Leu	Pro
625					630					635					640
Glu	Ile	Asp	Glu	Val	Cys	Leu	Thr	Leu	Val	Glu	Phe	Asp	Tyr	Leu	
				645				650					655		
Ile	Thr	Lys	Lys	Lys	Leu	Glu	Glu	Glu	Asp	Phe	Ile	Asp	Val	Leu	Asn
			660					665					670		
Pro	Cys	Thr	Lys	Lys	Glu	Thr	Leu	Ala	Tyr	Gly	Asp	Ser	Asn	Met	Arg
		675					680					685			
Asn	Leu	Gln	Arg	Gly	Asp	Leu	Leu	Gln	Leu	Glu	Arg	Lys	Gly	Tyr	Phe

PF59083SeqList PF59083.txt

690 695 700
 Arg Cys Asp Leu Pro Phe Ile Arg Pro Ser Gln Pro Ile Val Leu Tyr
 705 710 715 720
 Ala Ile Pro Asp Gly Arg Gln Gln Thr Ser Leu Lys

<210> 9981
 <211> 2388
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(2388)

<400> 9981
 atg gtc gac ggg gag aag gcc tcg gcc ccg ccc ctg ctg cgg ctg gag 48
 Met Val Asp Gly Glu Lys Ala Ser Ala Pro Pro Leu Leu Arg Leu Glu
 1 5 10 15
 acg ctg ctc gcg ctc ggc ctc gac cag cgc acg gcc gag aac gcg ctg 96
 Thr Leu Leu Ala Leu Gly Leu Asp Gln Arg Thr Ala Glu Asn Ala Leu
 20 25 30
 gtc aat agc aag gtc acc gcc aac cta gcc gcc gtc gta gcc gag gct 144
 Val Asn Ser Lys Val Thr Ala Asn Leu Ala Ala Val Val Ala Glu Ala
 35 40 45
 ggg ata act gga tgc gac aag tcc gtc ggg aat ctt ctg tac gca gtt 192
 Gly Ile Thr Gly Cys Asp Lys Ser Val Gly Asn Leu Leu Tyr Ala Val
 50 55 60
 gcc acg aag tac cca aat aat gca ctt gtc cat cgt cct gct ctc att 240
 Ala Thr Lys Tyr Pro Asn Ala Leu Val His Arg Pro Ala Leu Ile
 65 70 75 80
 agc tac atc gtt tcg acc aag atc aag aac cct gca cag cta gat gct 288
 Ser Tyr Ile Val Ser Thr Lys Ile Lys Asn Pro Ala Gln Leu Asp Ala
 85 90 95
 gct ctg tcg ttt ctt act aat acc ggt cct gaa tct ttg gat att ggg 336
 Ala Leu Ser Phe Leu Thr Asn Thr Gly Pro Glu Ser Leu Asp Ile Gly
 100 105 110
 aag ttt gaa gaa gcc tgt ggt gta ggt gtg gtt gtt tct att gaa gag 384
 Lys Phe Glu Glu Ala Cys Gly Val Gly Val Val Val Ser Ile Glu Glu
 115 120 125
 att cag tca act gtc tct gag gtt ctg aag gaa aac ctg gaa gct ata 432
 Ile Gln Ser Thr Val Ser Glu Val Leu Lys Glu Asn Leu Glu Ala Ile
 130 135 140
 ttg gag cag cgc tat cac ata aat gtt ggt ggc cta tgc gga cag gtc 480
 Leu Glu Gln Arg Tyr His Ile Asn Val Gly Gly Leu Cys Gly Gln Val
 145 150 155 160
 agg aag cgg cac ccc tgg ggc gat gcc aag gca aca aag gag gag att 528
 Arg Lys Arg His Pro Trp Gly Asp Ala Lys Ala Thr Lys Glu Glu Ile
 165 170 175
 gag aag aag ctt gct gag ata cta ggt ccg aag acg gaa gct gac aat 576
 Glu Lys Lys Leu Ala Glu Ile Leu Gly Pro Lys Thr Glu Ala Asp Asn
 180 185 190
 gta aaa cca gtg aaa aag aag aag gag aaa ccg gca aaa gtt gag gag 624
 Val Lys Pro Val Lys Lys Lys Lys Glu Lys Pro Ala Lys Val Glu Glu
 195 200 205
 aaa aag gtt gca gta gcc act gcc gcc cca cca tct gag gag gaa ttg 672
 Lys Lys Val Ala Val Ala Thr Ala Ala Pro Pro Ser Glu Glu Glu Leu
 210 215 220
 aat cct tat aca ata ttt ccc cag cca gcg gaa aac aat aag gtt cat 720
 Asn Pro Tyr Thr Ile Phe Pro Gln Pro Ala Glu Asn Asn Lys Val His
 225 230 235 240
 aca gaa ata ttc ttc agc gat ggg aac ata tgg agg gcg cat aac acg 768
 Thr Glu Ile Phe Phe Ser Asp Gly Asn Ile Trp Arg Ala His Asn Thr
 245 250 255
 aag gag ata tta gag aaa cat ctt aag gca act ggt gga aaa gtg atg 816
 Lys Glu Ile Leu Glu Lys His Leu Lys Ala Thr Gly Gly Lys Val Met
 260 265 270
 acg cgt ttc cca cca gaa cct aat gga tac ctt cat atc ggt cat gct 864
 Thr Arg Phe Pro Pro Glu Pro Asn Gly Tyr Leu His Ile Gly His Ala

PF59083SeqList PF59083.txt

aag Lys	gct Ala	atg Met	ttt Phe	att Ile	gat Asp	ttt Phe	gga Gly	ttg Leu	gct Ala	aaa Lys	gag Glu	cga Arg	aat Asn	ggt Gly	cac His	912
tgt Cys	tat Tyr	ctc Leu	agg Arg	ttt Phe	gat Asp	gac Asp	aca Thr	aat Asn	cca Pro	gaa Glu	gct Ala	gaa Glu	aag Lys	aaa Lys	gaa Glu	960
tat Tyr	ata Ile	gac Asp	cac His	atc Ile	cag Gln	gag Glu	ata Ile	gtc Val	aag Lys	tgg Trp	atg Met	ggg Gly	tgg Trp	gag Glu	ccc Pro	1008
tat Tyr	aaa Lys	gtt Val	aca Thr	tat Tyr	aca Thr	agt Ser	gat Asp	tat Tyr	ttc Phe	caa Gln	gct Ala	tta Leu	tat Tyr	gag Glu	cat His	1056
gca Ala	gtt Val	gag Glu	tta Leu	ata Ile	cgg Arg	aaa Lys	ggg Gly	cta Leu	gcc Ala	tat Tyr	gtg Val	gat Asp	cac His	cag Gln	act Thr	1104
gca Ala	gaa Glu	caa Gln	atc Ile	aag Lys	gaa Glu	tac Tyr	agg Arg	gaa Glu	aag Lys	aag Lys	atg Met	gat Asp	agt Ser	cca Pro	tgg Trp	1152
agg Arg	gac Asp	agg Arg	ccc Pro	att Ile	gaa Glu	gag Glu	tct Ser	ttg Leu	cag Gln	tta Leu	ttt Phe	gaa Glu	gac Asp	atg Met	cgg Arg	1200
cgt Arg	ggg Gly	ttg Leu	att Ile	gct Ala	gag Glu	ggt Gly	gct Ala	gca Ala	act Thr	ctc Leu	cga Arg	atg Met	aag Lys	cag Gln	gac Asp	1248
atg Met	cag Gln	aat Asn	gat Asp	aac Asn	aag Lys	aac Asn	atg Met	tct Ser	gat Asp	tta Leu	ata Ile	gca Ala	tat Tyr	aga Arg	ata Ile	1296
aaa Lys	ttc Phe	act Thr	cct Pro	cat His	cca Pro	cat His	gct Ala	ggc Gly	gac Asp	aaa Lys	tgg Trp	tgt Cys	atc Ile	tat Tyr	cca Pro	1344
agc Ser	tat Tyr	gac Asp	tat Tyr	gct Ala	cat His	tgc Cys	atg Met	gtg Val	gat Asp	tca Ser	ctt Leu	gaa Glu	aac Asn	att Ile	aca Thr	1392
cat His	tct Ser	ttg Leu	tgc Cys	acg Thr	ctt Leu	gag Glu	ttc Phe	gac Asp	ata Ile	cgc Arg	cgc Arg	ccg Pro	tca Ser	tac Tyr	tac Tyr	1440
tgg Trp	cta Leu	ctt Leu	ggt Val	gcc Ala	ttg Leu	ggt Gly	ttg Leu	tac Tyr	cag Gln	cca Pro	cat His	ggt Val	tgg Trp	gag Glu	tat Tyr	1488
tcg Ser	agg Arg	cta Leu	aac Asn	ata Ile	tca Ser	cat His	act Thr	atg Met	atg Met	tcc Ser	aaa Lys	aga Arg	aag Lys	ttg Leu	aat Asn	1536
cgg Arg	ctt Leu	gtg Val	aca Thr	gag Glu	aag Lys	tgg Trp	gta Val	gat Asp	ggg Gly	tgg Trp	gat Asp	gat Asp	cct Pro	cgt Arg	ttg Leu	1584
ttg Leu	act Thr	ttg Leu	gcg Ala	gga Gly	ctg Leu	agg Arg	cga Arg	cgg Arg	gga Gly	gta Val	tca Ser	gca Ala	act Thr	gcg Ala	atc Ile	1632
aat Asn	tca Ser	ttt Phe	atc Ile	cgt Arg	gga Gly	att Ile	ggg Gly	ata Ile	acg Thr	aga Arg	agt Ser	gac Asp	aat Asn	agc Ser	tta Leu	1680
att Ile	cgt Arg	gtt Val	gac Asp	cgt Arg	ctt Leu	gaa Glu	tat Tyr	cat His	atc Ile	aga Arg	gaa Glu	gaa Glu	ctg Leu	aat Asn	aaa Lys	1728
aca Thr	gct Ala	tct Ser	cga Arg	acc Thr	atg Met	gtt Val	gtt Val	ttg Leu	cat His	cct Pro	cta Leu	aag Lys	gtt Val	gta Val	ata Ile	1776
acc Thr	aac Asn	ttg Leu	gaa Glu	gat Asp	gga Gly	aaa Lys	gtc Val	ata Ile	gac Asp	ctt Leu	gat Asp	gga Gly	aaa Lys	aag Lys	tgg Trp	1824
cct Pro	gat Asp	gct Ala	cct Pro	gct Ala	gat Asp	gaa Glu	gca Ala	tcg Ser	tcc Ser	tac Tyr	tac Tyr	aag Lys	gtt Val	cct Pro	ttc Phe	1872
tca Ser	aaa Lys	att Ile	gtc Val	tac Tyr	att Ile	gaa Glu	aaa Lys	act Thr	gat Asp	ttt Phe	cgc Arg	gtg Val	aaa Lys	gac Asp	tcg Ser	1920
aaa Lys	gat Asp	tac Tyr	tat Tyr	ggg Gly	ctg Leu	gca Ala	cct Pro	ggt Gly	aaa Lys	tct Ser	gcc Ala	ctg Leu	ctg Leu	agg Arg	tat Tyr	1968

PF59083SeqList PF59083.txt

				645					650				655				
gca	ttc	ccg	ata	aaa	tgc	aca	gag	gtt	att	tat	ggt	gat	aat	cca	gat		2016
Ala	Phe	Pro	Ile	Lys	Cys	Thr	Glu	Val	Ile	Tyr	Gly	Asp	Asn	Pro	Asp		
			660						665				670				
gat	att	gtt	gaa	att	cga	gcc	gag	tat	gac	ccc	tca	aag	acc	tcc	aaa		2064
Asp	Ile	Val	Glu	Ile	Arg	Ala	Glu	Tyr	Asp	Pro	Ser	Lys	Thr	Ser	Lys		
		675					680					685					
cct	aag	ggt	gtt	ctg	cac	tgg	gtt	gcc	cag	cca	gca	cct	gga	gtt	gag		2112
Pro	Lys	Gly	Val	Leu	His	Trp	Val	Ala	Gln	Pro	Ala	Pro	Gly	Val	Glu		
	690					695					700						
cca	tta	aag	gtc	gaa	ata	aga	ttg	ttt	gag	aaa	tta	ttc	tta	tcg	gag		2160
Pro	Leu	Lys	Val	Glu	Ile	Arg	Leu	Phe	Glu	Lys	Leu	Phe	Leu	Ser	Glu		
705					710				715						720		
aat	cct	gcc	gaa	ttg	gaa	gat	tgg	ctt	ggt	gat	ctt	aac	ccg	cac	tcg		2208
Asn	Pro	Ala	Glu	Leu	Glu	Asp	Trp	Leu	Gly	Asp	Leu	Asn	Pro	His	Ser		
			725						730					735			
aaa	gag	gtt	gta	aag	gac	gcc	tat	gct	gta	ccg	tca	ctc	gcc	acc	gcg		2256
Lys	Glu	Val	Val	Lys	Asp	Ala	Tyr	Ala	Val	Pro	Ser	Leu	Ala	Thr	Ala		
		740					745					750					
gtt	gtg	ggc	gac	aat	ttc	cag	ttt	gag	cgg	ctt	ggc	tac	ttt	gct	gtg		2304
Val	Val	Gly	Asp	Asn	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Phe	Ala	Val		
		755				760					765						
gac	acg	gac	tcg	act	ccc	gag	aag	ctt	gtg	ttc	aac	agg	act	gta	acc		2352
Asp	Thr	Asp	Ser	Thr	Pro	Glu	Lys	Leu	Val	Phe	Asn	Arg	Thr	Val	Thr		
	770					775					780						
ctg	cgc	gac	tct	tat	ggg	aag	gct	gga	ccc	aag	tga						2388
Leu	Arg	Asp	Ser	Tyr	Gly	Lys	Ala	Gly	Pro	Lys							
785					790					795							

<210> 9982

<211> 795

<212> PRT

<213> Hordeum vulgare

<400> 9982

Met	Val	Asp	Gly	Glu	Lys	Ala	Ser	Ala	Pro	Pro	Leu	Leu	Arg	Leu	Glu	
1				5					10					15		
Thr	Leu	Leu	Ala	Leu	Gly	Leu	Asp	Gln	Arg	Thr	Ala	Glu	Asn	Ala	Leu	
			20					25					30			
Val	Asn	Ser	Lys	Val	Thr	Ala	Asn	Leu	Ala	Ala	Val	Val	Ala	Glu	Ala	
		35					40					45				
Gly	Ile	Thr	Gly	Cys	Asp	Lys	Ser	Val	Gly	Asn	Leu	Leu	Tyr	Ala	Val	
	50					55				60						
Ala	Thr	Lys	Tyr	Pro	Asn	Ala	Leu	Val	His	Arg	Pro	Ala	Leu	Ile		
65					70				75					80		
Ser	Tyr	Ile	Val	Ser	Thr	Lys	Ile	Lys	Asn	Pro	Ala	Gln	Leu	Asp	Ala	
				85					90					95		
Ala	Leu	Ser	Phe	Leu	Thr	Asn	Thr	Gly	Pro	Glu	Ser	Leu	Asp	Ile	Gly	
			100					105					110			
Lys	Phe	Glu	Glu	Ala	Cys	Gly	Val	Gly	Val	Val	Val	Ser	Ile	Glu	Glu	
		115					120						125			
Ile	Gln	Ser	Thr	Val	Ser	Glu	Val	Leu	Lys	Glu	Asn	Leu	Glu	Ala	Ile	
	130					135					140					
Leu	Glu	Gln	Arg	Tyr	His	Ile	Asn	Val	Gly	Gly	Leu	Cys	Gly	Gln	Val	
145					150				155						160	
Arg	Lys	Arg	His	Pro	Trp	Gly	Asp	Ala	Lys	Ala	Thr	Lys	Glu	Glu	Ile	
			165					170						175		
Glu	Lys	Lys	Leu	Ala	Glu	Ile	Leu	Gly	Pro	Lys	Thr	Glu	Ala	Asp	Asn	
			180					185					190			
Val	Lys	Pro	Val	Lys	Lys	Lys	Lys	Glu	Lys	Pro	Ala	Lys	Val	Glu	Glu	
		195					200					205				
Lys	Lys	Val	Ala	Val	Ala	Thr	Ala	Ala	Pro	Pro	Ser	Glu	Glu	Glu	Leu	
	210					215					220					
Asn	Pro	Tyr	Thr	Ile	Phe	Pro	Gln	Pro	Ala	Glu	Asn	Asn	Lys	Val	His	
225					230					235					240	
Thr	Glu	Ile	Phe	Phe	Ser	Asp	Gly	Asn	Ile	Trp	Arg	Ala	His	Asn	Thr	
			245					250					255			
Lys	Glu	Ile	Leu	Glu	Lys	His	Leu	Lys	Ala	Thr	Gly	Gly	Lys	Val	Met	
			260				265						270			

PF59083SeqList PF59083.txt

Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ala
		275					280					285			
Lys	Ala	Met	Phe	Ile	Asp	Phe	Gly	Leu	Ala	Lys	Glu	Arg	Asn	Gly	His
	290					295					300				
Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys	Lys	Glu
305					310					315					320
Tyr	Ile	Asp	His	Ile	Gln	Glu	Ile	Val	Lys	Trp	Met	Gly	Trp	Glu	Pro
				325					330					335	
Tyr	Lys	Val	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Gln	Ala	Leu	Tyr	Glu	His
			340					345					350		
Ala	Val	Glu	Leu	Ile	Arg	Lys	Gly	Leu	Ala	Tyr	Val	Asp	His	Gln	Thr
		355					360					365			
Ala	Glu	Gln	Ile	Lys	Glu	Tyr	Arg	Glu	Lys	Lys	Met	Asp	Ser	Pro	Trp
	370					375					380				
Arg	Asp	Arg	Pro	Ile	Glu	Glu	Ser	Leu	Gln	Leu	Phe	Glu	Asp	Met	Arg
385					390					395					400
Arg	Gly	Leu	Ile	Ala	Glu	Gly	Ala	Ala	Thr	Leu	Arg	Met	Lys	Gln	Asp
				405					410					415	
Met	Gln	Asn	Asp	Asn	Lys	Asn	Met	Ser	Asp	Leu	Ile	Ala	Tyr	Arg	Ile
			420					425					430		
Lys	Phe	Thr	Pro	His	Pro	His	Ala	Gly	Asp	Lys	Trp	Cys	Ile	Tyr	Pro
		435					440					445			
Ser	Tyr	Asp	Tyr	Ala	His	Cys	Met	Val	Asp	Ser	Leu	Glu	Asn	Ile	Thr
	450					455					460				
His	Ser	Leu	Cys	Thr	Leu	Glu	Phe	Asp	Ile	Arg	Arg	Pro	Ser	Tyr	Tyr
465					470					475					480
Trp	Leu	Leu	Val	Ala	Leu	Gly	Leu	Tyr	Gln	Pro	His	Val	Trp	Glu	Tyr
				485					490					495	
Ser	Arg	Leu	Asn	Ile	Ser	His	Thr	Met	Met	Ser	Lys	Arg	Lys	Leu	Asn
			500					505					510		
Arg	Leu	Val	Thr	Glu	Lys	Trp	Val	Asp	Gly	Trp	Asp	Asp	Pro	Arg	Leu
		515					520					525			
Leu	Thr	Leu	Ala	Gly	Leu	Arg	Arg	Arg	Gly	Val	Ser	Ala	Thr	Ala	Ile
	530					535					540				
Asn	Ser	Phe	Ile	Arg	Gly	Ile	Gly	Ile	Thr	Arg	Ser	Asp	Asn	Ser	Leu
545					550					555					560
Ile	Arg	Val	Asp	Arg	Leu	Glu	Tyr	His	Ile	Arg	Glu	Glu	Leu	Asn	Lys
				565					570					575	
Thr	Ala	Ser	Arg	Thr	Met	Val	Val	Leu	His	Pro	Leu	Lys	Val	Val	Ile
			580					585					590		
Thr	Asn	Leu	Glu	Asp	Gly	Lys	Val	Ile	Asp	Leu	Asp	Gly	Lys	Lys	Trp
		595					600					605			
Pro	Asp	Ala	Pro	Ala	Asp	Glu	Ala	Ser	Ser	Tyr	Tyr	Lys	Val	Pro	Phe
	610					615					620				
Ser	Lys	Ile	Val	Tyr	Ile	Glu	Lys	Thr	Asp	Phe	Arg	Val	Lys	Asp	Ser
625					630					635					640
Lys	Asp	Tyr	Tyr	Gly	Leu	Ala	Pro	Gly	Lys	Ser	Ala	Leu	Leu	Arg	Tyr
				645					650					655	
Ala	Phe	Pro	Ile	Lys	Cys	Thr	Glu	Val	Ile	Tyr	Gly	Asp	Asn	Pro	Asp
			660						665				670		
Asp	Ile	Val	Glu	Ile	Arg	Ala	Glu	Tyr	Asp	Pro	Ser	Lys	Thr	Ser	Lys
		675					680					685			
Pro	Lys	Gly	Val	Leu	His	Trp	Val	Ala	Gln	Pro	Ala	Pro	Gly	Val	Glu
	690					695					700				
Pro	Leu	Lys	Val	Glu	Ile	Arg	Leu	Phe	Glu	Lys	Leu	Phe	Leu	Ser	Glu
705					710					715					720
Asn	Pro	Ala	Glu	Leu	Glu	Asp	Trp	Leu	Gly	Asp	Leu	Asn	Pro	His	Ser
				725					730					735	
Lys	Glu	Val	Val	Lys	Asp	Ala	Tyr	Ala	Val	Pro	Ser	Leu	Ala	Thr	Ala
				740				745					750		
Val	Val	Gly	Asp	Asn	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Phe	Ala	Val
		755					760					765			
Asp	Thr	Asp	Ser	Thr	Pro	Glu	Lys	Leu	Val	Phe	Asn	Arg	Thr	Val	Thr
	770					775					780				
Leu	Arg	Asp	Ser	Tyr	Gly	Lys	Ala	Gly	Pro	Lys					
785					790					795					

<210> 9983

<211> 2163

PF59083SeqList PF59083.txt

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (1)..(2163)

<400> 9983

atg gag ctc aaa cga gca ttc ccc cag gac agc ctc cca ctt tcc atc	48
Met Glu Leu Lys Arg Ala Phe Pro Gln Asp Ser Leu Pro Leu Ser Ile	
1 5 10 15	
att tcg gct gct aag att gca ggt gtt cct cta atc att gat ccg acc	96
Ile Ser Ala Ala Lys Ile Ala Gly Val Pro Leu Ile Ile Asp Pro Thr	
20 25 30	
ctt gcc tca ggt tca gtg ccc aca cta cac ttc agt tct ggg gat ttt	144
Leu Ala Ser Gly Ser Val Pro Thr Leu His Phe Ser Ser Gly Asp Phe	
35 40 45	
ata cat ggt gtc aac aca att ctc cgg tac att gca cgt gct gca tct	192
Ile His Gly Val Asn Thr Ile Leu Arg Tyr Ile Ala Arg Ala Ala Ser	
50 55 60	
gtt tcc agc ttc tat ggc caa gac cat att cag gca tca cat gtt gac	240
Val Ser Ser Phe Tyr Gly Gln Asp His Ile Gln Ala Ser His Val Asp	
65 70 75 80	
caa tgg ctc gag tat gca cca ctc att ctg tca ggc tct gaa ttt gaa	288
Gln Trp Leu Glu Tyr Ala Pro Leu Ile Leu Ser Gly Ser Glu Phe Glu	
85 90 95	
gct gct tgc tca ttt ctt gat gga tac ttg tca tct cga acc ttt ttg	336
Ala Ala Cys Ser Phe Leu Asp Gly Tyr Leu Ser Ser Arg Thr Phe Leu	
100 105 110	
gtt ggt tat ggt tta tca att gct gat att gtt gtg tgg tca aat ctc	384
Val Gly Tyr Gly Leu Ser Ile Ala Asp Ile Val Val Trp Ser Asn Leu	
115 120 125	
aca gga act ggt caa cga tgg gaa agt cta agg agg tca aag aaa tat	432
Thr Gly Thr Gly Gln Arg Trp Glu Ser Leu Arg Arg Ser Lys Lys Tyr	
130 135 140	
cag agc ctt gtc cgc tgg ttc aac agt gta gct gca gac tat gcg gat	480
Gln Ser Leu Val Arg Trp Phe Asn Ser Val Ala Ala Asp Tyr Ala Asp	
145 150 155 160	
gca cta gat gaa gtt aca tct gct tat gtt gga aag cgt gga att ggc	528
Ala Leu Asp Glu Val Thr Ser Ala Tyr Val Gly Lys Arg Gly Ile Gly	
165 170 175	
aaa tct cct gct cca agc ttg aaa gaa aag gtg cct ggt ttg aag gag	576
Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val Pro Gly Leu Lys Glu	
180 185 190	
aat acg tcg ggt cat gaa ata gat ctc cca ggt gcc aca gtt ggc gaa	624
Asn Thr Ser Gly His Glu Ile Asp Leu Pro Gly Ala Thr Val Gly Glu	
195 200 205	
gtt tgc gtt cgt ttt gct cca gag cct agc ggg tat ctc cac att ggt	672
Val Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly	
210 215 220	
cat gca aag gct gca ctg ttg aac aag tat ttt gca gaa aga tat aaa	720
His Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Lys	
225 230 235 240	
ggg cgt cta ata gtt cga ttt gat gac aca aat cct tct aaa gaa agc	768
Gly Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser	
245 250 255	
aat gaa ttt gtt gag aat gtc ctg aaa gat att gag aca ctt ggt gtt	816
Asn Glu Phe Val Glu Asn Val Leu Lys Asp Ile Glu Thr Leu Gly Val	
260 265 270	
aaa tac gat gta gtt aca tac aca tca gat cat ttt cca aag cta atg	864
Lys Tyr Asp Val Val Thr Tyr Thr Ser Asp His Phe Pro Lys Leu Met	
275 280 285	
gaa atg gct gaa agt ttg att aag cag gga aag gca tat gtt gat gat	912
Glu Met Ala Glu Ser Leu Ile Lys Gln Gly Lys Ala Tyr Val Asp Asp	
290 295 300	
aca ccc aag gag caa atg agg agt gaa agg atg gat ggt gtg gaa tct	960
Thr Pro Lys Glu Gln Met Arg Ser Glu Arg Met Asp Gly Val Glu Ser	
305 310 315 320	
aag cgt aga aac agt act gtc gag gag aac ttg tcg ttg tgg aaa gag	1008

PF59083SeqList PF59083.txt

Lys	Arg	Arg	Asn	Ser	Thr	Val	Glu	Glu	Asn	Leu	Ser	Leu	Trp	Lys	Glu	
atg	ggt	aat	ggc	acc	aaa	agg	ggt	acc	gag	tgc	tgt	gta	cgt	ggt	aaa	1056
Met	Val	Asn	Gly	Thr	Lys	Arg	Gly	Thr	Glu	Cys	Cys	Val	Arg	Gly	Lys	
			340					345					350			
ctt	gac	atg	cag	gac	cca	aac	aaa	tca	ctc	cga	gat	cct	ggt	tac	tac	1104
Leu	Asp	Met	Gln	Asp	Pro	Asn	Lys	Ser	Leu	Arg	Asp	Pro	Val	Tyr	Tyr	
		355					360					365				
cgt	tgc	aac	cct	gat	ccc	cat	cat	cgc	ggt	ggc	tca	aaa	tac	aag	gtc	1152
Arg	Cys	Asn	Pro	Asp	Pro	His	His	Arg	Val	Gly	Ser	Lys	Tyr	Lys	Val	
		370				375					380					
tat	cca	act	tat	gac	ttt	gct	tgc	cca	ttt	gtg	gat	gca	cta	gaa	gga	1200
Tyr	Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Phe	Val	Asp	Ala	Leu	Glu	Gly	
385					390				395					400		
gtc	act	cat	gct	ctt	cgt	tca	agc	gaa	tac	cat	gat	cgg	aat	gca	cag	1248
Val	Thr	His	Ala	Leu	Arg	Ser	Ser	Glu	Tyr	His	Asp	Arg	Asn	Ala	Gln	
				405					410					415		
tac	tat	cgt	att	ctt	caa	gac	atg	ggc	ctg	cgg	agg	gta	gaa	atc	tat	1296
Tyr	Tyr	Arg	Ile	Leu	Gln	Asp	Met	Gly	Leu	Arg	Arg	Val	Glu	Ile	Tyr	
			420					425					430			
gag	ttc	agc	agg	ctg	aat	atg	ggt	tat	acc	ggt	ctt	agc	aag	cgc	aag	1344
Glu	Phe	Ser	Arg	Leu	Asn	Met	Val	Tyr	Thr	Val	Leu	Ser	Lys	Arg	Lys	
		435				440						445				
ctt	ctg	tgg	ttc	gtc	caa	aac	agg	atg	gtg	gag	gac	tgg	acc	gac	cca	1392
Leu	Leu	Trp	Phe	Val	Gln	Asn	Arg	Met	Val	Glu	Asp	Trp	Thr	Asp	Pro	
	450					455					460					
cgc	ttt	ccc	act	gta	caa	ggc	ata	gta	cgc	cgt	ggc	ttg	aag	att	gaa	1440
Arg	Phe	Pro	Thr	Val	Gln	Gly	Ile	Val	Arg	Arg	Gly	Leu	Lys	Ile	Glu	
465					470				475					480		
gca	ttg	atc	caa	ttt	ata	ctg	gaa	cag	ggg	gct	tca	aaa	aat	ctc	aat	1488
Ala	Leu	Ile	Gln	Phe	Ile	Leu	Glu	Gln	Gly	Ala	Ser	Lys	Asn	Leu	Asn	
				485					490					495		
ctt	atg	gag	tgg	gat	aaa	ctc	tgg	aca	atc	aac	aag	aag	ata	gtt	gat	1536
Leu	Met	Glu	Trp	Asp	Lys	Leu	Trp	Thr	Ile	Asn	Lys	Lys	Ile	Val	Asp	
			500					505					510			
cca	gta	tgt	gga	agg	cat	act	gct	gtg	ctg	aaa	gac	aaa	tgt	gtg	ctt	1584
Pro	Val	Cys	Gly	Arg	His	Thr	Ala	Val	Leu	Lys	Asp	Lys	Cys	Val	Leu	
		515				520						525				
ttg	aca	ctc	act	aat	ggt	cca	gag	gaa	cca	ttt	ggt	cga	atc	tta	cca	1632
Leu	Thr	Leu	Thr	Asn	Gly	Pro	Glu	Glu	Pro	Phe	Val	Arg	Ile	Leu	Pro	
	530				535						540					
agg	cac	aag	aaa	cac	gag	ggt	gct	ggg	aag	aag	gct	aca	acg	ttc	gcc	1680
Arg	His	Lys	Lys	His	Glu	Gly	Ala	Gly	Lys	Lys	Ala	Thr	Thr	Phe	Ala	
545					550				555					560		
aac	aga	att	tgg	cta	gag	tat	gct	gat	gca	tca	gtc	ggt	agc	gtg	ggc	1728
Asn	Arg	Ile	Trp	Leu	Glu	Tyr	Ala	Asp	Ala	Ser	Val	Val	Ser	Val	Gly	
				565					570					575		
gag	gaa	ggt	act	ttg	atg	gac	tgg	gga	aat	gct	atc	att	aga	gaa	atc	1776
Glu	Glu	Val	Thr	Leu	Met	Asp	Trp	Gly	Asn	Ala	Ile	Ile	Arg	Glu	Ile	
			580					585					590			
aag	aca	aat	aat	gga	aca	ggt	act	caa	cta	ggt	ggt	gaa	ctc	cat	ctt	1824
Lys	Thr	Asn	Asn	Gly	Thr	Val	Thr	Gln	Leu	Val	Gly	Glu	Leu	His	Leu	
		595				600						605				
gaa	ggg	tct	gtg	aag	atg	aca	aag	ctg	aaa	cta	aca	tgg	cta	tca	gat	1872
Glu	Gly	Ser	Val	Lys	Met	Thr	Lys	Leu	Lys	Leu	Thr	Trp	Leu	Ser	Asp	
	610					615					620					
att	gaa	gat	ctt	gtg	tct	ctc	tct	ttg	gta	gat	ttt	gac	tac	cta	att	1920
Ile	Glu	Asp	Leu	Val	Ser	Leu	Ser	Leu	Val	Asp	Phe	Asp	Tyr	Leu	Ile	
625					630					635				640		
aat	aaa	aag	aag	ctg	gaa	gaa	gat	gag	gac	ttc	ctt	gac	aat	ctc	aat	1968
Asn	Lys	Lys	Lys	Leu	Glu	Glu	Asp	Glu	Asp	Phe	Leu	Asp	Asn	Leu	Asn	
				645					650					655		
cca	tgc	act	cga	cga	gaa	gct	tta	gct	ctt	ggg	gac	cca	aac	atg	cgg	2016
Pro	Cys	Thr	Arg	Arg	Glu	Ala	Leu	Ala	Leu	Gly	Asp	Pro	Asn	Met	Arg	
			660					665					670			
aac	gtc	aag	aaa	gga	gaa	ggt	ata	cag	ctc	gaa	agg	aaa	gga	tat	tac	2064
Asn	Val	Lys	Lys	Gly	Glu	Val	Ile	Gln	Leu	Glu	Arg	Lys	Gly	Tyr	Tyr	
		675					680					685				
agg	tgt	gat	ggt	cca	ttt	gtc	cgg	tcg	tcc	aaa	cca	att	atg	ctt	ttt	2112

PF59083SeqList PF59083.txt

Arg	Cys	Asp	Val	Pro	Phe	Val	Arg	Ser	Ser	Lys	Pro	Ile	Met	Leu	Phe	
690						695					700					
gcc	att	cca	gat	ggc	cgg	cag	aag	tcc	acg	tcg	att	gtt	act	gga	gca	2160
Ala	Ile	Pro	Asp	Gly	Arg	Gln	Lys	Ser	Thr	Ser	Ile	Val	Thr	Gly	Ala	
705					710					715					720	
tag																2163

<210> 9984
 <211> 720
 <212> PRT
 <213> Hordeum vulgare

<400> 9984

Met	Glu	Leu	Lys	Arg	Ala	Phe	Pro	Gln	Asp	Ser	Leu	Pro	Leu	Ser	Ile	
1				5					10					15		
Ile	Ser	Ala	Ala	Lys	Ile	Ala	Gly	Val	Pro	Leu	Ile	Ile	Asp	Pro	Thr	
		20					25						30			
Leu	Ala	Ser	Gly	Ser	Val	Pro	Thr	Leu	His	Phe	Ser	Ser	Gly	Asp	Phe	
		35					40					45				
Ile	His	Gly	Val	Asn	Thr	Ile	Leu	Arg	Tyr	Ile	Ala	Arg	Ala	Ala	Ser	
	50				55					60						
Val	Ser	Ser	Phe	Tyr	Gly	Gln	Asp	His	Ile	Gln	Ala	Ser	His	Val	Asp	
65					70					75					80	
Gln	Trp	Leu	Glu	Tyr	Ala	Pro	Leu	Ile	Leu	Ser	Gly	Ser	Glu	Phe	Glu	
			85					90						95		
Ala	Ala	Cys	Ser	Phe	Leu	Asp	Gly	Tyr	Leu	Ser	Ser	Arg	Thr	Phe	Leu	
		100					105						110			
Val	Gly	Tyr	Gly	Leu	Ser	Ile	Ala	Asp	Ile	Val	Val	Trp	Ser	Asn	Leu	
		115					120					125				
Thr	Gly	Thr	Gly	Gln	Arg	Trp	Glu	Ser	Leu	Arg	Arg	Ser	Lys	Lys	Tyr	
	130				135					140						
Gln	Ser	Leu	Val	Arg	Trp	Phe	Asn	Ser	Val	Ala	Ala	Asp	Tyr	Ala	Asp	
145					150					155					160	
Ala	Leu	Asp	Glu	Val	Thr	Ser	Ala	Tyr	Val	Gly	Lys	Arg	Gly	Ile	Gly	
			165					170						175		
Lys	Ser	Pro	Ala	Pro	Ser	Leu	Lys	Glu	Lys	Val	Pro	Gly	Leu	Lys	Glu	
		180					185						190			
Asn	Thr	Ser	Gly	His	Glu	Ile	Asp	Leu	Pro	Gly	Ala	Thr	Val	Gly	Glu	
		195					200					205				
Val	Cys	Val	Arg	Phe	Ala	Pro	Glu	Pro	Ser	Gly	Tyr	Leu	His	Ile	Gly	
	210				215					220						
His	Ala	Lys	Ala	Ala	Leu	Asn	Lys	Tyr	Phe	Ala	Glu	Arg	Tyr	Lys		
225					230				235					240		
Gly	Arg	Leu	Ile	Val	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Ser	Lys	Glu	Ser	
			245					250						255		
Asn	Glu	Phe	Val	Glu	Asn	Val	Leu	Lys	Asp	Ile	Glu	Thr	Leu	Gly	Val	
		260					265						270			
Lys	Tyr	Asp	Val	Val	Thr	Tyr	Thr	Ser	Asp	His	Phe	Pro	Lys	Leu	Met	
		275					280					285				
Glu	Met	Ala	Glu	Ser	Leu	Ile	Lys	Gln	Gly	Lys	Ala	Tyr	Val	Asp	Asp	
	290					295					300					
Thr	Pro	Lys	Glu	Gln	Met	Arg	Ser	Glu	Arg	Met	Asp	Gly	Val	Glu	Ser	
305					310					315					320	
Lys	Arg	Arg	Asn	Ser	Thr	Val	Glu	Glu	Asn	Leu	Ser	Leu	Trp	Lys	Glu	
			325						330					335		
Met	Val	Asn	Gly	Thr	Lys	Arg	Gly	Thr	Glu	Cys	Cys	Val	Arg	Gly	Lys	
		340					345						350			
Leu	Asp	Met	Gln	Asp	Pro	Asn	Lys	Ser	Leu	Arg	Asp	Pro	Val	Tyr	Tyr	
		355					360					365				
Arg	Cys	Asn	Pro	Asp	Pro	His	His	Arg	Val	Gly	Ser	Lys	Tyr	Lys	Val	
	370					375					380					
Tyr	Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Phe	Val	Asp	Ala	Leu	Glu	Gly	
385					390					395					400	
Val	Thr	His	Ala	Leu	Arg	Ser	Ser	Glu	Tyr	His	Asp	Arg	Asn	Ala	Gln	
			405					410						415		
Tyr	Tyr	Arg	Ile	Leu	Gln	Asp	Met	Gly	Leu	Arg	Arg	Val	Glu	Ile	Tyr	
			420					425					430			

PF59083SeqList PF59083.txt

Glu Phe Ser Arg Leu Asn Met Val Tyr Thr Val Leu Ser Lys Arg Lys
 435 440 445
 Leu Leu Trp Phe Val Gln Asn Arg Met Val Glu Asp Trp Thr Asp Pro
 450 455 460
 Arg Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Ile Glu
 465 470 475 480
 Ala Leu Ile Gln Phe Ile Leu Glu Gln Gly Ala Ser Lys Asn Leu Asn
 485 490 495
 Leu Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Val Asp
 500 505 510
 Pro Val Cys Gly Arg His Thr Ala Val Leu Lys Asp Lys Cys Val Leu
 515 520 525
 Leu Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro
 530 535 540
 Arg His Lys Lys His Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala
 545 550 555 560
 Asn Arg Ile Trp Leu Glu Tyr Ala Asp Ala Ser Val Val Ser Val Gly
 565 570 575
 Glu Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Ile Arg Glu Ile
 580 585 590
 Lys Thr Asn Asn Gly Thr Val Thr Gln Leu Val Gly Glu Leu His Leu
 595 600 605
 Glu Gly Ser Val Lys Met Thr Lys Leu Lys Leu Thr Trp Leu Ser Asp
 610 615 620
 Ile Glu Asp Leu Val Ser Leu Ser Leu Val Asp Phe Asp Tyr Leu Ile
 625 630 635 640
 Asn Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn
 645 650 655
 Pro Cys Thr Arg Glu Ala Leu Ala Leu Gly Asp Pro Asn Met Arg
 660 665 670
 Asn Val Lys Lys Gly Glu Val Ile Gln Leu Glu Arg Lys Gly Tyr Tyr
 675 680 685
 Arg Cys Asp Val Pro Phe Val Arg Ser Ser Lys Pro Ile Met Leu Phe
 690 695 700
 Ala Ile Pro Asp Gly Arg Gln Lys Ser Thr Ser Ile Val Thr Gly Ala
 705 710 715 720

<210> 9985
 <211> 2388
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (1)..(2388)

<400> 9985
 atg gtc gac ggc gag aag gcc ccg gcc ccg gcc ctg ctg cag ctg gag 48
 Met Val Asp Gly Glu Lys Ala Pro Ala Pro Ala Leu Leu Gln Leu Glu 15
 1 5 10 15
 acg ctg ctg gcg ctc ggc ctc gac cag cgc acg gcc gag aac gcg ctg 96
 Thr Leu Leu Ala Leu Gly Leu Asp Gln Arg Thr Ala Glu Asn Ala Leu 20 25 30
 20 25 30
 gtc aat agc aag gtc acc gcc aac cta gcc gcc gtc gta gcc gag gct 144
 Val Asn Ser Lys Val Thr Ala Asn Leu Ala Val Val Ala Glu Ala 35 40 45
 35 40 45
 ggt ata act gga tgc gac aag tcc gtt ggg aat ctt ctg tac gca gtt 192
 Gly Ile Thr Gly Cys Asp Lys Ser Val Gly Asn Leu Leu Tyr Ala Val 50 55 60
 50 55 60
 gcc acg aaa tac cca aat aat gca ctt gtc cat cgt ccc gct ctc att 240
 Ala Thr Lys Tyr Pro Asn Asn Ala Leu Val His Arg Pro Ala Leu Ile 65 70 75 80
 65 70 75 80
 aac tac atc gtt tcg acg aag att aag aac cct gca cag cta gat gct 288
 Asn Tyr Ile Val Ser Thr Lys Ile Lys Asn Pro Ala Gln Leu Asp Ala 85 90 95
 85 90 95
 gct ctg tcg ttt ctt acc aac act ggt cct gaa tct ttg gat att ggg 336
 Ala Leu Ser Phe Leu Thr Asn Thr Gly Pro Glu Ser Leu Asp Ile Gly 100 105 110
 100 105 110
 aag ttt gaa gaa gcc tgt ggt gta ggt gtg gtt gtt tct att gaa gag 384
 105 110 115 120
 Seite 10566

PF59083SeqList PF59083.txt															
Lys	Phe	Glu	Glu	Ala	Cys	Gly	Val	Gly	Val	Val	Ser	Ile	Glu	Glu	
att	cag	tca	act	ggt	gct	gag	ggt	cta	aag	gaa	aac	atg	gaa	gct	ata
Ile	Gln	Ser	Thr	Val	Ala	Glu	Val	Leu	Lys	Glu	Asn	Met	Glu	Ala	Ile
130						135					140				
tta	gag	cag	cgg	tat	cac	ata	aat	ggt	ggt	ggc	cta	tgc	gga	cag	gtc
Leu	Glu	Gln	Arg	Tyr	His	Ile	Asn	Val	Gly	Gly	Leu	Cys	Gly	Gln	Val
145					150					155					160
agg	aag	cgg	cac	ccc	tgg	ggc	gat	gct	aag	gca	aca	aag	gag	gag	att
Arg	Lys	Arg	His	Pro	Trp	Gly	Asp	Ala	Lys	Ala	Thr	Lys	Glu	Glu	Ile
				165					170						175
gag	aag	aag	ctt	gct	gag	ata	cta	ggt	cca	aag	acg	gaa	gct	gac	aat
Glu	Lys	Lys	Leu	Ala	Glu	Ile	Leu	Gly	Pro	Lys	Thr	Glu	Ala	Asp	Asn
			180					185					190		
gta	aaa	cca	gtg	aaa	aag	aag	aag	gaa	aaa	cca	gca	aaa	ggt	gag	gag
Val	Lys	Pro	Val	Lys	Lys	Lys	Lys	Glu	Lys	Pro	Ala	Lys	Val	Glu	Glu
		195					200					205			
aaa	aaa	ggt	gca	gta	gcc	act	gct	gcc	cca	cca	tct	gag	gag	gaa	ctg
Lys	Lys	Val	Ala	Val	Ala	Thr	Ala	Ala	Pro	Pro	Ser	Glu	Glu	Glu	Leu
210						215					220				
aat	cct	tat	aca	ata	ttt	ccc	cag	cca	gag	gaa	aac	aat	aag	ggt	cat
Asn	Pro	Tyr	Thr	Ile	Phe	Pro	Gln	Pro	Glu	Glu	Asn	Asn	Lys	Val	His
225					230					235					240
aca	gaa	ata	ttc	ttc	agc	gat	ggg	aac	ata	tgg	agg	gca	cac	aac	aca
Thr	Glu	Ile	Phe	Phe	Ser	Asp	Gly	Asn	Ile	Trp	Arg	Ala	His	Asn	Thr
				245				250						255	
aag	gag	ata	tta	gag	aaa	cat	ctt	aag	gca	act	ggt	gga	aaa	gtg	atg
Lys	Glu	Ile	Leu	Glu	Lys	His	Leu	Lys	Ala	Thr	Gly	Gly	Lys	Val	Met
			260					265					270		
acc	cgt	ttc	ccg	cca	gaa	cct	aat	gga	tat	ctt	cat	atc	ggt	cat	gct
Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	Ala
		275					280					285			
aag	gct	atg	ttt	att	gat	ttt	gga	ttg	gct	aaa	gag	cga	aat	ggt	cac
Lys	Ala	Met	Phe	Ile	Asp	Phe	Gly	Leu	Ala	Lys	Glu	Arg	Asn	Gly	His
290						295					300				
tgt	tat	ctc	agg	ttt	gat	gac	aca	aat	cca	gaa	gct	gaa	aag	aaa	gaa
Cys	Tyr	Leu	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys	Lys	Glu
305					310					315					320
tat	ata	gac	cac	att	cag	gag	ata	gtc	aag	tgg	atg	gga	tgg	gag	ccc
Tyr	Ile	Asp	His	Ile	Gln	Glu	Ile	Val	Lys	Trp	Met	Gly	Trp	Glu	Pro
				325				330						335	
tat	aaa	ggt	aca	tat	aca	agt	gat	tat	ttc	caa	gat	tta	tat	gag	cat
Tyr	Lys	Val	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Gln	Asp	Leu	Tyr	Glu	His
			340					345					350		
gca	ggt	gag	tta	ata	cgg	aaa	ggg	cta	gcc	tat	gtg	gat	cac	cag	act
Ala	Val	Glu	Leu	Ile	Arg	Lys	Gly	Leu	Ala	Tyr	Val	Asp	His	Gln	Thr
		355					360					365			
gca	gaa	caa	atc	aag	gaa	tac	agg	gaa	aag	aag	atg	gat	agt	cca	tgg
Ala	Glu	Gln	Ile	Lys	Glu	Tyr	Arg	Glu	Lys	Lys	Met	Asp	Ser	Pro	Trp
370						375					380				
agg	gat	agg	ccc	att	gaa	gag	tct	ctg	cag	tta	ttt	gaa	gac	atg	cga
Arg	Asp	Arg	Pro	Ile	Glu	Glu	Ser	Leu	Gln	Leu	Phe	Glu	Asp	Met	Arg
385					390					395					400
cgc	ggg	ttg	att	gct	gag	ggt	gca	gca	act	ctc	cga	atg	aag	cag	gac
Arg	Gly	Leu	Ile	Ala	Glu	Gly	Ala	Ala	Thr	Leu	Arg	Met	Lys	Gln	Asp
				405				410						415	
atg	cag	aat	gat	aac	aag	aac	atg	tct	gat	tta	ata	gca	tat	aga	ata
Met	Gln	Asn	Asp	Asn	Lys	Asn	Met	Ser	Asp	Leu	Ile	Ala	Tyr	Arg	Ile
			420				425						430		
aaa	ttc	act	cct	cat	ccg	cat	gct	ggc	gac	aaa	tgg	tgt	atc	tat	cca
Lys	Phe	Thr	Pro	His	Pro	His	Ala	Gly	Asp	Lys	Trp	Cys	Ile	Tyr	Pro
		435					440				445				
agc	tat	gac	tat	gct	cat	tgc	atg	gtg	gat	tca	ctt	gaa	aac	att	aca
Ser	Tyr	Asp	Tyr	Ala	His	Cys	Met	Val	Asp	Ser		Glu	Asn	Ile	Thr
450						455					460				
cat	tct	ttg	tgc	acg	ctc	gag	ttc	gac	att	cgt	cgc	ccg	tca	tac	tac
His	Ser	Leu	Cys	Thr	Leu	Glu	Phe	Asp	Ile	Arg	Arg	Pro	Ser	Tyr	Tyr
465					470					475					480
tgg	cta	ctt	ggt	gcc	ttg	ggc	ttg	tac	cag	cca	tat	ggt	tgg	gag	tat

PF59083SeqList PF59083.txt

Trp	Leu	Leu	Val	Ala	Leu	Gly	Leu	Tyr	Gln	Pro	Tyr	Val	Trp	Glu	Tyr	
				485					490					495		
tca	agg	cta	aac	ata	tca	cat	act	atg	atg	tcc	aaa	aga	aag	ttg	aat	1536
Ser	Arg	Leu	Asn	Ile	Ser	His	Thr	Met	Met	Ser	Lys	Arg	Lys	Leu	Asn	
			500					505					510			
cgg	ctt	gtg	aca	gag	aag	tgg	gta	gat	ggg	tgg	gat	gat	cct	cgc	ttg	1584
Arg	Leu	Val	Thr	Glu	Lys	Trp	Val	Asp	Gly	Trp	Asp	Asp	Pro	Arg	Leu	
		515					520					525				
ttg	act	ttg	gca	gga	ctg	agg	cga	cgg	gga	gta	tca	gca	aat	gcg	atc	1632
Leu	Thr	Leu	Ala	Gly	Leu	Arg	Arg	Arg	Gly	Val	Ser	Ala	Asn	Ala	Ile	
	530					535					540					
aat	tca	ttt	atc	cgt	gga	att	ggg	ata	acg	aga	agt	gac	aat	agc	tta	1680
Asn	Ser	Phe	Ile	Arg	Gly	Ile	Gly	Ile	Thr	Arg	Ser	Asp	Asn	Ser	Leu	
	545				550					555					560	
att	cgt	gtt	gac	cgt	ctt	gaa	tat	cat	atc	aga	gaa	gaa	ctg	aat	aaa	1728
Ile	Arg	Val	Asp	Arg	Leu	Glu	Tyr	His	Ile	Arg	Glu	Glu	Leu	Asn	Lys	
				565					570					575		
aca	gct	tct	cga	acc	atg	gtg	gtt	ttg	cat	cct	cta	aag	gtt	gta	ata	1776
Thr	Ala	Ser	Arg	Thr	Met	Val	Val	Leu	His	Pro	Leu	Lys	Val	Val	Ile	
			580					585					590			
act	aac	ttg	gaa	gat	gga	aaa	gtc	ata	gac	ctt	gat	gga	aaa	aag	tg	1824
Thr	Asn	Leu	Glu	Asp	Gly	Lys	Val	Ile	Asp	Leu	Asp	Gly	Lys	Lys	Trp	
		595					600					605				
cct	gat	gct	cct	gct	gat	gaa	gct	tcg	tcc	tac	tac	aag	gtt	cct	ttc	1872
Pro	Asp	Ala	Pro	Ala	Asp	Glu	Ala	Ser	Ser	Tyr	Tyr	Lys	Val	Pro	Phe	
	610					615					620					
tca	aaa	atc	atc	tac	att	gaa	aaa	act	gat	ttt	cgc	gtg	aag	gac	tcc	1920
Ser	Lys	Ile	Ile	Tyr	Ile	Glu	Lys	Thr	Asp	Phe	Arg	Val	Lys	Asp	Ser	
					630					635					640	
aaa	gat	tac	tat	gga	ctg	gct	cct	gg	aaa	tct	gcc	ctg	ctg	agg	tat	1968
Lys	Asp	Tyr	Tyr	Gly	Leu	Ala	Pro	Gly	Lys	Ser	Ala	Leu	Leu	Arg	Tyr	
				645					650					655		
gca	ttc	ccg	ata	aaa	tgc	aca	gag	gtt	att	tat	gg	gat	aat	cca	gat	2016
Ala	Phe	Pro	Ile	Lys	Cys	Thr	Glu	Val	Ile	Tyr	Gly	Asp	Asn	Pro	Asp	
			660					665					670			
gat	att	gtt	gaa	att	cga	gcc	gag	tat	gac	cct	tca	aag	acc	tct	aaa	2064
Asp	Ile	Val	Glu	Ile	Arg	Ala	Glu	Tyr	Asp	Pro	Ser	Lys	Thr	Ser	Lys	
		675					680					685				
cct	aag	gg	gtt	ctg	cac	tgg	gtt	gcc	cag	cca	gca	cct	gga	gtt	gat	2112
Pro	Lys	Gly	Val	Leu	His	Trp	Val	Ala	Gln	Pro	Ala	Pro	Gly	Val	Asp	
		690				695					700					
ccg	tta	aag	gtt	gaa	ata	aga	tta	ttt	gag	aaa	tta	ttc	cta	tct	gag	2160
Pro	Leu	Lys	Val	Glu	Ile	Arg	Leu	Phe	Glu	Lys	Leu	Phe	Leu	Ser	Glu	
				710					715						720	
aat	ccc	gcc	gaa	ttg	gaa	gac	tgg	ctg	gg	ctt	aac	ccg	cac	tca		2208
Asn	Pro	Ala	Glu	Leu	Glu	Asp	Trp	Leu	Gly	Asp	Leu	Asn	Pro	His	Ser	
				725					730					735		
aag	gag	gta	gta	aag	gac	gcc	tat	gct	gta	cct	tca	ctg	gcc	acc	gcg	2256
Lys	Glu	Val	Val	Lys	Asp	Ala	Tyr	Ala	Val	Pro	Ser	Leu	Ala	Thr	Ala	
			740					745					750			
gtt	ctg	ggc	gac	aag	ttc	cag	ttt	gag	cga	ctt	ggc	tac	ttc	gct	gtg	2304
Val	Leu	Gly	Asp	Lys	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Phe	Ala	Val	
		755					760					765				
gac	acg	gac	tcg	acg	ccc	gag	aag	ctt	gtg	ttc	aac	agg	act	gta	acc	2352
Asp	Thr	Asp	Ser	Thr	Pro	Glu	Lys	Leu	Val	Phe	Asn	Arg	Thr	Val	Thr	
		770				775					780					
ctg	cgc	gac	tct	tat	ggg	aag	gct	gga	ccc	aag	tga					2388
Leu	Arg	Asp	Ser	Tyr	Gly	Lys	Ala	Gly	Pro	Lys						
				785		790				795						

<210> 9986

<211> 795

<212> PRT

<213> Triticum aestivum

<400> 9986

Met	Val	Asp	Gly	Glu	Lys	Ala	Pro	Ala	Pro	Ala	Leu	Leu	Gln	Leu	Glu
1				5					10					15	
Thr	Leu	Leu	Ala	Leu	Gly	Leu	Asp	Gln	Arg	Thr	Ala	Glu	Asn	Ala	Leu

Seite 10568

PF59083SeqList PF59083.txt

Seite 10569

PF59083SeqList PF59083.txt

Thr Ala Ser Arg Thr Met Val Val Leu His Pro Leu Lys Val Val Ile
 580 585 590
 Thr Asn Leu Glu Asp Gly Lys Val Ile Asp Leu Asp Gly Lys Lys Trp
 595 600 605
 Pro Asp Ala Pro Ala Asp Glu Ala Ser Ser Tyr Tyr Lys Val Pro Phe
 610 615 620
 Ser Lys Ile Ile Tyr Ile Glu Lys Thr Asp Phe Arg Val Lys Asp Ser
 625 630 635 640
 Lys Asp Tyr Tyr Gly Leu Ala Pro Gly Lys Ser Ala Leu Leu Arg Tyr
 645 650 655
 Ala Phe Pro Ile Lys Cys Thr Glu Val Ile Tyr Gly Asp Asn Pro Asp
 660 665 670
 Asp Ile Val Glu Ile Arg Ala Glu Tyr Asp Pro Ser Lys Thr Ser Lys
 675 680 685
 Pro Lys Gly Val Leu His Trp Val Ala Gln Pro Ala Pro Gly Val Asp
 690 695 700
 Pro Leu Lys Val Glu Ile Arg Leu Phe Glu Lys Leu Phe Leu Ser Glu
 705 710 715 720
 Asn Pro Ala Glu Leu Glu Asp Trp Leu Gly Asp Leu Asn Pro His Ser
 725 730 735
 Lys Glu Val Val Lys Asp Ala Tyr Ala Val Pro Ser Leu Ala Thr Ala
 740 745 750
 Val Leu Gly Asp Lys Phe Gln Phe Glu Arg Leu Gly Tyr Phe Ala Val
 755 760 765
 Asp Thr Asp Ser Thr Pro Glu Lys Leu Val Phe Asn Arg Thr Val Thr
 770 775 780
 Leu Arg Asp Ser Tyr Gly Lys Ala Gly Pro Lys
 785 790 795

<210> 9987
 <211> 2388
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(2388)

<400> 9987
 atg ccg gcg aag gac gac ggc tcc gac aag gag aag tgc ctc gat ctc 48
 Met Pro Ala Lys Asp Asp Gly Ser Asp Lys Glu Lys Cys Leu Asp Leu
 1 5 10 15
 ttt ctc aag atc ggc tta gac gag cgc acg gct aaa aac acg gtc gcc 96
 Phe Leu Lys Ile Gly Leu Asp Glu Arg Thr Ala Lys Asn Thr Val Ala
 20 25 30
 aac aac aaa gtc act gcc aat ctc act tcc gtc atc gac gag gcc ggt 144
 Asn Asn Lys Val Thr Ala Asn Leu Thr Ser Val Ile Asp Glu Ala Gly
 35 40 45
 gct act gat gga tgc agc cga acg gtc gga aat ttt ctt tac acg gtt 192
 Ala Thr Asp Gly Cys Ser Arg Thr Val Gly Asn Phe Leu Tyr Thr Val
 50 55 60
 gcg acg aag tac cct gca aat gcc ttg ccg cat cgc cca aca tta cta 240
 Ala Thr Lys Tyr Pro Ala Asn Ala Leu Pro His Arg Pro Thr Leu Leu
 65 70 75 80
 cag tac att gtc tgc tta aag gtg aaa aca act gcc cag tta gat gca 288
 Gln Tyr Ile Val Ser Leu Lys Val Lys Thr Thr Ala Gln Leu Asp Ala
 85 90 95
 gca tta tca ttt ctt gct acc aca ggc tcc gag aat ctt gat ttg gac 336
 Ala Leu Ser Phe Leu Ala Thr Thr Gly Ser Glu Asn Leu Asp Leu Asp
 100 105 110
 cgg ttt gaa gaa gct tgt ggt gtt ggt gtt gag gtt tca gaa gaa gat 384
 Arg Phe Glu Glu Ala Cys Gly Val Gly Val Glu Val Ser Glu Glu Asp
 115 120 125
 atc aaa caa gct gtt agt gaa gtt gtt gag gag aac aag gct aca att 432
 Ile Lys Gln Ala Val Ser gaa gtt gtt Val Val Glu Glu Asn Lys Ala Thr Ile
 130 135 140
 ttg gag cta cgt tat cga aca aat gtg ggt gag ttg ctg ggg cat gtg 480
 Leu Glu Leu Arg Tyr Arg Thr Asn Val Gly Glu Leu Leu Gly His Val
 145 150 155 160

PF59083SeqList PF59083.txt																
cgc	aag	agg	ctg	cca	tgg	ggt	gat	gca	aaa	ggt	tgc	caa	ggc	aac	ttg	528
Arg	Lys	Arg	Leu	Pro	Trp	Gly	Asp	Ala	Lys	Gly	Cys	Gln	Gly	Asn	Leu	
				165					170					175		
ttg	atg	caa	aac	tat	atg	aac	tta	ctt	ggt	gat	cgg	aca	gca	gca	gat	576
Leu	Met	Gln	Asn	Tyr	Met	Asn	Leu	Leu	Gly	Asp	Arg	Thr	Ala	Ala	Asp	
			180					185					190			
gat	gaa	aag	cct	tct	aga	aag	aag	aag	gag	aaa	cct	gct	aaa	gta	gag	624
Asp	Glu	Lys	Pro	Ser	Arg	Lys	Lys	Lys	Glu	Lys	Pro	Ala	Lys	Val	Glu	
		195					200				205					
gat	aag	gca	gct	cct	ggt	tct	acc	cct	gaa	aag	tca	cct	gaa	gaa	gac	672
Asp	Lys	Ala	Ala	Pro	Val	Ser	Thr	Pro	Glu	Lys	Pro	Pro	Glu	Glu	Asp	
	210					215					220					
ctt	aat	cca	ttt	tta	ata	ttc	cct	aat	cca	gag	gaa	aat	ttc	aag	gtg	720
Leu	Asn	Pro	Phe	Leu	Ile	Phe	Pro	Asn	Pro	Glu	Glu	Asn	Phe	Lys	Val	
225				230					235						240	
cat	act	gaa	gtg	cct	agt	gat	ggt	agt	att	ttg	aga	tgt	tgc	aat		768
His	Thr	Glu	Val	Pro	Phe	Ser	Asp	Gly	Ser	Ile	Leu	Arg	Cys	Cys	Asn	
			245				250						255			
aca	aga	gat	ctg	ctt	gac	aaa	cac	tta	aaa	gca	aca	ggt	gga	aaa	gtc	816
Thr	Arg	Asp	Leu	Leu	Asp	Lys	His	Leu	Lys	Ala	Thr	Gly	Gly	Lys	Val	
			260				265					270				
ttg	acc	cgg	ttt	cca	ccc	gaa	cct	aat	gga	tat	ttg	cat	att	ggc	cat	864
Leu	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Asn	Gly	Tyr	Leu	His	Ile	Gly	His	
		275					280				285					
gca	aaa	gca	atg	ttt	att	gat	ttt	ggg	ttg	gcg	aaa	gac	agg	gat	gga	912
Ala	Lys	Ala	Met	Phe	Ile	Asp	Phe	Gly	Leu	Ala	Lys	Asp	Arg	Asp	Gly	
	290					295					300					
ggt	ggc	act	tcc	agg	tat	gat	gat	aca	aat	cct	gaa	gca	gaa	aag	aaa	960
Gly	Gly	Thr	Ser	Arg	Tyr	Asp	Asp	Thr	Asn	Pro	Glu	Ala	Glu	Lys	Lys	
305					310					315					320	
gag	tat	att	gat	cat	att	gaa	gaa	att	gtc	cag	tgg	atg	ggt	tgg	aaa	1008
Glu	Tyr	Ile	Asp	His	Ile	Glu	Glu	Ile	Val	Gln	Trp	Met	Gly	Trp	Lys	
			325					330					335			
cca	ttt	aag	att	act	tac	aca	agt	gat	tac	ttc	caa	gaa	ttg	tac	gaa	1056
Pro	Phe	Lys	Ile	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Gln	Glu	Leu	Tyr	Glu	
			340				345						350			
tta	gca	gtg	gag	ctc	ata	aaa	aag	ggt	cat	gct	tat	ggt	gat	cat	cag	1104
Leu	Ala	Val	Glu	Leu	Ile	Lys	Lys	Gly	His	Ala	Tyr	Val	Asp	His	Gln	
		355				360					365					
aca	cct	gat	gag	ata	aag	gag	tat	agg	gag	aag	aaa	ctg	aac	agt	cct	1152
Thr	Pro	Asp	Glu	Ile	Lys	Glu	Tyr	Arg	Glu	Lys	Lys	Leu	Asn	Ser	Pro	
	370					375					380					
tgg	aga	gac	aga	cca	att	tca	gag	tca	ttg	aaa	ctc	ttt	gag	gat	atg	1200
Trp	Arg	Asp	Arg	Pro	Ile	Ser	Glu	Ser	Leu	Lys	Leu	Phe	Glu	Asp	Met	
385					390					395					400	
aaa	aat	ggc	agt	atc	gaa	gaa	gga	aaa	gcc	act	ctt	aga	atg	aag	cag	1248
Lys	Asn	Gly	Ser	Ile	Glu	Glu	Gly	Lys	Ala	Thr	Leu	Arg	Met	Lys	Gln	
			405				410						415			
gac	atg	cag	agt	gat	aac	tac	aat	atg	tat	gac	ctt	att	gca	tat	aga	1296
Asp	Met	Gln	Ser	Asp	Asn	Tyr	Asn	Met	Tyr	Asp	Leu	Ile	Ala	Tyr	Arg	
			420				425						430			
att	aag	ttt	acc	cca	cac	cct	cat	gct	gga	gac	aaa	tgg	tgt	atc	tat	1344
Ile	Lys	Phe	Thr	Pro	His	Pro	His	Ala	Gly	Asp	Lys	Trp	Cys	Ile	Tyr	
		435				440					445					
cca	agt	tat	gat	tat	gca	cac	tgc	att	gtg	gat	tct	cta	gag	aat	atc	1392
Pro	Ser	Tyr	Asp	Tyr	Ala	His	Cys	Ile	Val	Asp	Ser	Leu	Glu	Asn	Ile	
			450			455					460					
aca	cat	tca	ctg	tgt	aca	ctt	gaa	ttt	gag	aca	cgt	cgt	gca	tca	tac	1440
Thr	His	Ser	Leu	Cys	Thr	Leu	Glu	Phe	Glu	Thr	Arg	Arg	Ala	Ser	Tyr	
465				470					475						480	
tat	tgg	ttg	ttg	cat	gcg	tta	ggc	att	tac	caa	cct	tat	gtg	tgg	gag	1488
Tyr	Trp	Leu	Leu	His	Ala	Leu	Gly	Ile	Tyr	Gln	Pro	Tyr	Val	Trp	Glu	
			485				490						495			
tat	tca	agg	ttg	aat	gtc	tct	aac	aca	ggt	atg	tca	aag	cgt	aag	cta	1536
Tyr	Ser	Arg	Leu	Asn	Val	Ser	Asn	Thr	Val	Met	Ser	Lys	Arg	Lys	Leu	
			500				505						510			
aat	cgt	cta	ggt	aca	gag	aag	tgg	ggt	gat	ggg	tgg	gat	gat	cct	cgt	1584
Asn	Arg	Leu	Val	Thr	Glu	Lys	Trp	Val	Asp	Gly	Trp	Asp	Asp	Pro	Arg	
		515					520					525				

PF59083SeqList PF59083.txt

ttg atg aca cta gct ggt ttg cgg cgt aga ggc atg acc cca act gca	1632
Leu Met Thr Leu Ala Gly Leu Arg Arg Arg Gly Met Thr Pro Thr Ala	
530	
atc aat gct ttt gtc cga gga att gga ata act aga agt gat ggc act	1680
Ile Asn Ala Phe Val Arg Gly Ile Gly Ile Thr Arg Ser Asp Gly Thr	
545	
ttg att tct gtg gaa cgc ctt gaa tat cat gtt agg gaa gaa ttg aac	1728
Leu Ile Ser Val Glu Arg Leu Glu Tyr His Val Arg Glu Glu Leu Asn	
565	
aaa aca gca cct cgt gca atg gtt gtc cta cat cca ctc aag gtt gtc	1776
Lys Thr Ala Pro Arg Ala Met Val Val Leu His Pro Leu Lys Val Val	
580	
att act aat ctt gaa gcc aac tca gca att gag gtt gat gca aag aaa	1824
Ile Thr Asn Leu Glu Ala Asn Ser Ala Ile Glu Val Asp Ala Lys Lys	
595	
tgg cct gat gct caa gct gat gat gct tct gct ttc tac aag att cca	1872
Trp Pro Asp Ala Gln Ala Asp Asp Ala Ser Ala Phe Tyr Lys Ile Pro	
610	
ttt tcc aat gtt gta tat att gaa cat tcg gac ttc cgg atg caa gat	1920
Phe Ser Asn Val Val Tyr Ile Glu His Ser Asp Phe Arg Met Gln Asp	
625	
tca aaa gat tat tat ggc ctt gct cct ggg aaa tct gtg ata ctc aga	1968
Ser Lys Asp Tyr Tyr Gly Leu Ala Pro Gly Lys Ser Val Ile Leu Arg	
645	
tat gca ttt cct ata aag tgc act gaa gtt att cta gct gat gat aat	2016
Tyr Ala Phe Pro Ile Lys Cys Thr Glu Val Ile Leu Ala Asp Asp Asn	
660	
gag act att ctt gaa att cga gcc gag tat gat cct tca aag aag acc	2064
Glu Thr Ile Leu Glu Ile Arg Ala Glu Tyr Asp Pro Ser Lys Lys Thr	
675	
aag cct aag ggg gtt ctc cat tgg gtt gct caa cct tct cct gga gtt	2112
Lys Pro Lys Gly Val Leu His Trp Val Ala Gln Pro Ser Pro Gly Val	
690	
gat cca ttg aag gtg gaa gtc aga ttg ttt gag agg cta ttc cta tca	2160
Asp Pro Leu Lys Val Glu Val Arg Leu Phe Glu Arg Leu Phe Leu Ser	
705	
gag aat ccc gct gaa ctt gac aac tgg ctt ggc gat ttg aac cca aat	2208
Glu Asn Pro Ala Glu Leu Asp Asn Trp Leu Gly Asp Leu Asn Pro Asn	
725	
tcc aaa gtg ata att ccc gat gca tat ggt gtg tct tcc ata cag aat	2256
Ser Lys Val Ile Ile Pro Asp Ala Tyr Gly Val Ser Ser Ile Gln Asn	
740	
gca aaa gtt ggg gac aat ttc caa ttt gaa aga tta ggc tat ttt gtg	2304
Ala Lys Val Gly Asp Asn Phe Gln Phe Glu Arg Leu Gly Tyr Phe Val	
755	
gtt gac cgg gac tcg aca tca gaa aaa ctt gtt ttt aat agg act gtc	2352
Val Asp Arg Asp Ser Thr Ser Glu Lys Leu Val Phe Asn Arg Thr Val	
770	
acc tta aag ggc agc tat agc aaa ggt gga aag tag	2388
Thr Leu Lys Gly Ser Tyr Ser Lys Gly Gly Lys	
785	
790	

<210> 9988

<211> 795

<212> PRT

<213> Glycine max

<400> 9988

Met Pro Ala Lys Asp Asp Gly Ser Asp Lys Glu Lys Cys Leu Asp Leu	
1 Phe Leu Lys Ile Gly Leu Asp Glu Arg Thr Ala Lys Asn Thr Val Ala	
20 Asn Asn Lys Val Thr Ala Asn Leu Thr Ser Val Ile Asp Glu Ala Gly	
35 Ala Thr Asp Gly Cys Ser Arg Thr Val Gly Asn Phe Leu Tyr Thr Val	
50 Ala Thr Lys Tyr Pro Ala Asn Ala Leu Pro His Arg Pro Thr Leu Leu	
65 Gln Tyr Ile Val Ser Leu Lys Val Lys Thr Thr Ala Gln Leu Asp Ala	
70	
75	
80	

PF59083SeqList PF59083.txt

				85					90				95		
Ala	Leu	Ser	Phe 100	Leu	Ala	Thr	Thr	Gly 105	Ser	Glu	Asn	Leu	Asp 110	Leu	Asp
Arg	Phe	Glu 115	Glu	Ala	Cys	Gly	Val 120	Gly	Val	Glu	Val	Ser 125	Glu	Glu	Asp
Ile	Lys 130	Gln	Ala	Val	Ser	Glu 135	Val	Val	Glu	Glu	Asn 140	Lys	Ala	Thr	Ile
Leu 145	Glu	Leu	Arg	Tyr	Arg 150	Thr	Asn	Val	Gly	Glu 155	Leu	Leu	Gly	His	Val 160
Arg	Lys	Arg	Leu	Pro 165	Trp	Gly	Asp	Ala	Lys 170	Gly	Cys	Gln	Gly	Asn 175	Leu
Leu	Met	Gln	Asn 180	Tyr	Met	Asn	Leu	Leu 185	Gly	Asp	Arg	Thr	Ala 190	Ala	Asp
Asp	Glu	Lys 195	Pro	Ser	Arg	Lys	Lys 200	Lys	Glu	Lys	Pro	Ala 205	Lys	Val	Glu
Asp	Lys 210	Ala	Ala	Pro	Val	Ser 215	Thr	Pro	Glu	Lys	Ser 220	Pro	Glu	Glu	Asp
Leu 225	Asn	Pro	Phe	Leu	Ile 230	Phe	Pro	Asn	Pro	Glu 235	Glu	Asn	Phe	Lys	Val 240
His	Thr	Glu	Val	Pro 245	Phe	Ser	Asp	Gly	Ser 250	Ile	Leu	Arg	Cys	Cys 255	Asn
Thr	Arg	Asp	Leu 260	Leu	Asp	Lys	His	Leu 265	Lys	Ala	Thr	Gly	Gly 270	Lys	Val
Leu	Thr	Arg 275	Phe	Pro	Pro	Glu	Pro 280	Asn	Gly	Tyr	Leu	His 285	Ile	Gly	His
Ala	Lys 290	Ala	Met	Phe	Ile	Asp 295	Phe	Gly	Leu	Ala	Lys 300	Asp	Arg	Asp	Gly
Gly 305	Gly	Thr	Ser	Arg	Tyr 310	Asp	Asp	Thr	Asn	Pro 315	Glu	Ala	Glu	Lys	Lys 320
Glu	Tyr	Ile	Asp	His 325	Ile	Glu	Glu	Ile	Val 330	Gln	Trp	Met	Gly	Trp 335	Lys
Pro	Phe	Lys	Ile 340	Thr	Tyr	Thr	Ser	Asp 345	Tyr	Phe	Gln	Glu	Leu 350	Tyr	Glu
Leu	Ala	Val 355	Glu	Leu	Ile	Lys	Lys 360	Gly	His	Ala	Tyr	Val 365	Asp	His	Gln
Thr	Pro 370	Asp	Glu	Ile	Lys	Glu 375	Tyr	Arg	Glu	Lys	Lys 380	Leu	Asn	Ser	Pro
Trp 385	Arg	Asp	Arg	Pro	Ile 390	Ser	Glu	Ser	Leu	Lys 395	Leu	Phe	Glu	Asp	Met 400
Lys	Asn	Gly	Ser	Ile 405	Glu	Glu	Gly	Lys	Ala 410	Thr	Leu	Arg	Met	Lys 415	Gln
Asp	Met	Gln	Ser 420	Asp	Asn	Tyr	Asn	Met 425	Tyr	Asp	Leu	Ile	Ala 430	Tyr	Arg
Ile	Lys	Phe 435	Thr	Pro	His	Pro	His 440	Ala	Gly	Asp	Lys	Trp 445	Cys	Ile	Tyr
Pro	Ser 450	Tyr	Asp	Tyr	Ala	His 455	Cys	Ile	Val	Asp	Ser 460	Leu	Glu	Asn	Ile
Thr 465	His	Ser	Leu	Cys	Thr 470	Leu	Glu	Phe	Glu	Thr 475	Arg	Arg	Ala	Ser	Tyr 480
Tyr	Trp	Leu	Leu	His 485	Ala	Leu	Gly	Ile	Tyr 490	Gln	Pro	Tyr	Val	Trp 495	Glu
Tyr	Ser	Arg	Leu 500	Asn	Val	Ser	Asn	Thr 505	Val	Met	Ser	Lys	Arg 510	Lys	Leu
Asn	Arg	Leu 515	Val	Thr	Glu	Lys	Trp 520	Val	Asp	Gly	Trp	Asp 525	Asp	Pro	Arg
Leu	Met 530	Thr	Leu	Ala	Gly	Leu 535	Arg	Arg	Arg	Gly	Met 540	Thr	Pro	Thr	Ala
Ile 545	Asn	Ala	Phe	Val	Arg 550	Gly	Ile	Gly	Ile	Thr 555	Arg	Ser	Asp	Gly	Thr 560
Leu	Ile	Ser	Val	Glu 565	Arg	Leu	Glu	Tyr	His 570	Val	Arg	Glu	Glu	Leu 575	Asn
Lys	Thr	Ala	Pro 580	Arg	Ala	Met	Val	Val 585	Leu	His	Pro	Leu	Lys 590	Val	Val
Ile	Thr	Asn 595	Leu	Glu	Ala	Asn	Ser 600	Ala	Ile	Glu	Val	Asp 605	Ala	Lys	Lys
Trp	Pro 610	Asp	Ala	Gln	Ala	Asp 615	Asp	Ala	Ser	Ala	Phe 620	Tyr	Lys	Ile	Pro
Phe 625	Ser	Asn	Val	Val											

PF59083SeqList PF59083.txt

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

<210> 9989
 <211> 2148
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(2148)

<400> 9989

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

PF59083SeqList PF59083.txt																	
195200205																	
tgc Cys	ggt Val 210	cgt Arg	ttt Phe	gcc Ala	cca Pro	gag Glu 215	cct Pro	agt Ser	ggt Gly	tac Tyr	ctc Leu 220	cat His	att Ile	ggg Gly	cat His	672	
gca Ala 225	aag Lys	gct Ala	gca Ala	cta Leu	ttg Leu 230	aac Asn	aaa Lys	tac Tyr	ttt Phe	gct Ala 235	gaa Glu	aga Arg	tat Tyr	caa Gln	ggg Gly 240	720	
cgc Arg	tta Leu	ata Ile	gtt Val	cga Arg 245	ttt Phe	gat Asp	gac Asp	aca Thr	aac Asn 250	cct Pro	tca Ser	aaa Lys	gaa Glu	agc Ser 255	aat Asn	768	
gag Glu	ttt Phe	ggt Val	gag Glu 260	aat Asn	ctt Leu	ttg Leu	aaa Lys	gat Asp 265	att Ile	gag Glu	acg Thr	ttg Leu 270	ggg Gly 270	atc Ile	aaa Lys	816	
tat Tyr	gat Asp	gct Ala 275	gtc Val	aca Thr	tac Tyr	aca Thr	tct Ser 280	gat Asp	tat Tyr	ttc Phe	cca Pro	aag Lys 285	cta Leu	atg Met	gaa Glu	864	
atg Met	gct Ala 290	gag Glu	agt Ser	ttg Leu	ata Ile	aag Lys 295	cag Gln	ggt Gly	aaa Lys	gca Ala	tat Tyr 300	att Ile	gat Asp	gac Asp	aca Thr	912	
cca Pro 305	aag Lys	gag Glu	caa Gln	atg Met	agg Arg 310	aaa Lys	gag Glu	agg Arg	atg Met	gac Asp 315	ggt Gly	att Ile	gag Glu	tca Ser	agg Arg 320	960	
tgc Cys	aga Arg	aat Asn	aat Asn	acc Thr 325	gtg Val	gag Glu	gaa Glu	aat Asn	ctc Leu 330	tca Ser	tta Leu	tgg Trp	aaa Lys	gag Glu 335	atg Met	1008	
gtt Val	aat Asn	gga Gly	act Thr 340	gaa Glu	agg Arg	ggc Gly	atg Met	cag Gln 345	tgc Cys	tgt Cys	gta Val	cgg Arg	ggt Gly 350	aaa Lys	ctt Leu	1056	
gac Asp	atg Met	cag Gln 355	gat Asp	cct Pro	aac Asn	aag Lys	tca Ser 360	ctc Leu	agg Arg	gat Asp	cct Pro	ggt Val 365	tac Tyr	tac Tyr	cgc Arg	1104	
tgt Cys	aat Asn 370	act Thr	gat Asp	cca Pro	cac His	cat His 375	cgt Arg	ggt Val	ggt Gly	tcg Ser	aag Lys 380	tac Tyr	aag Lys	gtc Val	tat Tyr	1152	
cca Pro 385	aca Thr	tat Tyr	gac Asp	ttt Phe	gcg Ala 390	tgc Cys	cca Pro	ttt Phe	ggt Val 395	gat Asp	gca Ala	ttg Leu	gag Glu	ggg Gly	gta Val 400	1200	
aca Thr	cat His	gct Ala	ctt Leu	cgt Arg 405	tcc Ser	agt Ser	gaa Glu	tat Tyr	cat His 410	gac Asp	aga Arg	aat Asn	gca Ala	caa Gln 415	tat Tyr	1248	
tat Tyr	cga Arg	att Ile	ctt Leu 420	caa Gln	gac Asp	atg Met	ggg Gly	ttg Leu 425	agg Arg	aga Arg	gtg Val	gaa Glu	att Ile 430	tat Tyr	gaa Glu	1296	
ttc Phe	agc Ser	cga Arg 435	ttg Leu	aat Asn	atg Met	ggt Val 440	tac Tyr	ctt Thr	ctt Leu	cta Leu	agc Ser	aag Lys 445	cga Arg	aag Lys	ctt Leu	1344	
ctt Leu	tgg Trp 450	ttt Phe	gta Val	caa Gln	aac Asn	aag Lys 455	aag Lys	gtc Val	gaa Glu	gat Asp	tgg Trp 460	aca Thr	gac Asp	cca Pro	cgt Arg	1392	
ttt Phe 465	ccc Pro	act Thr	gtc Val	caa Gln	ggc Gly 470	ata Ile	gta Val	cgt Arg	cgg Arg	ggc Gly 475	ttg Leu	aag Lys	ggt Val	gag Glu	gca Ala 480	1440	
ttg Leu	ata Ile	cag Gln	ttt Phe	ata Ile 485	ctc Leu	caa Gln	cag Gln	ggt Gly	gct Ala 490	tca Ser	aaa Lys	aat Asn	ctg Leu 495	aat Asn	ctc Leu	1488	
atg Met	gag Glu	tgg Trp	gat Asp 500	aaa Lys	ctc Leu	tgg Trp	aca Thr	atc Ile 505	aac Asn	aag Lys	aag Lys	ata Ile 510	att Ile	gat Asp	cca Pro	1536	
gtg Val	tgc Cys	gca Ala 515	agg Arg	cat His	act Thr	gct Ala 520	gtg Val 520	cta Leu	aaa Lys	gac Asp	cag Gln	cgt Arg 525	gtc Val	atc Ile	ttt Phe	1584	
act Thr	ctt Leu 530	aca Thr	aat Asn	ggt Gly	cca Pro	gag Glu 535	gag Glu	cca Pro	ttt Phe	ggt Val	cga Arg 540	att Ile	tta Leu	cca Pro	aga Arg	1632	
cat His 545	aag Lys	aaa Lys															

PF59083SeqList PF59083.txt

565																1776
gaa	gta	acc	ctt	atg	gat	tgg	ggg	aat	gct	att	gtt	aaa	gag	atc	aag	
Glu	Val	Thr	Leu	Met	Asp	Trp	Gly	Asn	Ala	Ile	Val	Lys	Glu	Ile	Lys	
580																
gtg	gag	agt	gga	gta	att	act	gaa	cta	gtt	gga	gaa	ctg	cat	ctt	gag	1824
Val	Glu	Ser	Gly	Val	Ile	Thr	Glu	Leu	Val	Gly	Glu	Leu	His	Leu	Glu	
595																
ggg	tct	gtg	aaa	aca	aca	aaa	ttg	aag	atc	aca	tgg	cta	gca	gat	ata	1872
Gly	Ser	Val	Lys	Thr	Thr	Lys	Leu	Lys	Ile	Thr	Trp	Leu	Ala	Asp	Ile	
610																
gag	gag	cta	gtt	ccc	ctt	tca	ttg	gtt	gaa	ttt	gat	tac	ctc	atc	agc	1920
Glu	Glu	Leu	Val	Pro	Leu	Ser	Leu	Val	Glu	Phe	Asp	Tyr	Leu	Ile	Ser	
625																
aag	aaa	aag	cta	gag	gaa	gac	gag	gac	ttc	ctc	gac	aat	ctc	aac	cct	1968
Lys	Lys	Lys	Leu	Glu	Glu	Asp	Glu	Asp	Phe	Leu	Asp	Asn	Leu	Asn	Pro	
645																
tgc	act	cga	cgg	gaa	atc	cca	gcc	ctt	gga	gat	gcg	aac	atg	agg	aac	2016
Cys	Thr	Arg	Arg	Glu	Ile	Pro	Ala	Leu	Gly	Asp	Ala	Asn	Met	Arg	Asn	
660																
atc	aag	cgt	gga	gag	atc	ata	cag	ctc	gag	agg	aaa	ggc	tac	tat	agg	2064
Ile	Lys	Arg	Gly	Glu	Ile	Ile	Gln	Leu	Glu	Arg	Lys	Gly	Tyr	Tyr	Arg	
675																
tgt	gat	gcc	cct	ttt	atc	aga	tcg	tcc	aaa	ccg	gtg	gtc	ctg	ttt	gcg	2112
Cys	Asp	Ala	Pro	Phe	Ile	Arg	Ser	Ser	Lys	Pro	Val	Val	Leu	Phe	Ala	
690																
atc	cca	gat	ggc	agg	cag	cag	gcc	tcg	ctt	agc	tag					2148
Ile	Pro	Asp	Gly	Arg	Gln	Gln	Ala	Ser	Leu	Ser						
705																
710																
715																

<210>	9990
<211>	715
<212>	PRT
<213>	Zea mays

<400> 9990

Met 1	Glu	Ala	Ala	Leu 5	Ser	Phe	Ser	Lys	Asp 10	Ser	Pro	Pro	Ile	Ser 15	Ile
Ile	Cys	Ala	Ala 20	Lys	Leu	Val	Gly	Leu 25	Pro	Leu	Thr	Ile	Asn 30	His	Ser
Leu	Ala	Ala 35	Gly	Ser	Ala	Pro	Thr 40	Leu	Gln	Phe	Ala	Ser 45	Gly	Glu	Ser
Leu	His 50	Gly	Val	Asn	Pro	Ile 55	Ile	Leu	Tyr	Ile	Ala 60	Arg	Gly	Ala	Thr
Ile 65	Pro	Ser	Leu	Ser	Gly 70	Lys	Asn	Asp	Ile	Glu 75	Phe	Gly	His	Val	Val 80
Glu	Trp	Leu	Glu	Tyr 85	Ala	Pro	Thr	Phe	Leu 90	Ser	Gly	Ser	Glu	Phe 95	Glu
Asn	Ala	Cys	Leu 100	Phe	Val	Asp	Gly	Phe 105	Leu	Ala	Ser	Arg	Thr 110	Phe	Leu
Val	Gly	His 115	Gly	Leu	Thr	Ile	Ala 120	Asp	Ile	Ala	Val	Trp 125	Ser	Asn	Leu
Ala	Gly 130	Ile	Gly	Gln	Arg	Trp 135	Glu	Ser	Leu	Arg	Lys 140	Ser	Lys	Lys	Tyr
Gln 145	Asn	Leu	Val	Arg	Trp 150	Phe	Asn	Ser	Ile	Asp 155	Ser	Glu	Tyr	Lys	Glu 160
Ala	Leu	Asn	Glu 165	Val	Val	Ala	Ala	Phe	Val 170	Gly	Lys	Arg	Gly	Ile 175	Gly
Lys	Ser	Pro	Ala 180	Pro	Ser	Leu	Lys	Glu 185	Lys	Val	His	Asp	Ser 190	Lys	Asp
Pro	Ser	Ala 195	Pro	Glu	Val	Asp	Leu 200	Pro	Gly	Ala	Lys	Val 205	Gly	Lys	Val
Cys	Val 210	Arg	Phe	Ala	Pro	Glu 215	Pro	Ser	Gly	Tyr	Leu 220	His	Ile	Gly	His
Ala 225	Lys	Ala	Ala	Leu	Leu 230	Asn	Lys	Tyr	Phe	Ala 235	Glu	Arg	Tyr	Gln	Gly 240
Arg	Leu	Ile	Val	Arg 245	Phe	Asp	Asp	Thr	Asn 250	Pro	Ser	Lys	Glu	Ser 255	Asn
Glu	Phe	Val	Glu 260	Asn	Leu	Leu	Lys	Asp 265	Ile	Glu	Thr	Leu	Gly 270	Ile	Lys

PF59083SeqList PF59083.txt

Tyr Asp Ala Val Thr Tyr Thr Ser Asp Tyr Phe Pro Lys Leu Met Glu
 275 280 285
 Met Ala Glu Ser Leu Ile Lys Gln Gly Lys Ala Tyr Ile Asp Asp Thr
 290 295 300
 Pro Lys Glu Gln Met Arg Lys Glu Arg Met Asp Gly Ile Glu Ser Arg
 305 310 315 320
 Cys Arg Asn Asn Thr Val Glu Glu Asn Leu Ser Leu Trp Lys Glu Met
 325 330 335
 Val Asn Gly Thr Glu Arg Gly Met Gln Cys Cys Val Arg Gly Lys Leu
 340 345 350
 Asp Met Gln Asp Pro Asn Lys Ser Leu Arg Asp Pro Val Tyr Tyr Arg
 355 360 365
 Cys Asn Thr Asp Pro His His Arg Val Gly Ser Lys Tyr Lys Val Tyr
 370 375 380
 Pro Thr Tyr Asp Phe Ala Cys Pro Phe Val Asp Ala Leu Glu Gly Val
 385 390 395 400
 Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln Tyr
 405 410 415
 Tyr Arg Ile Leu Gln Asp Met Gly Leu Arg Arg Val Glu Ile Tyr Glu
 420 425 430
 Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys Leu
 435 440 445
 Leu Trp Phe Val Gln Asn Lys Lys Val Glu Asp Trp Thr Asp Pro Arg
 450 455 460
 Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Val Glu Ala
 465 470 475 480
 Leu Ile Gln Phe Ile Leu Gln Gln Gly Ala Ser Lys Asn Leu Asn Leu
 485 490 495
 Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp Pro
 500 505 510
 Val Cys Ala Arg His Thr Ala Val Leu Lys Asp Gln Arg Val Ile Phe
 515 520 525
 Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro Arg
 530 535 540
 His Lys Lys Phe Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala Asn
 545 550 555 560
 Arg Ile Trp Leu Asp Tyr Ala Asp Ala Ala Ala Ile Ser Lys Gly Glu
 565 570 575
 Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys
 580 585 590
 Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu
 595 600 605
 Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile
 610 615 620
 Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser
 625 630 635 640
 Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro
 645 650 655
 Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn
 660 665 670
 Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg
 675 680 685
 Cys Asp Ala Pro Phe Ile Arg Ser Ser Lys Pro Val Val Leu Phe Ala
 690 695 700
 Ile Pro Asp Gly Arg Gln Gln Ala Ser Leu Ser
 705 710 715

<210> 9991

<211> 2391

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1)..(2391)

<400> 9991

atg ggc aca ggg gga gac ggg gat aag gcg ggg ccg gcg ctg ccg ctg
 Met Gly Thr Gly Gly Asp Gly Asp Lys Ala Gly Pro Ala Leu Pro Leu
 Seite 10577

PF59083SeqList PF59083.txt

1	5	10	15													
gag Glu	gcg Ala	ctt Leu	ttg Leu	gcg Ala	ctc Leu	ggg Gly	ctc Leu	gac Asp	cag Gln	cgc Arg	acc Thr	gcc Ala	gag Glu	aac Asn	gcg Ala	96
ctc Leu	gtc Val	aac Asn	gcc Ala	aag Lys	gtc Val	acc Thr	gcc Ala	aac Asn	ctc Leu	gcc Ala	gcc Ala	gtc Val	ata Ile	gct Ala	gag Glu	144
gct Ala	ggt Gly	ata Ile	aag Lys	gaa Glu	tgt Cys	gac Asp	aag Lys	tca Ser	att Ile	ggt Gly	aat Asn	ctt Leu	cta Leu	tat Tyr	gca Ala	192
gtt Val	gcc Ala	acc Thr	aag Lys	tac Tyr	cca Pro	act Thr	aat Asn	gca Ala	ctt Leu	gtt Val	cat His	cgc Arg	cct Pro	gtc Val	ctt Leu	240
att Ile	agc Ser	tat Tyr	gtc Val	ttg Leu	tca Ser	aca Thr	aag Lys	ata Ile	aag Lys	agc Ser	cct Pro	gca Ala	cag Gln	cta Leu	gat Asp	288
gct Ala	gcc Ala	ctc Leu	tca Ser	ttt Phe	ctt Leu	act Thr	aat Asn	act Thr	ggt Gly	cct Pro	gat Asp	tct Ser	cta Leu	gat Asp	gtg Val	336
gac Asp	aag Lys	ttt Phe	gaa Glu	gaa Glu	gca Ala	tgt Cys	ggt Gly	gta Val	ggc Gly	gtg Val	gtt Val	gtt Val	tct Ser	att Ile	gag Glu	384
gaa Glu	att Ile	aaa Lys	tct Ser	act Thr	gtt Val	act Thr	gac Asp	att Ile	ctt Leu	gag Glu	gag Glu	aat Asn	atg Met	gaa Glu	gct Ala	432
ata Ile	aag Lys	gag Glu	cag Gln	cgg Arg	tat Tyr	cac His	ata Ile	aat Asn	gtt Val	ggt Gly	atg Met	cta Leu	tgt Cys	gga Gly	cag Gln	480
gtt Val	agg Arg	aag Lys	aga Arg	cac His	ccc Pro	tgg Trp	ggt Gly	gat Asp	gct Ala	aag Lys	gca Ala	gta Val	aag Lys	gag Glu	gaa Glu	528
att Ile	gac Asp	aag Lys	agg Arg	ctt Leu	gca Ala	gaa Glu	atc Ile	cta Leu	ggt Gly	cca Pro	aag Lys	aca Thr	gaa Glu	gct Ala	gac Asp	576
agt Ser	ata Ile	aaa Lys	cca Pro	gtg Val	aaa Lys	aag Lys	aag Lys	gaa Glu	aaa Lys	aca Thr	gca Ala	aaa Lys	gtt Val	gag Glu		624
gag Glu	aaa Lys	aaa Lys	gtt Val	gca Ala	gtt Val	gcc Ala	act Thr	act Thr	gcc Ala	cca Pro	cca Pro	tct Ser	gag Glu	gag Glu	gaa Glu	672
ttg Leu	aac Asn	ccg Pro	tat Tyr	act Thr	ata Ile	ttt Phe	ccc Pro	caa Gln	cca Pro	gag Glu	gaa Glu	aac Asn	ttt Phe	aag Lys	gtt Val	720
cat His	aca Thr	gaa Glu	ata Ile	ttt Phe	ttc Phe	agt Ser	gat Asp	ggg Gly	aac Asn	ata Ile	tgg Trp	aga Arg	gca Ala	cat His	aac Asn	768
aca Thr	aag Lys	gaa Glu	att Ile	ttg Leu	gaa Glu	aaa Lys	cat His	ctc Leu	aag Lys	gca Ala	act Thr	gga Gly	gga Gly	aaa Lys	gtg Val	816
atg Met	acc Thr	cgf Arg	ttt Phe	cca Pro	cca Pro	gaa Glu	cct Pro	aat Asn	gga Gly	tat Tyr	ctt Leu	cat His	att Ile	ggt Gly	cat His	864
gcc Ala	aag Lys	gct Ala	atg Met	ttt Phe	atc Ile	gat Asp	ttt Phe	ggt Gly	ctg Leu	gct Ala	aag Lys	gag Glu	cga Arg	aat Asn	ggc Gly	912
cat His	tgc Cys	tac Tyr	ctt Leu	agg Arg	ttt Phe	gac Asp	gac Asp	aca Thr	aat Asn	ccg Pro	gaa Glu	gct Ala	gaa Glu	aag Lys	aaa Lys	960
gaa Glu	tac Tyr	ata Ile	gat Asp	cac His	att Ile	cag Gln	gaa Glu	atc Ile	gtc Val	cat His	tgg Trp	atg Met	gga Gly	tgg Trp	gag Glu	1008
ccc Pro	tac Tyr	aaa Lys	gta Val	aca Thr	tac Tyr	acg Thr	agt Ser	gac Asp	tat Tyr	ttc Phe	caa Gln	gct Ala	ttg Leu	tat Tyr	gaa Glu	1056
cat His	gcc Ala	gtt Val	gag Glu	tta Leu	ata Ile	cag Gln	aaa Lys	ggg Gly	cta Leu	gca Ala	tat Tyr	gtg Val	gat Asp	cac His	cag Gln	1104
act Thr	gca Ala	gaa Glu	gaa Glu	atc Ile	aag Lys	gaa Glu	tac Tyr	agg Arg	gaa Glu	aag Lys	aag Lys	atg Met	gat Asp	agt Ser	cca Pro	1152

PF59083SeqList PF59083.txt

370	agg	ggt	agg	cca	att	gaa	gag	tct	ctg	aaa	tta	ttt	gaa	gac	atg	1200
Trp	Arg	Gly	Arg	Pro	Ile	Glu	Glu	Ser	Leu	Lys	Leu	Phe	Glu	Asp	Met	
385					390					395					400	
agg	cgt	ggg	ttg	att	gca	gag	ggt	gca	gca	act	ctc	cgt	atg	aag	cag	1248
Arg	Arg	Gly	Leu	Ile	Ala	Glu	Gly	Ala	Ala	Thr	Leu	Arg	Met	Lys	Gln	
				405					410					415		
gat	atg	caa	aat	gag	aac	aaa	aat	atg	tct	gac	tta	ata	gca	tat	aga	1296
Asp	Met	Gln	Asn	Glu	Asn	Lys	Asn	Met	Ser	Asp	Leu	Ile	Ala	Tyr	Arg	
			420					425					430			
ata	aaa	ttc	acc	ccc	cat	cca	cat	gct	ggc	gac	aag	tgg	tgt	gtc	tat	1344
Ile	Lys	Phe	Thr	Pro	His	Pro	His	Ala	Gly	Asp	Lys	Trp	Cys	Val	Tyr	
		435					440					445				
ccg	agc	tat	gac	tac	gct	cat	tgc	atg	gtg	gat	tct	ctt	gaa	aac	atc	1392
Pro	Ser	Tyr	Asp	Tyr	Ala	His	Cys	Met	Val	Asp	Ser	Leu	Glu	Asn	Ile	
	450					455					460					
aca	cat	tcg	ctg	tgc	aca	ctt	gag	ttt	gac	ata	cgt	cgc	cct	tca	tac	1440
Thr	His	Ser	Leu	Cys	Thr	Leu	Glu	Phe	Asp	Ile	Arg	Arg	Pro	Ser	Tyr	
465				470					475						480	
tac	tgg	cta	ctt	gtt	gcc	ttg	ggc	ctt	tat	caa	cca	tat	gtg	tgg	gaa	1488
Tyr	Trp	Leu	Leu	Val	Ala	Leu	Gly	Leu	Tyr	Gln	Pro	Tyr	Val	Trp	Glu	
				485					490					495		
tat	tcg	agg	cta	aac	ata	tca	aat	act	gtg	atg	tct	aaa	aga	aag	ttg	1536
Tyr	Ser	Arg	Leu	Asn	Ile	Ser	Asn	Thr	Val	Met	Ser	Lys	Arg	Lys	Leu	
			500					505					510			
aat	cga	ctt	gtg	aca	gag	aag	tgg	gta	gat	ggg	tgg	gat	gat	ccc	cgc	1584
Asn	Arg	Leu	Val	Thr	Glu	Lys	Trp	Val	Asp	Gly	Trp	Asp	Asp	Pro	Arg	
	515						520				525					
ttg	ttg	aca	ctg	gct	ggt	ctc	cgg	cga	cgg	gga	gta	tca	tca	act	gca	1632
Leu	Leu	Thr	Leu	Ala	Gly	Leu	Arg	Arg	Arg	Gly	Val	Ser	Ser	Thr	Ala	
	530				535						540					
ata	aat	tcc	ttt	att	cgt	gga	atc	ggg	ata	acg	aga	agt	gac	aat	agc	1680
Ile	Asn	Ser	Phe	Ile	Arg	Gly	Ile	Gly	Ile	Thr	Arg	Ser	Asp	Asn	Ser	
545				550					555						560	
tta	att	cgt	gtt	gat	cgt	cta	gaa	tat	cac	atc	agg	gag	gag	ctt	aac	1728
Leu	Ile	Arg	Val	Asp	Arg	Leu	Glu	Tyr	His	Ile	Arg	Glu	Glu	Leu	Asn	
				565					570					575		
aaa	aca	gcc	cct	cga	acc	atg	gtt	gtt	ttg	cga	cct	cta	aag	gtg	gta	1776
Lys	Thr	Ala	Pro	Arg	Thr	Met	Val	Val	Leu	Arg	Pro	Leu	Lys	Val	Val	
			580					585					590			
ata	act	aac	ttg	gaa	gaa	gga	aaa	gta	cta	gac	ctt	gat	ggc	aaa	atg	1824
Ile	Thr	Asn	Leu	Glu	Glu	Gly	Lys	Val	Leu	Asp	Leu	Asp	Gly	Lys	Met	
	595					600						605				
tgg	cct	gat	gct	tct	gat	act	gat	gct	tcc	tcc	cac	tat	aag	gtt	ccg	1872
Trp	Pro	Asp	Ala	Ser	Asp	Thr	Asp	Ala	Ser	Ser	His	Tyr	Lys	Val	Pro	
	610				615						620					
ttc	tca	aga	act	gtc	tac	att	gag	aaa	act	gat	ttt	cgc	cta	aag	gac	1920
Phe	Ser	Arg	Thr	Val	Tyr	Ile	Glu	Lys	Thr	Asp	Phe	Arg	Leu	Lys	Asp	
625				630						635					640	
tca	aaa	gac	tac	tat	ggg	cta	gcc	cct	ggt	aaa	tct	gtc	atg	cta	agg	1968
Ser	Lys	Asp	Tyr	Tyr	Gly	Leu	Ala	Pro	Gly	Lys	Ser	Val	Met	Leu	Arg	
				645					650					655		
tat	gcg	ttc	ccc	ata	aaa	tgc	aca	gat	gtt	atc	tct	ggt	gat	agt	cct	2016
Tyr	Ala	Phe	Pro	Ile	Lys	Cys	Thr	Asp	Val	Ile	Ser	Gly	Asp	Ser	Pro	
			660					665					670			
gat	gat	att	gtt	gaa	att	cga	gct	gaa	tat	gat	cct	ttg	aag	act	tct	2064
Asp	Asp	Ile	Val	Glu	Ile	Arg	Ala	Glu	Tyr	Asp	Pro	Leu	Lys	Thr	Ser	
		675				680						685				
aaa	ctg	aag	ggt	gtt	ctt	cac	tgg	att	gct	gag	cca	gca	cct	ggt	gta	2112
Lys	Leu	Lys	Gly	Val	Leu	His	Trp	Ile	Ala	Glu	Pro	Ala	Pro	Gly	Val	
	690				695						700					
gag	cca	ttg	aag	gtg	gaa	gta	aga	tta	ttc	gag	aaa	ttg	ttc	atg	tca	2160
Glu	Pro	Leu	Lys	Val	Glu	Val	Arg	Leu	Phe	Glu	Lys	Leu	Phe	Met	Ser	
705				710						715					720	
gag	aat	cct	gct	gaa	ttg	gaa	gat	tgg	ctt	ggc	gat	ctt	aac	cca	cac	2208
Glu	Asn	Pro	Ala	Glu	Leu	Glu	Asp	Trp	Leu	Gly	Asp	Leu	Asn	Pro	His	
				725					730					735		
tcg	aaa	gag	gtg	ata	aag	gat	gct	tat	gct	gta	cca	tca	ctt	gcc	act	2256
Ser	Lys	Glu	Val	Ile	Lys	Asp	Ala	Tyr	Ala	Val	Pro	Ser	Leu	Ala	Thr	

PF59083SeqList PF59083.txt

gcg	gtt	ctg	ggt	gac	aag	ttc	cag	ttt	gag	cgg	ctt	ggt	tac	ttc	gcc	2304
Ala	Val	Leu	Gly	Asp	Lys	Phe	Gln	Phe	Glu	Arg	Leu	Gly	Tyr	Phe	Ala	
		755					760					765				
gtg	gat	act	gac	tcc	aca	cct	gag	aaa	ctc	gtg	ttc	aac	aga	act	gtt	2352
Val	Asp	Thr	Asp	Ser	Thr	Pro	Glu	Lys	Leu	Val	Phe	Asn	Arg	Thr	Val	
		770				775					780					
acc	ctc	cgt	gat	tcg	ttc	ggg	aaa	gct	gga	ccc	aag	tga				2391
Thr	Leu	Arg	Asp	Ser	Phe	Gly	Lys	Ala	Gly	Pro	Lys					
785					790					795						

<210> 9992
 <211> 796
 <212> PRT
 <213> Zea mays

<400> 9992
 Met Gly Thr Gly Gly Asp Gly Asp Lys Ala Gly Pro Ala Leu Pro Leu
 1 5 10 15
 Glu Ala Leu Leu Ala Leu Gly Leu Asp Gln Arg Thr Ala Glu Asn Ala
 20 25 30
 Leu Val Asn Ala Lys Val Thr Ala Asn Leu Ala Ala Val Ile Ala Glu
 35 40 45
 Ala Gly Ile Lys Glu Cys Asp Lys Ser Ile Gly Asn Leu Leu Tyr Ala
 50 55 60
 Val Ala Thr Lys Tyr Pro Thr Asn Ala Leu Val His Arg Pro Val Leu
 65 70 75 80
 Ile Ser Tyr Val Leu Ser Thr Lys Ile Lys Ser Pro Ala Gln Leu Asp
 85 90 95
 Ala Ala Leu Ser Phe Leu Thr Asn Thr Gly Pro Asp Ser Leu Asp Val
 100 105 110
 Asp Lys Phe Glu Glu Ala Cys Gly Val Gly Val Val Ser Ile Glu
 115 120 125
 Glu Ile Lys Ser Thr Val Thr Asp Ile Leu Glu Glu Asn Met Glu Ala
 130 135 140
 Ile Lys Glu Gln Arg Tyr His Ile Asn Val Gly Met Leu Cys Gly Gln
 145 150 155 160
 Val Arg Lys Arg His Pro Trp Gly Asp Ala Lys Ala Val Lys Glu Glu
 165 170 175
 Ile Asp Lys Arg Leu Ala Glu Ile Leu Gly Pro Lys Thr Glu Ala Asp
 180 185 190
 Ser Ile Lys Pro Val Lys Lys Lys Lys Glu Lys Thr Ala Lys Val Glu
 195 200 205
 Glu Lys Lys Val Ala Val Ala Thr Thr Ala Pro Pro Ser Glu Glu Glu
 210 215 220
 Leu Asn Pro Tyr Thr Ile Phe Pro Gln Pro Glu Glu Asn Phe Lys Val
 225 230 235 240
 His Thr Glu Ile Phe Phe Ser Asp Gly Asn Ile Trp Arg Ala His Asn
 245 250 255
 Thr Lys Glu Ile Leu Glu Lys His Leu Lys Ala Thr Gly Gly Lys Val
 260 265 270
 Met Thr Arg Phe Pro Pro Glu Pro Asn Gly Tyr Leu His Ile Gly His
 275 280 285
 Ala Lys Ala Met Phe Ile Asp Phe Gly Leu Ala Lys Glu Arg Asn Gly
 290 295 300
 His Cys Tyr Leu Arg Phe Asp Asp Thr Asn Pro Glu Ala Glu Lys Lys
 305 310 315 320
 Glu Tyr Ile Asp His Ile Gln Glu Ile Val His Trp Met Gly Trp Glu
 325 330 335
 Pro Tyr Lys Val Thr Tyr Thr Ser Asp Tyr Phe Gln Ala Leu Tyr Glu
 340 345 350
 His Ala Val Glu Leu Ile Gln Lys Gly Leu Ala Tyr Val Asp His Gln
 355 360 365
 Thr Ala Glu Glu Ile Lys Glu Tyr Arg Glu Lys Lys Met Asp Ser Pro
 370 375 380
 Trp Arg Gly Arg Pro Ile Glu Glu Ser Leu Lys Leu Phe Glu Asp Met
 385 390 395 400
 Arg Arg Gly Leu Ile Ala Glu Gly Ala Ala Thr Leu Arg Met Lys Gln
 405 410 415

PF59083SeqList PF59083.txt

Asp Met Gln Asn Glu Asn Lys Asn Met Ser Asp Leu Ile Ala Tyr Arg
 420 425 430
 Ile Lys Phe Thr Pro His Pro His Ala Gly Asp Lys Trp Cys Val Tyr
 435 440 445
 Pro Ser Tyr Asp Tyr Ala His Cys Met Val Asp Ser Leu Glu Asn Ile
 450 455 460
 Thr His Ser Leu Cys Thr Leu Glu Phe Asp Ile Arg Arg Pro Ser Tyr
 465 470 475 480
 Tyr Trp Leu Leu Val Ala Leu Gly Leu Tyr Gln Pro Tyr Val Trp Glu
 485 490 495
 Tyr Ser Arg Leu Asn Ile Ser Asn Thr Val Met Ser Lys Arg Lys Leu
 500 505 510
 Asn Arg Leu Val Thr Glu Lys Trp Val Asp Gly Trp Asp Asp Pro Arg
 515 520 525
 Leu Leu Thr Leu Ala Gly Leu Arg Arg Arg Gly Val Ser Ser Thr Ala
 530 535 540
 Ile Asn Ser Phe Ile Arg Gly Ile Gly Ile Thr Arg Ser Asp Asn Ser
 545 550 555 560
 Leu Ile Arg Val Asp Arg Leu Glu Tyr His Ile Arg Glu Glu Leu Asn
 565 570 575
 Lys Thr Ala Pro Arg Thr Met Val Val Leu Arg Pro Leu Lys Val Val
 580 585 590
 Ile Thr Asn Leu Glu Glu Gly Lys Val Leu Asp Leu Asp Gly Lys Met
 595 600 605
 Trp Pro Asp Ala Ser Asp Thr Asp Ala Ser Ser His Tyr Lys Val Pro
 610 615 620
 Phe Ser Arg Thr Val Tyr Ile Glu Lys Thr Asp Phe Arg Leu Lys Asp
 625 630 635 640
 Ser Lys Asp Tyr Tyr Gly Leu Ala Pro Gly Lys Ser Val Met Leu Arg
 645 650 655
 Tyr Ala Phe Pro Ile Lys Cys Thr Asp Val Ile Ser Gly Asp Ser Pro
 660 665 670
 Asp Asp Ile Val Glu Ile Arg Ala Glu Tyr Asp Pro Leu Lys Thr Ser
 675 680 685
 Lys Leu Lys Gly Val Leu His Trp Ile Ala Glu Pro Ala Pro Gly Val
 690 695 700
 Glu Pro Leu Lys Val Glu Val Arg Leu Phe Glu Lys Leu Phe Met Ser
 705 710 715 720
 Glu Asn Pro Ala Glu Leu Glu Asp Trp Leu Gly Asp Leu Asn Pro His
 725 730 735
 Ser Lys Glu Val Ile Lys Asp Ala Tyr Ala Val Pro Ser Leu Ala Thr
 740 745 750
 Ala Val Leu Gly Asp Lys Phe Gln Phe Glu Arg Leu Gly Tyr Phe Ala
 755 760 765
 Val Asp Thr Asp Ser Thr Pro Glu Lys Leu Val Phe Asn Arg Thr Val
 770 775 780
 Thr Leu Arg Asp Ser Phe Gly Lys Ala Gly Pro Lys
 785 790 795

<210> 9993

<211> 2148

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1)..(2148)

<400> 9993

atg gag gca gct ttg tca ttc tcc aag gac agc cca cca att tcg ata	48
Met Glu Ala Ala Leu Ser Phe Ser Lys Asp Ser Pro Pro Ile Ser Ile	
1 5 10 15	
att tgt gct gca aag att gtg ggt cta ccc cta acc atc aat cat agc	96
Ile Cys Ala Ala Lys Ile Val Gly Leu Pro Leu Thr Ile Asn His Ser	
20 25 30	
ctc gct gct ggc tcg gca ccc acc cta cag ttt gct tct gga gaa tca	144
Leu Ala Ala Gly Ser Ala Pro Thr Leu Gln Phe Ala Ser Gly Glu Ser	
35 40 45	
ctc cat ggt gtc aac cca atc atc ctc tac att gct aga ggt gca tca	192

PF59083SeqList PF59083.txt

Leu	His	Gly	Val	Asn	Pro	Ile	Ile	Leu	Tyr	Ile	Ala	Arg	Gly	Ala	Ser	
50						55				60						
att	gcc	tcc	tta	tct	gga	aag	aat	gat	att	gag	ttt	ggg	cat	gtt	gtt	240
Ile	Ala	Ser	Leu	Ser	Gly	Lys	Asn	Asp	Ile	Glu	Phe	Gly	His	Val	Val	
65					70					75					80	
gaa	tgg	ctt	gaa	tat	gcc	ccc	acc	ttc	ctt	tca	ggc	tct	gaa	ttt	gaa	288
Glu	Trp	Leu	Glu	Tyr	Ala	Pro	Thr	Phe	Leu	Ser	Gly	Ser	Glu	Phe	Glu	
				85					90					95		
aat	gca	tgc	tta	ttt	gtt	gat	gga	ttc	ttg	gcc	tcc	cgg	acc	ttt	ctg	336
Asn	Ala	Cys	Leu	Phe	Val	Asp	Gly	Phe	Leu	Ala	Ser	Arg	Thr	Phe	Leu	
				100				105					110			
gtt	ggg	cat	ggc	ctg	aca	att	gct	gac	att	gca	gtt	tgg	tca	aat	ctt	384
Val	Gly	His	Gly	Leu	Thr	Ile	Ala	Asp	Ile	Ala	Val	Trp	Ser	Asn	Leu	
				115				120				125				
gct	gga	att	ggg	cag	cgg	tgg	gag	agt	cta	agg	aaa	tca	aag	aaa	tac	432
Ala	Gly	Ile	Gly	Gln	Arg	Trp	Glu	Ser	Leu	Arg	Lys	Ser	Lys	Lys	Tyr	
						135					140					
caa	aat	ctt	gtt	cgc	tgg	ttc	aac	agc	ata	gat	tca	gaa	tac	aaa	gag	480
Gln	Asn	Leu	Val	Arg	Trp	Phe	Asn	Ser	Ile	Asp	Ser	Glu	Tyr	Lys	Glu	
145					150					155					160	
gca	ctg	aac	gaa	gtt	gtg	gct	gca	ttt	gtt	ggg	aaa	cga	ggg	att	gga	528
Ala	Leu	Asn	Glu	Val	Val	Ala	Ala	Phe	Val	Gly	Lys	Arg	Gly	Ile	Gly	
				165					170					175		
aaa	tct	cct	gca	cct	agc	ctt	aag	gag	aag	gta	cat	gac	tca	aag	gac	576
Lys	Ser	Pro	Ala	Pro	Ser	Leu	Lys	Glu	Lys	Val	His	Asp	Ser	Lys	Asp	
				180				185					190			
cca	tca	gct	cca	gaa	gtt	gat	ctc	cct	ggg	gca	aaa	gtt	ggg	aaa	gtc	624
Pro	Ser	Ala	Pro	Glu	Val	Asp	Leu	Pro	Gly	Ala	Lys	Val	Gly	Lys	Val	
				195				200				205				
tgc	gtt	cgt	ttt	gcc	cca	gag	cct	agt	ggg	tac	ctc	cat	att	ggg	cat	672
Cys	Val	Arg	Phe	Ala	Pro	Glu	Pro	Ser	Gly	Tyr	Leu	His	Ile	Gly	His	
						215					220					
gca	aag	gct	gca	cta	ttg	aac	aaa	tac	ttt	gct	gaa	aga	tat	caa	ggg	720
Ala	Lys	Ala	Ala	Leu	Leu	Asn	Lys	Tyr	Phe	Ala	Glu	Arg	Tyr	Gln	Gly	
225					230					235					240	
cgc	tta	ata	gtt	cga	ttt	gat	gac	aca	aac	cct	tca	aaa	gaa	agc	aat	768
Arg	Leu	Ile	Val	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Ser	Lys	Glu	Ser	Asn	
				245					250					255		
gag	ttt	gtt	gag	aat	ctt	ttg	aaa	gat	att	gag	acg	ttg	ggg	atc	aaa	816
Glu	Phe	Val	Glu	Asn	Leu	Leu	Lys	Asp	Ile	Glu	Thr	Leu	Gly	Ile	Lys	
				260				265					270			
tat	gat	gct	gtc	aca	tac	aca	tct	gat	tat	ttc	cca	aag	cta	atg	gaa	864
Tyr	Asp	Ala	Val	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Pro	Lys	Leu	Met	Glu	
				275				280				285				
atg	gct	gag	agt	ttg	ata	aag	cag	ggg	aaa	gca	tat	att	gat	gac	aca	912
Met	Ala	Glu	Ser	Leu	Ile	Lys	Gln	Gly	Lys	Ala	Tyr	Ile	Asp	Asp	Thr	
						295					300					
cca	aag	gag	caa	atg	agg	aaa	gag	agg	atg	gac	ggg	att	gag	tca	agg	960
Pro	Lys	Glu	Gln	Met	Arg	Lys	Glu	Arg	Met	Asp	Gly	Ile	Glu	Ser	Arg	
305					310					315					320	
tgc	aga	aat	aat	acc	gtg	gag	gaa	aat	ctc	tca	tta	tgg	aaa	gag	atg	1008
Cys	Arg	Asn	Asn	Thr	Val	Glu	Glu	Asn	Leu	Ser	Leu	Trp	Lys	Glu	Met	
				325					330					335		
gtt	aat	gga	act	gaa	agg	ggc	atg	cag	tgc	tgt	gta	cgg	ggg	aaa	ctt	1056
Val	Asn	Gly	Thr	Glu	Arg	Gly	Met	Gln	Cys	Cys	Val	Arg	Gly	Lys	Leu	
				340				345					350			
gac	atg	cag	gat	cct	aac	aag	tca	ctc	agg	gat	cct	gtt	tac	tac	cgc	1104
Asp	Met	Gln	Asp	Pro	Asn	Lys	Ser	Leu	Arg	Asp	Pro	Val	Tyr	Tyr	Arg	
				355				360				365				
tgt	aat	act	gat	cca	cac	cat	cgt	gtt	ggg	tcg	aag	tac	aag	gtc	tat	1152
Cys	Asn	Thr	Asp	Pro	His	His	Arg	Val	Gly	Ser	Lys	Tyr	Lys	Val	Tyr	
				370				375				380				
cca	aca	tat	gac	ttt	gcg	tcg	cca	ttt	gtt	gat	gca	ttg	gag	ggg	gta	1200
Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Phe	Val	Asp	Ala	Leu	Glu	Gly	Val	
385					390					395					400	
aca	cat	gct	ctt	cgt	tcc	agt	gaa	tat	cat	gac	aga	aat	gca	caa	tat	1248
Thr	His	Ala	Leu	Arg	Ser	Ser	Glu	Tyr	His	Asp	Arg	Asn	Ala	Gln	Tyr	
				405					410					415		
tat	cga	att	ctt	caa	gac	atg	ggg	ttg	agg	aga	gta	gaa	att	tat	gag	1296

PF59083SeqList PF59083.txt

Tyr	Arg	Ile	Leu	Gln	Asp	Met	Gly	Leu	Arg	Arg	Val	Glu	Ile	Tyr	Glu	
420			420				425					430				
ttc	agc	cga	ttg	aat	atg	gtt	tac	act	ctt	cta	agc	aag	cga	aag	ctt	1344
Phe	Ser	Arg	Leu	Asn	Met	Val	Tyr	Thr	Leu	Leu	Ser	Lys	Arg	Lys	Leu	
435							440					445				
ctt	tgg	ttt	gta	caa	aac	aag	aag	ctc	gaa	gat	tgg	aca	gac	cca	cgt	1392
Leu	Trp	Phe	Val	Gln	Asn	Lys	Lys	Val	Glu	Asp	Trp	Thr	Asp	Pro	Arg	
450						455					460					
ttt	ccc	act	gtc	caa	ggc	ata	gta	cgt	cgg	ggc	ttg	aag	gtt	gag	gca	1440
Phe	Pro	Thr	Val	Gln	Gly	Ile	Val	Arg	Arg	Gly	Leu	Lys	Val	Glu	Ala	
465					470					475					480	
ttg	ata	cag	ttt	ata	ctc	caa	cag	ggg	gct	tca	aaa	aat	ctg	aat	ctc	1488
Leu	Ile	Gln	Phe	Ile	Leu	Gln	Gln	Gly	Ala	Ser	Lys	Asn	Leu	Asn	Leu	
485								490						495		
atg	gag	tgg	gat	aaa	ctc	tgg	aca	atc	aac	aag	aag	ata	att	gat	cca	1536
Met	Glu	Trp	Asp	Lys	Leu	Trp	Thr	Ile	Asn	Lys	Lys	Ile	Ile	Asp	Pro	
500							505						510			
gtg	tgc	gca	agg	cat	act	gct	gtg	cta	aaa	gac	cag	cgt	gtc	atc	ttc	1584
Val	Cys	Ala	Arg	His	Thr	Ala	Val	Leu	Lys	Asp	Gln	Arg	Val	Ile	Phe	
515						520						525				
act	ctt	aca	aat	ggg	cca	gag	gag	cca	ttt	gtt	cga	att	tta	cca	aga	1632
Thr	Leu	Thr	Asn	Gly	Pro	Glu	Glu	Pro	Phe	Val	Arg	Ile	Leu	Pro	Arg	
530						535					540					
cat	aag	aaa	ttt	gag	ggg	gct	gga	aag	aag	gct	aca	acc	ttt	gcc	aac	1680
His	Lys	Lys	Phe	Glu	Gly	Ala	Gly	Lys	Lys	Ala	Thr	Thr	Phe	Ala	Asn	
545					550					555					560	
aga	att	tgg	ctc	gat	tat	gct	gat	gcg	gca	gct	att	agc	aag	ggg	gag	1728
Arg	Ile	Trp	Leu	Asp	Tyr	Ala	Asp	Ala	Ala	Ala	Ile	Ser	Lys	Gly	Glu	
565								570						575		
gaa	gta	acc	ctt	atg	gat	tgg	ggg	aat	gct	att	gtt	aaa	gag	atc	aag	1776
Glu	Val	Thr	Leu	Met	Asp	Trp	Gly	Asn	Ala	Ile	Val	Lys	Glu	Ile	Lys	
580							585						590			
gtg	gag	agt	gga	gta	att	act	gaa	cta	gtt	gga	gaa	ctg	cat	ctt	gag	1824
Val	Glu	Ser	Gly	Val	Ile	Thr	Glu	Leu	Val	Gly	Glu	Leu	His	Leu	Glu	
595							600					605				
ggg	tct	gtg	aaa	aca	aca	aaa	ttg	aag	atc	aca	tgg	cta	gca	gat	ata	1872
Gly	Ser	Val	Lys	Thr	Thr	Lys	Leu	Lys	Ile	Thr	Trp	Leu	Ala	Asp	Ile	
610						615					620					
gag	gag	cta	gtt	ccc	ctt	tca	ttg	gtt	gaa	ttt	gat	tac	ctc	atc	agc	1920
Glu	Glu	Leu	Val	Pro	Leu	Ser	Leu	Val	Glu	Phe	Asp	Tyr	Leu	Ile	Ser	
625					630					635					640	
aag	aaa	aag	cta	gag	gaa	gac	gag	gac	ttc	ctc	gac	aat	ctc	aac	cct	1968
Lys	Lys	Lys	Leu	Glu	Glu	Asp	Glu	Asp	Phe	Leu	Asp	Asn	Leu	Asn	Pro	
645									650					655		
tgc	act	cga	cgg	gaa	atc	cca	gcc	ctt	gga	gat	gcg	aac	atg	agg	aac	2016
Cys	Thr	Arg	Arg	Glu	Ile	Pro	Ala	Leu	Gly	Asp	Ala	Asn	Met	Arg	Asn	
660							665						670			
atc	aag	cgt	gga	gag	atc	ata	cag	ctc	gag	agg	aaa	ggc	tac	tat	agg	2064
Ile	Lys	Arg	Gly	Glu	Ile	Ile	Gln	Leu	Glu	Arg	Lys	Gly	Tyr	Tyr	Arg	
675							680					685				
tgt	gat	gcc	cct	ttt	atc	aga	tcg	tcc	aaa	ccg	gtg	gtc	ctg	ttt	gcg	2112
Cys	Asp	Ala	Pro	Phe	Ile	Arg	Ser	Ser	Lys	Pro	Val	Val	Leu	Phe	Ala	
690						695					700					
atc	cca	gat	ggc	agg	cag	cag	gcc	tcg	ctt	agc	tag					2148
Ile	Pro	Asp	Gly	Arg	Gln	Gln	Ala	Ser	Leu	Ser						
705					710					715						

<210> 9994
 <211> 715
 <212> PRT
 <213> Zea mays

<400> 9994
 Met Glu Ala Ala Leu Ser Phe Ser Lys Asp Ser Pro Pro Ile Ser Ile
 1 5 10 15
 Ile Cys Ala Ala Lys Ile Val Gly Leu Pro Leu Thr Ile Asn His Ser
 20 25 30
 Leu Ala Ala Gly Ser Ala Pro Thr Leu Gln Phe Ala Ser Gly Glu Ser
 35 40 45

PF59083SeqList PF59083.txt

Leu His Gly Val Asn Pro Ile Ile Leu Tyr Ile Ala Arg Gly Ala Ser
 50 55 60
 Ile Ala Ser Leu Ser Gly Lys Asn Asp Ile Glu Phe Gly His Val Val
 65 70 75 80
 Glu Trp Leu Glu Tyr Ala Pro Thr Phe Leu Ser Gly Ser Glu Phe Glu
 85 90 95
 Asn Ala Cys Leu Phe Val Asp Gly Phe Leu Ala Ser Arg Thr Phe Leu
 100 105 110
 Val Gly His Gly Leu Thr Ile Ala Asp Ile Ala Val Trp Ser Asn Leu
 115 120 125
 Ala Gly Ile Gly Gln Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys Tyr
 130 135 140
 Gln Asn Leu Val Arg Trp Phe Asn Ser Ile Asp Ser Glu Tyr Lys Glu
 145 150 155 160
 Ala Leu Asn Glu Val Val Ala Ala Phe Val Gly Lys Arg Gly Ile Gly
 165 170 175
 Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val His Asp Ser Lys Asp
 180 185 190
 Pro Ser Ala Pro Glu Val Asp Leu Pro Gly Ala Lys Val Gly Lys Val
 195 200 205
 Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His
 210 215 220
 Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Gln Gly
 225 230 235 240
 Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser Asn
 245 250 255
 Glu Phe Val Glu Asn Leu Leu Lys Asp Ile Glu Thr Leu Gly Ile Lys
 260 265 270
 Tyr Asp Ala Val Thr Tyr Thr Ser Asp Tyr Phe Pro Lys Leu Met Glu
 275 280 285
 Met Ala Glu Ser Leu Ile Lys Gln Gly Lys Ala Tyr Ile Asp Asp Thr
 290 295 300
 Pro Lys Glu Gln Met Arg Lys Glu Arg Met Asp Gly Ile Glu Ser Arg
 305 310 315 320
 Cys Arg Asn Asn Thr Val Glu Glu Asn Leu Ser Leu Trp Lys Glu Met
 325 330 335
 Val Asn Gly Thr Glu Arg Gly Met Gln Cys Cys Val Arg Gly Lys Leu
 340 345 350
 Asp Met Gln Asp Pro Asn Lys Ser Leu Arg Asp Pro Val Tyr Tyr Arg
 355 360 365
 Cys Asn Thr Asp Pro His His Arg Val Gly Ser Lys Tyr Lys Val Tyr
 370 375 380
 Pro Thr Tyr Asp Phe Ala Cys Pro Phe Val Asp Ala Leu Glu Gly Val
 385 390 395 400
 Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln Tyr
 405 410 415
 Tyr Arg Ile Leu Gln Asp Met Gly Leu Arg Arg Val Glu Ile Tyr Glu
 420 425 430
 Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys Leu
 435 440 445
 Leu Trp Phe Val Gln Asn Lys Lys Val Glu Asp Trp Thr Asp Pro Arg
 450 455 460
 Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Val Glu Ala
 465 470 475 480
 Leu Ile Gln Phe Ile Leu Gln Gln Gly Ala Ser Lys Asn Leu Asn Leu
 485 490 495
 Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp Pro
 500 505 510
 Val Cys Ala Arg His Thr Ala Val Leu Lys Asp Gln Arg Val Ile Phe
 515 520 525
 Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro Arg
 530 535 540
 His Lys Lys Phe Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala Asn
 545 550 555 560
 Arg Ile Trp Leu Asp Tyr Ala Asp Ala Ala Ile Ser Lys Gly Glu
 565 570 575
 Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys
 580 585 590
 Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu

PF59083SeqList PF59083.txt

595 600 605
 Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile
 610 615 620
 Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser
 625 630 635 640
 Lys Lys Lys Leu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro
 645 650 655
 Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn
 660 665 670
 Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg
 675 680 685
 Cys Asp Ala Pro Phe Ile Arg Ser Ser Lys Pro Val Val Leu Phe Ala
 690 695 700
 Ile Pro Asp Gly Arg Gln Gln Ala Ser Leu Ser
 705 710 715

<210> 9995
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 9995
 atgtcttctg tagaagaatt gactc

25

<210> 9996
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 9996
 tcacttggaa gttgcgtcct tcaa

24

<210> 9997
 <211> 834
 <212> PRT
 <213> Artificial sequence

<220>
 <223> consensus sequence

<220>
 <221> Variant
 <222> (2)..(21)
 <223> Xaa in position 2 to 21 is any amino acid

<220>
 <221> Variant
 <222> (22)..(27)
 <223> Xaa in position 22 to 27 is any or no amino acid

<220>
 <221> Variant
 <222> (29)..(37)
 <223> Xaa in position 29 to 37 is any amino acid

<220>
 <221> Variant
 <222> (39)..(54)
 <223> Xaa in position 39 to 54 is any amino acid

<220>
 <221> Variant

```

<222> (55)..(59)
<223> Xaa in position 55 to 59 is any or no amino acid

<220>
<221> Variant
<222> (61)..(64)
<223> Xaa in position 61 to 64 is any amino acid

<220>
<221> Variant
<222> (66)..(66)
<223> Xaa in position 66 is any amino acid

<220>
<221> Variant
<222> (68)..(111)
<223> Xaa in position 68 to 111 is any amino acid

<220>
<221> Variant
<222> (112)..(114)
<223> Xaa in position 112 to 114 is any or no amino acid

<220>
<221> Variant
<222> (116)..(133)
<223> Xaa in position 116 to 133 is any amino acid

<220>
<221> Variant
<222> (134)..(134)
<223> Xaa in position 134 is any or no amino acid

<220>
<221> Variant
<222> (136)..(136)
<223> Xaa in position 136 is any amino acid

<220>
<221> Variant
<222> (138)..(167)
<223> Xaa in position 138 to 167 is any amino acid

<220>
<221> Variant
<222> (168)..(221)
<223> Xaa in position 168 to 221 is any or no amino acid

<220>
<221> Variant
<222> (223)..(225)
<223> Xaa in position 223 to 225 is any amino acid

<220>
<221> Variant
<222> (226)..(227)
<223> Xaa in position 226 to 227 is any or no amino acid

<220>
<221> Variant
<222> (229)..(229)
<223> Xaa in position 229 is any amino acid

<220>
<221> Variant
<222> (231)..(231)
<223> Xaa in position 231 is any amino acid

<220>

```

```

<221> Variant
<222> (241)..(241)
<223> Xaa in position 241 is any amino acid

<220>
<221> Variant
<222> (247)..(247)
<223> Xaa in position 247 is any amino acid

<220>
<221> Variant
<222> (250)..(253)
<223> Xaa in position 250 to 253 is any amino acid

<220>
<221> Variant
<222> (255)..(256)
<223> Xaa in position 255 to 256 is any amino acid

<220>
<221> Variant
<222> (258)..(261)
<223> Xaa in position 258 to 261 is any amino acid

<220>
<221> Variant
<222> (263)..(266)
<223> Xaa in position 263 to 266 is any amino acid

<220>
<221> Variant
<222> (268)..(268)
<223> Xaa in position 268 is any amino acid

<220>
<221> Variant
<222> (275)..(275)
<223> Xaa in position 275 is any amino acid

<220>
<221> Variant
<222> (277)..(283)
<223> Xaa in position 277 to 283 is any amino acid

<220>
<221> Variant
<222> (285)..(289)
<223> Xaa in position 285 to 289 is any amino acid

<220>
<221> Variant
<222> (291)..(291)
<223> Xaa in position 291 is any amino acid

<220>
<221> Variant
<222> (293)..(294)
<223> Xaa in position 293 to 294 is any amino acid

<220>
<221> Variant
<222> (296)..(297)
<223> Xaa in position 296 to 297 is any amino acid

<220>
<221> Variant
<222> (298)..(298)
<223> Xaa in position 298 is any or no amino acid

```

<220>
<221> Variant
<222> (301)..(301)
<223> Xaa in position 301 is any amino acid

<220>
<221> Variant
<222> (306)..(306)
<223> Xaa in position 306 is any amino acid

<220>
<221> Variant
<222> (307)..(307)
<223> Xaa in position 307 is any or no amino acid

<220>
<221> Variant
<222> (310)..(311)
<223> Xaa in position 310 to 311 is any amino acid

<220>
<221> Variant
<222> (313)..(314)
<223> Xaa in position 313 to 314 is any amino acid

<220>
<221> Variant
<222> (317)..(318)
<223> Xaa in position 317 to 318 is any amino acid

<220>
<221> Variant
<222> (320)..(320)
<223> Xaa in position 320 is any amino acid

<220>
<221> Variant
<222> (324)..(334)
<223> Xaa in position 324 to 334 is any amino acid

<220>
<221> Variant
<222> (336)..(341)
<223> Xaa in position 336 to 341 is any amino acid

<220>
<221> Variant
<222> (342)..(352)
<223> Xaa in position 342 to 352 is any or no amino acid

<220>
<221> Variant
<222> (354)..(357)
<223> Xaa in position 354 to 357 is any amino acid

<220>
<221> Variant
<222> (360)..(360)
<223> Xaa in position 360 is any amino acid

<220>
<221> Variant
<222> (362)..(363)
<223> Xaa in position 362 to 363 is any amino acid

<220>
<221> Variant
<222> (365)..(366)
<223> Xaa in position 365 to 366 is any amino acid

```

<220>
<221> Variant
<222> (368)..(369)
<223> Xaa in position 368 to 369 is any amino acid

<220>
<221> Variant
<222> (371)..(379)
<223> Xaa in position 371 to 379 is any amino acid

<220>
<221> Variant
<222> (381)..(381)
<223> Xaa in position 381 is any amino acid

<220>
<221> Variant
<222> (383)..(390)
<223> Xaa in position 383 to 390 is any amino acid

<220>
<221> Variant
<222> (391)..(393)
<223> Xaa in position 391 to 393 is any or no amino acid

<220>
<221> Variant
<222> (395)..(396)
<223> Xaa in position 395 to 396 is any amino acid

<220>
<221> Variant
<222> (400)..(403)
<223> Xaa in position 400 to 403 is any amino acid

<220>
<221> Variant
<222> (406)..(408)
<223> Xaa in position 406 to 408 is any amino acid

<220>
<221> Variant
<222> (410)..(410)
<223> Xaa in position 410 is any amino acid

<220>
<221> Variant
<222> (413)..(413)
<223> Xaa in position 413 is any amino acid

<220>
<221> Variant
<222> (417)..(417)
<223> Xaa in position 417 is any amino acid

<220>
<221> Variant
<222> (420)..(421)
<223> Xaa in position 420 to 421 is any amino acid

<220>
<221> Variant
<222> (424)..(425)
<223> Xaa in position 424 to 425 is any amino acid

<220>
<221> Variant
<222> (428)..(428)

```

<223> Xaa in position 428 is any amino acid

<220>
<221> Variant
<222> (430)..(430)
<223> Xaa in position 430 is any amino acid

<220>
<221> Variant
<222> (438)..(438)
<223> Xaa in position 438 is any amino acid

<220>
<221> Variant
<222> (441)..(443)
<223> Xaa in position 441 to 443 is any amino acid

<220>
<221> Variant
<222> (445)..(445)
<223> Xaa in position 445 is any amino acid

<220>
<221> Variant
<222> (448)..(448)
<223> Xaa in position 448 is any amino acid

<220>
<221> Variant
<222> (451)..(462)
<223> Xaa in position 451 to 462 is any amino acid

<220>
<221> Variant
<222> (464)..(465)
<223> Xaa in position 464 to 465 is any amino acid

<220>
<221> Variant
<222> (469)..(471)
<223> Xaa in position 469 to 471 is any amino acid

<220>
<221> Variant
<222> (473)..(474)
<223> Xaa in position 473 to 474 is any amino acid

<220>
<221> Variant
<222> (479)..(482)
<223> Xaa in position 479 to 482 is any amino acid

<220>
<221> Variant
<222> (484)..(487)
<223> Xaa in position 484 to 487 is any amino acid

<220>
<221> Variant
<222> (489)..(490)
<223> Xaa in position 489 to 490 is any amino acid

<220>
<221> Variant
<222> (496)..(497)
<223> Xaa in position 496 to 497 is any amino acid

<220>
<221> Variant

<222> (499)..(503)
<223> Xaa in position 499 to 503 is any amino acid

<220>
<221> Variant
<222> (507)..(510)
<223> Xaa in position 507 to 510 is any amino acid

<220>
<221> Variant
<222> (512)..(514)
<223> Xaa in position 512 to 514 is any amino acid

<220>
<221> Variant
<222> (516)..(519)
<223> Xaa in position 516 to 519 is any amino acid

<220>
<221> Variant
<222> (521)..(521)
<223> Xaa in position 521 is any amino acid

<220>
<221> Variant
<222> (523)..(537)
<223> Xaa in position 523 to 537 is any amino acid

<220>
<221> Variant
<222> (538)..(538)
<223> Xaa in position 538 is any or no amino acid

<220>
<221> Variant
<222> (540)..(541)
<223> Xaa in position 540 to 541 is any amino acid

<220>
<221> Variant
<222> (543)..(547)
<223> Xaa in position 543 to 547 is any amino acid

<220>
<221> Variant
<222> (549)..(549)
<223> Xaa in position 549 is any amino acid

<220>
<221> Variant
<222> (551)..(551)
<223> Xaa in position 551 is any amino acid

<220>
<221> Variant
<222> (554)..(557)
<223> Xaa in position 554 to 557 is any amino acid

<220>
<221> Variant
<222> (559)..(574)
<223> Xaa in position 559 to 574 is any amino acid

<220>
<221> Variant
<222> (575)..(577)
<223> Xaa in position 575 to 577 is any or no amino acid

<220>

<221> Variant
<222> (579)..(587)
<223> Xaa in position 579 to 587 is any amino acid

<220>
<221> Variant
<222> (588)..(592)
<223> Xaa in position 588 to 592 is any or no amino acid

<220>
<221> Variant
<222> (594)..(598)
<223> Xaa in position 594 to 598 is any amino acid

<220>
<221> Variant
<222> (600)..(602)
<223> Xaa in position 600 to 602 is any amino acid

<220>
<221> Variant
<222> (604)..(614)
<223> Xaa in position 604 to 614 is any amino acid

<220>
<221> Variant
<222> (615)..(615)
<223> Xaa in position 615 is any or no amino acid

<220>
<221> Variant
<222> (617)..(620)
<223> Xaa in position 617 to 620 is any amino acid

<220>
<221> Variant
<222> (621)..(623)
<223> Xaa in position 621 to 623 is any or no amino acid

<220>
<221> Variant
<222> (625)..(651)
<223> Xaa in position 625 to 651 is any amino acid

<220>
<221> Variant
<222> (652)..(662)
<223> Xaa in position 652 to 662 is any or no amino acid

<220>
<221> Variant
<222> (664)..(664)
<223> Xaa in position 664 is any amino acid

<220>
<221> Variant
<222> (666)..(669)
<223> Xaa in position 666 to 669 is any amino acid

<220>
<221> Variant
<222> (671)..(677)
<223> Xaa in position 671 to 677 is any amino acid

<220>
<221> Variant
<222> (678)..(684)
<223> Xaa in position 678 to 684 is any or no amino acid


```

<220>
<221> Variant
<222> (686)..(686)
<223> Xaa in position 686 is any amino acid

<220>
<221> Variant
<222> (688)..(691)
<223> Xaa in position 688 to 691 is any amino acid

<220>
<221> Variant
<222> (694)..(697)
<223> Xaa in position 694 to 697 is any amino acid

<220>
<221> Variant
<222> (699)..(702)
<223> Xaa in position 699 to 702 is any amino acid

<220>
<221> Variant
<222> (703)..(708)
<223> Xaa in position 703 to 708 is any or no amino acid

<220>
<221> Variant
<222> (710)..(712)
<223> Xaa in position 710 to 712 is any amino acid

<220>
<221> Variant
<222> (715)..(721)
<223> Xaa in position 715 to 721 is any amino acid

<220>
<221> Variant
<222> (722)..(722)
<223> Xaa in position 722 is any or no amino acid

<220>
<221> Variant
<222> (724)..(738)
<223> Xaa in position 724 to 738 is any amino acid

<220>
<221> Variant
<222> (739)..(793)
<223> Xaa in position 739 to 793 is any or no amino acid

<220>
<221> Variant
<222> (795)..(796)
<223> Xaa in position 795 to 796 is any amino acid

<220>
<221> Variant
<222> (798)..(798)
<223> Xaa in position 798 is any amino acid

<220>
<221> Variant
<222> (802)..(803)
<223> Xaa in position 802 to 803 is any amino acid

<220>
<221> Variant
<222> (805)..(812)
<223> Xaa in position 805 to 812 is any amino acid

```

PF59083SeqList PF59083.txt

```
<220>
<221> Variant
<222> (813)..(826)
<223> Xaa in position 813 to 826 is any or no amino acid
```

```
<220>
<221> Variant
<222> (828)..(828)
<223> Xaa in position 828 is any amino acid
```

```
<220>
<221> Variant
<222> (830)..(831)
<223> Xaa in position 830 to 831 is any amino acid
```

```
<220>
<221> Variant
<222> (833)..(833)
<223> Xaa in position 833 is any amino acid
```

<400>	9997														
Leu 1	Xaa	Xaa	Xaa	Xaa 5	Xaa	Xaa	Xaa	Xaa	Xaa 10	Xaa	Xaa	Xaa	Xaa 15	Xaa	Xaa
Xaa	Xaa	Xaa	Xaa 20	Xaa	Xaa	Xaa	Xaa	Xaa 25	Xaa	Xaa	Ile	Xaa	Xaa 30	Xaa	Xaa
Xaa	Xaa	Xaa 35	Xaa	Xaa	Gln	Xaa	Xaa 40	Xaa	Xaa	Xaa	Xaa	Xaa 45	Xaa	Xaa	Xaa
Xaa	Xaa 50	Xaa	Xaa	Xaa	Xaa	Xaa 55	Xaa	Xaa	Xaa	Xaa	Phe 60	Xaa	Xaa	Xaa	Xaa
Gly 65	Xaa	Gly	Xaa	Xaa	Xaa 70	Xaa	Xaa	Xaa	Xaa	Xaa 75	Xaa	Xaa	Xaa	Xaa	Xaa 80
Xaa	Xaa	Xaa	Xaa	Xaa 85	Xaa	Xaa	Xaa	Xaa	Xaa 90	Xaa	Xaa	Xaa	Xaa	Xaa 95	Xaa
Xaa	Xaa	Xaa	Xaa 100	Xaa	Xaa	Xaa	Xaa	Xaa 105	Xaa	Xaa	Xaa	Xaa	Xaa 110	Xaa	Xaa
Xaa	Xaa	Trp 115	Xaa	Xaa	Xaa	Xaa 120	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa 125	Xaa	Xaa	Xaa
Xaa	Xaa 130	Xaa	Xaa	Xaa	Xaa	Gly 135	Xaa	Lys	Xaa	Xaa	Xaa 140	Xaa	Xaa	Xaa	Xaa
Xaa 145	Xaa	Xaa	Xaa	Xaa	Xaa 150	Xaa	Xaa	Xaa	Xaa	Xaa 155	Xaa	Xaa	Xaa	Xaa	Xaa 160
Xaa	Xaa	Xaa	Xaa	Xaa 165	Xaa	Xaa	Xaa	Xaa	Xaa 170	Xaa	Xaa	Xaa	Xaa	Xaa 175	Xaa
Xaa	Xaa	Xaa	Xaa 180	Xaa	Xaa	Xaa	Xaa	Xaa 185	Xaa	Xaa	Xaa	Xaa	Xaa 190	Xaa	Xaa
Xaa	Xaa	Xaa 195	Xaa	Xaa	Xaa	Xaa	Xaa 200	Xaa	Xaa	Xaa	Xaa	Xaa 205	Xaa	Xaa	Xaa
Xaa	Xaa 210	Xaa	Xaa	Xaa	Xaa	Xaa 215	Xaa	Xaa	Xaa	Xaa	Xaa 220	Xaa	His	Xaa	Xaa
Xaa 225	Xaa	Xaa	Gly	Xaa	Val 230	Xaa	Thr	Arg	Phe	Pro 235	Pro	Glu	Pro	Asn	Gly 240
Xaa	Leu	His	Ile	Gly 245	His	Xaa	Lys	Ala	Xaa 250	Xaa	Xaa	Xaa	Phe	Xaa 255	Xaa
Ala	Xaa	Xaa	Xaa 260	Gly	Xaa	Xaa	Xaa	Xaa 265	Xaa	Arg	Xaa	Asp	Asp 270	Thr	Asn
Pro	Glu	Xaa 275	Glu	Xaa	Xaa	Xaa	Xaa 280	Xaa	Xaa	Xaa	Ile	Xaa 285	Xaa	Xaa	Xaa
Xaa	Trp 290	Xaa	Gly	Xaa	Xaa	Pro 295	Xaa	Xaa	Xaa	Thr	Tyr 300	Xaa	Ser	Asp	Tyr
Phe 305	Xaa	Xaa	Leu	Tyr	Xaa 310	Xaa	Ala	Xaa	Xaa	Leu 315	Ile	Xaa	Xaa	Gly	Xaa 320
Ala	Tyr	Val	Xaa	Xaa 325	Xaa	Xaa	Xaa	Xaa	Xaa 330	Xaa	Xaa	Xaa	Xaa	Arg 335	Xaa
Xaa	Xaa	Xaa	Xaa 340	Xaa	Xaa	Xaa	Xaa	Xaa 345	Xaa	Xaa	Xaa	Xaa	Xaa 350	Xaa	Xaa
Arg	Xaa	Xaa 355	Xaa	Xaa	Glu	Glu	Xaa 360	Leu	Xaa	Xaa	Phe	Xaa 365	Xaa	Met	Xaa
Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Lys	Xaa	Xaa

PF59083SeqList PF59083.txt															
370					375					380					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Ala	Tyr	Arg	Xaa
385					390				395						400
Xaa	Xaa	Xaa	Pro	His	Xaa	Xaa	Xaa	Gly	Xaa	Lys	Trp	Xaa	Ile	Tyr	Pro
				405					410					415	
Xaa	Tyr	Asp	Xaa	His	Cys	Xaa	Xaa	Asp	Ser	Xaa	Glu	Xaa	Ile	Thr	
			420					425					430		
His	Ser	Leu	Cys	Thr	Xaa	Glu	Phe	Xaa	Xaa	Xaa	Arg	Xaa	Ser	Tyr	Xaa
		435					440					445			
Trp	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	
	450					455					460				
Xaa	Arg	Leu	Asn	Xaa	Xaa	Xaa	Thr	Xaa	Xaa	Ser	Lys	Arg	Lys	Xaa	Xaa
465					470					475					480
Xaa	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Val	Xaa	Xaa	Trp	Asp	Asp	Pro	Arg	Xaa
				485					490					495	
Xaa	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Arg	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Xaa
			500					505					510		
Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		515					520					525			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Xaa	Leu	Xaa	Xaa
	530					535					540				
Xaa	Xaa	Xaa	Arg	Xaa	Met	Xaa	Val	Leu	Xaa	Xaa	Xaa	Xaa	Val	Xaa	Xaa
545					550					555					560
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				565					570					575	
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			580				585						590		
Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Xaa
		595				600						605			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	
	610					615					620				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
625					630					635					640
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				645					650					655	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Trp	Xaa	Xaa
			660				665						670		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Arg	Xaa
		675					680					685			
Xaa	Xaa	Xaa	Leu	Phe	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	690					695					700				
Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Asn	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
705					710					715					720
Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			725						730					735	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			740				745						750		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		755					760					765			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	770					775					780				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Xaa	Xaa	Arg	Xaa	Gly	Tyr
785					790					795					800
Phe	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			805						810					815	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Xaa	Asn	Xaa	Xaa	Val	
			820				825					830			
Xaa	Leu														

<210> 9998
 <211> 58
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

```

<220>
<221> Variant
<222> (2)..(3)
<223> Xaa in position 2 to 3 is any amino acid

<220>
<221> Variant
<222> (7)..(7)
<223> Xaa in position 7 is Ile or Val

<220>
<221> Variant
<222> (8)..(10)
<223> Xaa in position 8 to 10 is any amino acid

<220>
<221> Variant
<222> (11)..(11)
<223> Xaa in position 11 is Pro or Ser

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is any amino acid

<220>
<221> Variant
<222> (14)..(14)
<223> Xaa in position 14 is His, Lys or Arg

<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is Ala or Thr

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is Ala or Gly

<220>
<221> Variant
<222> (17)..(18)
<223> Xaa in position 17 to 18 is any amino acid

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is any amino acid

<220>
<221> Variant
<222> (21)..(21)
<223> Xaa in position 21 is Ile or Val

<220>
<221> Variant
<222> (24)..(24)
<223> Xaa in position 24 is Ser or Thr

<220>
<221> Variant
<222> (27)..(27)
<223> Xaa in position 27 is Phe or Tyr

<220>
<221> Variant
<222> (28)..(28)
<223> Xaa in position 28 is Ala or Thr

```

PF59083SeqList PF59083.txt

```

<220>
<221> Variant
<222> (31)..(31)
<223> Xaa in position 31 is any amino acid

<220>
<221> Variant
<222> (32)..(32)
<223> Xaa in position 32 is Cys or Val

<220>
<221> Variant
<222> (35)..(35)
<223> Xaa in position 35 is Phe, Ile, Leu or Met

<220>
<221> Variant
<222> (37)..(37)
<223> Xaa in position 37 is any amino acid

<220>
<221> Variant
<222> (38)..(38)
<223> Xaa in position 38 is Ile or Val

<220>
<221> Variant
<222> (39)..(39)
<223> Xaa in position 39 is Ser or Thr

<220>
<221> Variant
<222> (45)..(45)
<223> Xaa in position 45 is any amino acid

<220>
<221> Variant
<222> (48)..(49)
<223> Xaa in position 48 to 49 is any amino acid

<220>
<221> Variant
<222> (50)..(50)
<223> Xaa in position 50 is any or no amino acid

<220>
<221> Variant
<222> (52)..(52)
<223> Xaa in position 52 is any amino acid

<220>
<221> Variant
<222> (53)..(53)
<223> Xaa in position 53 is any or no amino acid

<220>
<221> Variant
<222> (56)..(56)
<223> Xaa in position 56 is any amino acid

<400> 9998
Asp Xaa Xaa Ala Tyr Arg Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa
1      5      10      15
Xaa Xaa Trp Xaa Xaa Tyr Pro Xaa Tyr Asp Xaa Xaa His Cys Xaa Xaa
20      25      30
Asp Ser Xaa Glu Xaa Xaa Xaa His Ser Leu Cys Thr Xaa Glu Phe Xaa
35      40      45
Xaa Xaa Arg Xaa Xaa Ser Tyr Xaa Trp Leu
                               Seite 10597

```

<210> 9999
 <211> 32
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (2)..(8)
 <223> Xaa in position 2 to 8 is any amino acid

<220>
 <221> Variant
 <222> (9)..(9)
 <223> Xaa in position 9 is Ile or Val

<220>
 <221> Variant
 <222> (10)..(10)
 <223> Xaa in position 10 is any amino acid

<220>
 <221> Variant
 <222> (20)..(20)
 <223> Xaa in position 20 is any amino acid

<220>
 <221> Variant
 <222> (26)..(26)
 <223> Xaa in position 26 is Ala, Ser or Val

<220>
 <221> Variant
 <222> (29)..(29)
 <223> Xaa in position 29 is Ile or Met

<220>
 <221> Variant
 <222> (30)..(30)
 <223> Xaa in position 30 is any amino acid

<220>
 <221> Variant
 <222> (31)..(31)
 <223> Xaa in position 31 is Phe, Ile or Val

<220>
 <221> Variant
 <222> (32)..(32)
 <223> Xaa in position 32 is Asp or Asn

<400> 9999
 His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg Phe Pro Pro Glu
 1 5 10 15
 Pro Asn Gly Xaa Leu His Ile Gly His Xaa Lys Ala Xaa Xaa Xaa Xaa
 20 25 30

<210> 10000
 <211> 26
 <212> PRT
 <213> Artificial sequence

```

<220>
<223> protein pattern

<220>
<221> Variant
<222> (2)..(2)
<223> Xaa in position 2 is His or Tyr

<220>
<221> Variant
<222> (3)..(3)
<223> Xaa in position 3 is Ala, Ser or Thr

<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is any amino acid

<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is Asp, Asn, Pro or Gln

<220>
<221> Variant
<222> (9)..(9)
<223> Xaa in position 9 is any amino acid

<220>
<221> Variant
<222> (11)..(13)
<223> Xaa in position 11 to 13 is any amino acid

<220>
<221> Variant
<222> (15)..(16)
<223> Xaa in position 15 to 16 is any amino acid

<220>
<221> Variant
<222> (19)..(20)
<223> Xaa in position 19 to 20 is any amino acid

<220>
<221> Variant
<222> (22)..(22)
<223> Xaa in position 22 is any amino acid

<220>
<221> Variant
<222> (23)..(23)
<223> Xaa in position 23 is Ala, Gly or Thr

<220>
<221> Variant
<222> (24)..(24)
<223> Xaa in position 24 is Phe or Tyr

<220>
<221> Variant
<222> (25)..(25)
<223> Xaa in position 25 is Ile or Val

<220>
<221> Variant
<222> (26)..(26)
<223> Xaa in position 26 is Cys or Asp

<400> 10000

```

PF59083SeqList PF59083.txt

Thr Xaa Xaa Ser Asp Xaa Phe Xaa Xaa Leu Xaa Xaa Xaa Ala Xaa Xaa
 1 5 10 15
 Leu Ile Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa
 20 25

<210> 10001
 <211> 21
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is Ala or Gly

<220>
 <221> Variant
 <222> (3)..(3)
 <223> Xaa in position 3 is any amino acid

<220>
 <221> Variant
 <222> (5)..(8)
 <223> Xaa in position 5 to 8 is any amino acid

<220>
 <221> Variant
 <222> (10)..(10)
 <223> Xaa in position 10 is any amino acid

<220>
 <221> Variant
 <222> (11)..(11)
 <223> Xaa in position 11 is Cys, Gly or Thr

<220>
 <221> Variant
 <222> (12)..(13)
 <223> Xaa in position 12 to 13 is any amino acid

<220>
 <221> Variant
 <222> (15)..(15)
 <223> Xaa in position 15 is Phe or Tyr

<400> 10001
 Phe Xaa Xaa Ala Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Arg Xaa Asp
 1 5 10 15
 Asp Thr Asn Pro Glu
 20

<210> 10002
 <211> 18
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is any amino acid

PF59083SeqList PF59083.txt

```

<220>
<221> Variant
<222> (3)..(3)
<223> Xaa in position 3 is Gln or Arg

<220>
<221> Variant
<222> (4)..(4)
<223> Xaa in position 4 is Pro, Ser or Thr

<220>
<221> Variant
<222> (5)..(5)
<223> Xaa in position 5 is any amino acid

<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is Glu, Gln or Ser

<220>
<221> Variant
<222> (7)..(7)
<223> Xaa in position 7 is any amino acid

<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is Asn or Ser

<220>
<221> Variant
<222> (9)..(9)
<223> Xaa in position 9 is Ile, Leu or Met

<220>
<221> Variant
<222> (10)..(11)
<223> Xaa in position 10 to 11 is any amino acid

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is Asp, Glu or Arg

<220>
<221> Variant
<222> (14)..(14)
<223> Xaa in position 14 is any amino acid

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is Lys or Arg

<220>
<221> Variant
<222> (17)..(17)
<223> Xaa in position 17 is any amino acid

<400> 10002
Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Met Xaa
1          5          10          15
Xaa Gly

```

```

<210> 10003
<211> 26

```

<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
<221> Variant
<222> (2)..(3)
<223> Xaa in position 2 to 3 is any or no amino acid

<220>
<221> Variant
<222> (5)..(8)
<223> Xaa in position 5 to 8 is any amino acid

<220>
<221> Variant
<222> (9)..(9)
<223> Xaa in position 9 is any or no amino acid

<220>
<221> Variant
<222> (11)..(11)
<223> Xaa in position 11 is any amino acid

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is any amino acid

<220>
<221> Variant
<222> (14)..(14)
<223> Xaa in position 14 is Ile, Leu or Val

<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is Leu or Pro

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is any amino acid

<220>
<221> Variant
<222> (17)..(17)
<223> Xaa in position 17 is Gly or Pro

<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is Ile, Leu or Val

<220>
<221> Variant
<222> (19)..(19)
<223> Xaa in position 19 is any amino acid

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is Ile, Leu or Val

<220>
<221> Variant
<222> (21)..(21)

<223> Xaa in position 21 is any amino acid

<220>

<221> Variant

<222> (22)..(22)

<223> Xaa in position 22 is Ile, Leu or Val

<220>

<221> Variant

<222> (23)..(23)

<223> Xaa in position 23 is any amino acid

<220>

<221> Variant

<222> (24)..(24)

<223> Xaa in position 24 is Asp or Asn

<220>

<221> Variant

<222> (25)..(25)

<223> Xaa in position 25 is any amino acid

<220>

<221> Variant

<222> (26)..(26)

<223> Xaa in position 26 is Asp, Glu, Pro or Ser

<400> 10003

Arg	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Met	Xaa	Xaa	Xaa	Xaa
1				5				10				15		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa					
			20				25							

<210> 10004

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (2)..(2)

<223> Xaa in position 2 is any amino acid

<220>

<221> Variant

<222> (3)..(4)

<223> Xaa in position 3 to 4 is any or no amino acid

<220>

<221> Variant

<222> (6)..(6)

<223> Xaa in position 6 is any amino acid

<220>

<221> Variant

<222> (7)..(7)

<223> Xaa in position 7 is Ala or Gly

<220>

<221> Variant

<222> (8)..(9)

<223> Xaa in position 8 to 9 is Phe or Tyr

<220>

<221> Variant

<222> (10)..(10)
 <223> Xaa in position 10 is Ala, Cys, Ser, Thr or Val
 <220>
 <221> Variant
 <222> (11)..(11)
 <223> Xaa in position 11 is Leu, Met or Val
 <220>
 <221> Variant
 <222> (13)..(14)
 <223> Xaa in position 13 to 14 is any amino acid
 <220>
 <221> Variant
 <222> (15)..(15)
 <223> Xaa in position 15 is Ser or Thr
 <400> 10004
 Phe Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa
 1 5 10 15

<210> 10005
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is any amino acid

<220>
 <221> Variant
 <222> (4)..(7)
 <223> Xaa in position 4 to 7 is any amino acid

<220>
 <221> Variant
 <222> (10)..(11)
 <223> Xaa in position 10 to 11 is any amino acid

<220>
 <221> Variant
 <222> (12)..(12)
 <223> Xaa in position 12 is Asp, Glu or Lys

<220>
 <221> Variant
 <222> (13)..(13)
 <223> Xaa in position 13 is Asp, Asn, Pro or Thr

<400> 10005
 Glu Xaa Arg Xaa Xaa Xaa Leu Phe Xaa Xaa Xaa Xaa Pro
 1 5 10

<210> 10006
 <211> 660
 <212> DNA
 <213> Escherichia coli K12

<220>
 <221> CDS
 <222> (1)..(660)
 <223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 10006
atg gat cgt att gtt agt tct tca cat gac cgt aca tca ctg ctt agc      48
Met Asp Arg Ile Val Ser Ser Ser His Asp Arg Thr Ser Leu Leu Ser
1      5      10      15
acc cat aag gtg ctg cgt aat acc tat ttt ctg ctg agc ctg acg ctg      96
Thr His Lys Val Leu Arg Asn Thr Tyr Phe Leu Leu Ser Leu Thr Leu
20      25      30
gcc ttt tcg gcg att acc gca act gcc agt acg gtg ctg atg ctg cca      144
Ala Phe Ser Ala Ile Thr Ala Thr Ala Ser Thr Val Leu Met Leu Pro
35      40      45
tct ccg ggt ctg att ctg acg ctg gtg ggt atg tat ggt ttg atg ttc      192
Ser Pro Gly Leu Ile Leu Thr Leu Val Gly Met Tyr Gly Leu Met Phe
50      55      60
ctg acc tat aaa acg gcg aat aag ccg acc ggg att atc tcc gca ttc      240
Leu Thr Tyr Lys Thr Ala Asn Lys Pro Thr Gly Ile Ile Ser Ala Phe
65      70      75      80
gcc ttt acc ggt ttt ctg ggt tat atc ctc gga cct att ctg aac acc      288
Ala Phe Thr Gly Phe Leu Gly Tyr Ile Leu Gly Pro Ile Leu Asn Thr
85      90      95
tat ctg tct gcc gga atg ggt gac gta atc gct atg gca ctg ggc gga      336
Tyr Leu Ser Ala Gly Met Gly Asp Val Ile Ala Met Ala Leu Gly Gly
100      105      110
acg gcg tta gtg ttc ttc tgc tgc tct gca tat gtg ctg acc acc cgc      384
Thr Ala Leu Val Phe Phe Cys Cys Ser Ala Tyr Val Leu Thr Thr Arg
115      120      125
aaa gat atg tcg ttc ctc ggc ggt atg ctg atg gcg ggt att gtg gtg      432
Lys Asp Met Ser Phe Leu Gly Gly Met Leu Met Ala Gly Ile Val Val
130      135      140
gtg ctg att ggt atg gtt gcg aat atc ttc ctg cag ctg cct gct ctg      480
Val Leu Ile Gly Met Val Ala Asn Ile Phe Leu Gln Leu Pro Ala Leu
145      150      155      160
cat ctg gcg atc agc gcg gtc ttc att ctg atc tcc tct ggc gct atc      528
His Leu Ala Ile Ser Ala Val Phe Ile Leu Ile Ser Ser Gly Ala Ile
165      170      175
ttg ttt gaa acc agc aac atc att cat ggc ggt gag acg aac tat att      576
Leu Phe Glu Thr Ser Asn Ile Ile His Gly Gly Glu Thr Asn Tyr Ile
180      185      190
cgt gcc acg gtt agc ctg tat gtt tcg ctg tac aac atc ttc gtc agc      624
Arg Ala Thr Val Ser Leu Tyr Val Ser Leu Tyr Asn Ile Phe Val Ser
195      200      205
ctg ctg agc att ctg ggc ttc gct agc cgc gat taa      660
Leu Leu Ser Ile Leu Gly Phe Ala Ser Arg Asp
210      215

```

```

<210> 10007
<211> 219
<212> PRT
<213> Escherichia coli K12

```

```

<400> 10007
Met Asp Arg Ile Val Ser Ser Ser His Asp Arg Thr Ser Leu Leu Ser
1      5      10      15
Thr His Lys Val Leu Arg Asn Thr Tyr Phe Leu Leu Ser Leu Thr Leu
20      25      30
Ala Phe Ser Ala Ile Thr Ala Thr Ala Ser Thr Val Leu Met Leu Pro
35      40      45
Ser Pro Gly Leu Ile Leu Thr Leu Val Gly Met Tyr Gly Leu Met Phe
50      55      60
Leu Thr Tyr Lys Thr Ala Asn Lys Pro Thr Gly Ile Ile Ser Ala Phe
65      70      75      80
Ala Phe Thr Gly Phe Leu Gly Tyr Ile Leu Gly Pro Ile Leu Asn Thr
85      90      95
Tyr Leu Ser Ala Gly Met Gly Asp Val Ile Ala Met Ala Leu Gly Gly
100      105      110
Thr Ala Leu Val Phe Phe Cys Cys Ser Ala Tyr Val Leu Thr Thr Arg
115      120      125
Lys Asp Met Ser Phe Leu Gly Gly Met Leu Met Ala Gly Ile Val Val
130      135      140

```

PF59083SeqList PF59083.txt

Val Leu Ile Gly Met Val Ala Asn Ile Phe Leu Gln Leu Pro Ala Leu
 145 150 155 160
 His Leu Ala Ile Ser Ala Val Phe Ile Leu Ile Ser Ser Gly Ala Ile
 165 170 175
 Leu Phe Glu Thr Ser Asn Ile Ile His Gly Gly Glu Thr Asn Tyr Ile
 180 185 190
 Arg Ala Thr Val Ser Leu Tyr Val Ser Leu Tyr Asn Ile Phe Val Ser
 195 200 205
 Leu Leu Ser Ile Leu Gly Phe Ala Ser Arg Asp
 210 215

<210> 10008
 <211> 735
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(735)

<400> 10008
 atg gac gcc ttc aat tcc ttc ttc gat tca aga aac cga tgg aat tac 48
 Met Asp Ala Phe Asn Ser Phe Phe Asp Ser Arg Asn Arg Trp Asn Tyr
 1 5 10 15
 gat act ctc aaa aac ttc cgt cag att tct ccg gtc gtg cag aat cac 96
 Asp Thr Leu Lys Asn Phe Arg Gln Ile Ser Pro Val Val Gln Asn His
 20 25 30
 ctg aag cag gtt tat ttt act ctg tgt ttt gcc gtg gtt gct gcg gct 144
 Leu Lys Gln Val Tyr Phe Thr Leu Cys Phe Ala Val Val Ala Ala Ala
 35 40 45
 gtc ggg gct tac ctt cat gtc ctc ttg aac att ggg ggt ttt ctt act 192
 Val Gly Ala Tyr Leu His Val Leu Leu Asn Ile Gly Gly Phe Leu Thr
 50 55 60
 aca gtg gca tgc atg gga agc agc ttt tgg tta ctc tcc aca cct cct 240
 Thr Val Ala Cys Met Gly Ser Ser Phe Trp Leu Ser Thr Pro Pro
 65 70 75 80
 ttt gaa gag agg aag agg gtg act ttg ttg atg gcc gca tca ctg ttt 288
 Phe Glu Glu Arg Lys Arg Val Thr Leu Leu Met Ala Ala Ser Leu Phe
 85 90 95
 cag ggt tcc tct att gga ccc ttg att gat ttg gct att cat atc gat 336
 Gln Gly Ser Ser Ile Gly Pro Leu Ile Asp Leu Ala Ile His Ile Asp
 100 105 110
 cca agc ctt atc ttt agt gca ttt gtg gga aca gct ttg gcc ttt gca 384
 Pro Ser Leu Ile Phe Ser Ala Phe Val Gly Thr Ala Leu Ala Phe Ala
 115 120 125
 tgc ttc tca gga gca gct ttg gtt gca agg cgt agg gag tac ctg tac 432
 Cys Phe Ser Gly Ala Ala Leu Val Ala Arg Arg Arg Glu Tyr Leu Tyr
 130 135 140
 ctt ggt ggc ttg gtt tct tct gga ttg tcc atc ctt ctc tgg ttg cac 480
 Leu Gly Gly Leu Val Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu His
 145 150 155 160
 ttt gct tct tcc atc ttt gga ggc tca aca gct ctc ttt aag ttt gag 528
 Phe Ala Ser Ser Ile Phe Gly Gly Ser Thr Ala Leu Phe Lys Phe Glu
 165 170 175
 ttg tac ttt ggg cta ttg gtg ttt gta ggt tac att gta gta gac acc 576
 Leu Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Ile Val Val Val Asp Thr
 180 185 190
 caa gaa ata gtt gag agg gca cac ttg ggc gat ctg gac tat gta aag 624
 Gln Glu Ile Val Glu Arg Ala His Leu Gly Asp Leu Asp Tyr Val Lys
 195 200 205
 cat gcc ttg acc ttg ttt acc gat ttg gtc gca gtt ttt gtc cgg att 672
 His Ala Leu Thr Leu Phe Thr Asp Leu Val Ala Val Phe Val Arg Ile
 210 215 220
 ctt gtt att atg ttg aag aat tcg act gag agg aat gag aag aaa aag 720
 Leu Val Ile Met Leu Lys Asn Ser Thr Glu Arg Asn Glu Lys Lys Lys
 225 230 235 240
 aag aga aga gat tga 735
 Lys Arg Arg Asp

PF59083SeqList PF59083.txt

<210> 10009
 <211> 244
 <212> PRT
 <213> Glycine max

<400> 10009
 Met Asp Ala Phe Asn Ser Phe Phe Asp Ser Arg Asn Arg Trp Asn Tyr
 1 5 10 15
 Asp Thr Leu Lys Asn Phe Arg Gln Ile Ser Pro Val Val Gln Asn His
 20 25 30
 Leu Lys Gln Val Tyr Phe Thr Leu Cys Phe Ala Val Val Ala Ala Ala
 35 40 45
 Val Gly Ala Tyr Leu His Val Leu Leu Asn Ile Gly Gly Phe Leu Thr
 50 55 60
 Thr Val Ala Cys Met Gly Ser Ser Phe Trp Leu Ser Thr Pro Pro
 65 70 75 80
 Phe Glu Glu Arg Lys Arg Val Thr Leu Leu Met Ala Ala Ser Leu Phe
 85 90 95
 Gln Gly Ser Ser Ile Gly Pro Leu Ile Asp Leu Ala Ile His Ile Asp
 100 105 110
 Pro Ser Leu Ile Phe Ser Ala Phe Val Gly Thr Ala Leu Ala Phe Ala
 115 120 125
 Cys Phe Ser Gly Ala Ala Leu Val Ala Arg Arg Arg Glu Tyr Leu Tyr
 130 135 140
 Leu Gly Gly Leu Val Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu His
 145 150 155 160
 Phe Ala Ser Ser Ile Phe Gly Gly Ser Thr Ala Leu Phe Lys Phe Glu
 165 170 175
 Leu Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Ile Val Val Asp Thr
 180 185 190
 Gln Glu Ile Val Glu Arg Ala His Leu Gly Asp Leu Asp Tyr Val Lys
 195 200 205
 His Ala Leu Thr Leu Phe Thr Asp Leu Val Ala Val Phe Val Arg Ile
 210 215 220
 Leu Val Ile Met Leu Lys Asn Ser Thr Glu Arg Asn Glu Lys Lys Lys
 225 230 235 240
 Lys Arg Arg Asp

<210> 10010
 <211> 549
 <212> DNA
 <213> Escherichia coli K12

<220>
 <221> CDS
 <222> (1)..(549)
 <223> transl_table=11

<400> 10010
 atg caa ttt aat atc cct acg ttg ctt aca ctg ttc cgt gtc atc ctt 48
 Met Gln Phe Asn Ile Pro Thr Leu Leu Thr 10 Leu Phe Arg Val Ile Leu 15
 1 5 10 15
 atc cca ttc ttt gta ttg gtc ttt tat ctg cct gtc acc tgg tcg ccg 96
 Ile Pro Phe Phe Val Leu Val Phe Tyr Leu Pro Val Thr Trp Ser Pro 20 25 30
 ttt gcc gcc gcg ctc att ttc tgc gtc gcg gcg gtg act gac tgg ttc 144
 Phe Ala Ala Ala Leu Ile Phe Cys Val Ala Ala Val Thr Asp Trp Phe 35 40 45
 gat ggt ttt ctg gca cgc cgc tgg aac cag agt acc cgg ttt ggt gct 192
 Asp Gly Phe Leu Ala Arg Arg Trp Asn Gln Ser Thr Arg Phe Gly Ala 50 55 60
 ttc ctt gac cct gtg gca gat aaa gtt ctc gtg gct atc gcc atg gtg 240
 Phe Leu Asp Pro Val Ala Asp Lys Val Leu Val Ala Ile Ala Met Val 65 70 75 80
 ctg gta acc gag cat tat cac agc tgg tgg gtg aca tta ccg gcg gca 288
 Leu Val Thr Glu His Tyr His Ser Trp Trp Val Thr Leu Pro Ala Ala 85 90 95

PF59083SeqList PF59083.txt

acg atg atc gcc cgt gaa att att att tct gcg cta cgc gaa tgg atg	336
Thr Met Ile Ala Arg Glu Ile Ile Ile Ser Ala Leu Arg Glu Trp Met	
100 105 110	
gcg gag ttg ggt aaa cgc agt agc gtg gcc gtc tcc tgg att ggg aaa	384
Ala Glu Leu Gly Lys Arg Ser Ser Val Ala Val Ser Trp Ile Gly Lys	
115 120 125	
gtg aaa acc act gcc cag atg gtg gcg ttg gca tgg ctg ctg tgg cgt	432
Val Lys Thr Thr Ala Gln Met Val Ala Leu Ala Trp Leu Leu Trp Arg	
130 135 140	
ccg aac att tgg gtt gag tac gcc ggt att gca ctt ttc ttt gtg gct	480
Pro Asn Ile Trp Val Glu Tyr Ala Gly Ile Ala Leu Phe Phe Val Ala	
145 150 155 160	
gcg gta ctg act ctg tgg tca atg ttg caa tat ttg agc gct gcg cgt	528
Ala Val Leu Thr Leu Trp Ser Met Leu Gln Tyr Leu Ser Ala Ala Arg	
165 170 175	
gca gat ttg ctt gat cag tga	549
Ala Asp Leu Leu Asp Gln	
180	

<210> 10011

<211> 182

<212> PRT

<213> Escherichia coli K12

<400> 10011

Met Gln Phe Asn Ile Pro Thr Leu Leu Thr Leu Phe Arg Val Ile Leu	
1 5 10 15	
Ile Pro Phe Phe Val Leu Val Phe Tyr Leu Pro Val Thr Trp Ser Pro	
20 25 30	
Phe Ala Ala Ala Leu Ile Phe Cys Val Ala Ala Val Thr Asp Trp Phe	
35 40 45	
Asp Gly Phe Leu Ala Arg Arg Trp Asn Gln Ser Thr Arg Phe Gly Ala	
50 55 60	
Phe Leu Asp Pro Val Ala Asp Lys Val Leu Val Ala Ile Ala Met Val	
65 70 75 80	
Leu Val Thr Glu His Tyr His Ser Trp Trp Val Thr Leu Pro Ala Ala	
85 90 95	
Thr Met Ile Ala Arg Glu Ile Ile Ile Ser Ala Leu Arg Glu Trp Met	
100 105 110	
Ala Glu Leu Gly Lys Arg Ser Ser Val Ala Val Ser Trp Ile Gly Lys	
115 120 125	
Val Lys Thr Thr Ala Gln Met Val Ala Leu Ala Trp Leu Leu Trp Arg	
130 135 140	
Pro Asn Ile Trp Val Glu Tyr Ala Gly Ile Ala Leu Phe Phe Val Ala	
145 150 155 160	
Ala Val Leu Thr Leu Trp Ser Met Leu Gln Tyr Leu Ser Ala Ala Arg	
165 170 175	
Ala Asp Leu Leu Asp Gln	
180	

<210> 10012

<211> 654

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(654)

<400> 10012

atg ggc gaa gaa gac gcc gcg gaa ttg gat cag aac agt tat aat ggt	48
Met Gly Glu Glu Asp Ala Ala Glu Leu Asp Gln Asn Ser Tyr Asn Gly	
1 5 10 15	
ggc gaa gat tct tcc aaa gtg ctt aca ttg ccc acc gta tta acc ctc	96
Gly Glu Asp Ser Lys Val Leu Thr Leu Pro Thr Val Leu Thr Leu	
20 25 30	
ggc cgt gtc gcc gcc gtt ccg atc ctc gtc gcg acc ttc tac gtt gat	144
Gly Arg Val Ala Ala Val Pro Ile Leu Val Ala Thr Phe Tyr Val Asp	
35 40 45	

PF59083SeqList PF59083.txt

tgc	tgg	tgg	ggg	aga	act	gcc	aca	acg	agt	atc	ttc	att	gca	gct	gcc	192
Cys	Trp	Trp	Gly	Arg	Thr	Ala	Thr	Thr	Ser	Ile	Phe	Ile	Ala	Ala	Ala	
	50					55				60						
att	acg	gat	tgg	ctt	gac	ggg	tac	att	gcg	aga	aag	atg	aga	tta	ggc	240
Ile	Thr	Asp	Trp	Leu	Asp	Gly	Tyr	Ile	Ala	Arg	Lys	Met	Arg	Leu	Gly	
	65				70				75					80		
tct	gcg	ttt	ggt	gct	ttt	ttg	gat	cca	gtt	gca	gat	aag	ctt	atg	gta	288
Ser	Ala	Phe	Gly	Ala	Phe	Leu	Asp	Pro	Val	Ala	Asp	Lys	Leu	Met	Val	
			85					90					95			
gca	gca	acg	ttg	ata	ctg	ctg	tgc	act	aaa	cct	atg	gac	gct	gtt	gtt	336
Ala	Ala	Thr	Leu	Ile	Leu	Leu	Cys	Thr	Lys	Pro	Met	Asp	Ala	Val	Val	
			100				105					110				
ttt	gga	cca	gtt	cct	tgg	tta	gtg	act	gta	cct	tca	att	gct	atc	att	384
Phe	Gly	Pro	Val	Pro	Trp	Leu	Val	Thr	Val	Pro	Ser	Ile	Ala	Ile	Ile	
		115				120					125					
ggt	aga	gag	att	act	atg	tcg	gca	gta	aga	gag	tgg	gct	gca	tct	cag	432
Gly	Arg	Glu	Ile	Thr	Met	Ser	Ala	Val	Arg	Glu	Trp	Ala	Ala	Ser	Gln	
	130					135				140						
aac	ggc	aag	ctt	tcg	aag	gct	gtt	gct	gta	aat	agc	ttg	gga	aag	tgg	480
Asn	Gly	Lys	Leu	Ser	Lys	Ala	Val	Ala	Val	Asn	Ser	Leu	Gly	Lys	Trp	
	145				150					155					160	
aaa	act	gca	acg	cag	atg	ata	gcg	ctg	acc	ata	ctg	ctt	gca	agc	cgg	528
Lys	Thr	Ala	Thr	Gln	Met	Ile	Ala	Leu	Thr	Ile	Leu	Leu	Ala	Ser	Arg	
			165			170							175			
gat	agc	agt	ttt	gag	agg	cta	tta	ccg	ccg	ggg	att	ggg	ttg	ctc	tat	576
Asp	Ser	Ser	Phe	Glu	Arg	Leu	Leu	Pro	Pro	Gly	Ile	Gly	Leu	Leu	Tyr	
			180			185						190				
gta	tct	gca	ggt	ctc	tct	ata	tgg	tct	tta	gtt	gtt	tat	atg	aga	cag	624
Val	Ser	Ala	Gly	Leu	Ser	Ile	Trp	Ser	Leu	Val	Val	Tyr	Met	Arg	Gln	
		195				200					205					
att	gtg	aga	gta	ctg	cta	aag	aag	tag								654
Ile	Val	Arg	Val	Leu	Leu	Lys	Lys	Lys								
	210					215										

<210> 10013
 <211> 217
 <212> PRT
 <213> Brassica napus

<400> 10013
 Met Gly Glu Glu Asp Ala Ala Glu Leu Asp Gln Asn Ser Tyr Asn Gly
 1 5 10 15
 Gly Glu Asp Ser Ser Lys Val Leu Thr Leu Pro Thr Val Leu Thr Leu
 20 25 30
 Gly Arg Val Ala Ala Val Pro Ile Leu Val Ala Thr Phe Tyr Val Asp
 35 40 45
 Cys Trp Trp Gly Arg Thr Ala Thr Thr Ser Ile Phe Ile Ala Ala Ala
 50 55 60
 Ile Thr Asp Trp Leu Asp Gly Tyr Ile Ala Arg Lys Met Arg Leu Gly
 65 70 75 80
 Ser Ala Phe Gly Ala Phe Leu Asp Pro Val Ala Asp Lys Leu Met Val
 85 90 95
 Ala Ala Thr Leu Ile Leu Leu Cys Thr Lys Pro Met Asp Ala Val Val
 100 105 110
 Phe Gly Pro Val Pro Trp Leu Val Thr Val Pro Ser Ile Ala Ile Ile
 115 120 125
 Gly Arg Glu Ile Thr Met Ser Ala Val Arg Glu Trp Ala Ala Ser Gln
 130 135 140
 Asn Gly Lys Leu Ser Lys Ala Val Ala Val Asn Ser Leu Gly Lys Trp
 145 150 155 160
 Lys Thr Ala Thr Gln Met Ile Ala Leu Thr Ile Leu Leu Ala Ser Arg
 165 170 175
 Asp Ser Ser Phe Glu Arg Leu Leu Pro Pro Gly Ile Gly Leu Leu Tyr
 180 185 190
 Val Ser Ala Gly Leu Ser Ile Trp Ser Leu Val Val Tyr Met Arg Gln
 195 200 205
 Ile Val Arg Val Leu Leu Lys Lys Lys

PF59083SeqList PF59083.txt

<210> 10014
<211> 813
<212> DNA
<213> Escherichia coli K12

<220>
<221> CDS
<222> (1)..(813)
<223> transl_table=11

```

<400> 10014
atg agc gat ctg cat aac gag tcc att ttt att acc ggc ggc gga tcg      48
Met Ser Asp Leu His Asn Glu Ser Ile Phe Ile Thr Gly Gly Gly Ser
  1          5          10          15
gga tta ggg ctg gcg ctg gtc gag cga ttt atc gaa gaa ggc gcg cag      96
Gly Leu Gly Leu Ala Leu Val Glu Arg Phe Ile Glu Glu Gly Ala Gln
          20          25          30
gtt gcc acg ctg gaa ctg tcg gcg gca aaa gtc gcc agt ctg cgt cag     144
Val Ala Thr Leu Glu Leu Ser Ala Ala Lys Val Ala Ser Leu Arg Gln
          35          40          45
cga ttt ggc gaa cat att ctg gcg gtg gaa ggt aac gtg acc tgt tat     192
Arg Phe Gly Glu His Ile Leu Ala Val Glu Gly Asn Val Thr Cys Tyr
          50          55          60
gcc gat tat caa cgc gcg gtc gat cag atc ctg act cgt tcc ggc aag     240
Ala Asp Tyr Gln Arg Ala Val Asp Gln Ile Leu Thr Arg Ser Gly Lys
          65          70          75
ctg gat tgt ttt atc ggc aat gca ggc atc tgg gat cac aat gcc tca     288
Leu Asp Cys Phe Ile Gly Asn Ala Gly Ile Trp Asp His Asn Ala Ser
          85          90          95
ctg gtt aat act ccc gca gag acg ctc gaa acc ggc ttc cac gag ctg     336
Leu Val Asn Thr Pro Ala Glu Thr Leu Glu Thr Gly Phe His Glu Leu
          100          105          110
ttt aac gtc aat gtt ctc ggt tac ctg ctg ggc gca aaa gcc tgc gct     384
Phe Asn Val Asn Val Leu Gly Tyr Leu Leu Gly Ala Lys Ala Cys Ala
          115          120          125
ccg gcg tta atc gcc agt gaa ggc agc atg att ttc aca ctg tca aat     432
Pro Ala Leu Ile Ala Ser Glu Gly Ser Met Ile Phe Thr Leu Ser Asn
          130          135          140
gcc gcc tgg tat cct ggc ggc ggt ggc ccg ctg tac acc gcc agt aaa     480
Ala Ala Trp Tyr Pro Gly Gly Gly Pro Leu Tyr Thr Ala Ser Lys
          145          150          155
cat gcc gca acc gga ctt att cgc caa ctg gct tat gaa ctg gca ccg     528
His Ala Ala Thr Gly Leu Ile Arg Gln Leu Ala Tyr Glu Leu Ala Pro
          165          170          175
aaa gtg cgg gtg aat ggc gtc ggc ccg tgt ggt atg gcc agc gac ctg     576
Lys Val Arg Val Asn Gly Val Gly Pro Cys Gly Met Ala Ser Asp Leu
          180          185          190
cgc ggc cca cag gcg ctc ggg caa agt gaa acc tcg ata atg cag tct     624
Arg Gly Pro Gln Ala Leu Gly Gln Ser Glu Thr Ser Ile Met Gln Ser
          195          200          205
ctg acg ccg gag aaa att gcc gcc att tta ccg ctg caa ttt ttc ccg     672
Leu Thr Pro Glu Lys Ile Ala Ala Ile Leu Pro Leu Gln Phe Phe Pro
          210          215          220
caa ccg gcg gat ttt acg ggg ccg tat gtg atg ttg aca tcg cgg cgc     720
Gln Pro Ala Asp Phe Thr Gly Pro Tyr Val Met Leu Thr Ser Arg Arg
          225          230          235
aat aat cgc gca tta agc ggt gtg atg atc aac gct gat gcg ggt tta     768
Asn Asn Arg Ala Leu Ser Gly Val Met Ile Asn Ala Asp Ala Gly Leu
          245          250          255
gcg att cgc ggc att cgc cac gta gcg gct ggg ctg gat ctt taa      813
Ala Ile Arg Gly Ile Arg His Val Ala Ala Gly Leu Asp Leu
          260          265          270

```

<210> 10015
<211> 270
<212> PRT
<213> Escherichia coli K12

<400> 10015

PF59083SeqList PF59083.txt

Met Ser Asp Leu His Asn Glu Ser Ile Phe Ile Thr Gly Gly Gly Ser
 1 Gly Leu Gly Leu Ala Leu Val Glu Arg Phe Ile Glu Glu Gly Ala Gln
 Val Ala Thr 20 Leu Glu Leu Ser Ala 25 Ala Lys Val Ala Ser 30 Leu Arg Gln
 Arg Phe Gly Glu His Ile Leu 35 Ala Val Glu Gly Asn 40 Val Thr Cys Tyr
 Ala Asp Tyr Gln Arg Ala 45 Val Asp Gln Ile Leu 50 Thr Arg Ser Gly Lys
 65 Leu Asp Cys Phe Ile 55 Gly Asn Ala Gly Ile 60 Trp Asp His Asn Ala Ser
 Leu Val Asn Thr Pro Ala Glu Thr Leu 65 Glu Thr Gly Phe His Glu Leu
 Phe Asn Val Asn Val Leu Gly Tyr 70 Leu Leu Gly Ala Lys 75 Ala Cys Ala
 Pro Ala Leu Ile Ala Ser Glu Gly Ser Met Ile Phe Thr Leu Ser Asn
 130 Ala Ala Trp Tyr Pro Gly 135 Gly Gly Gly Pro Leu Tyr Thr Ala Ser Lys
 145 His Ala Ala Thr Gly 150 Leu Ile Arg Gln Leu Ala Tyr Glu Leu Ala Pro
 Lys Val Arg Val Asn Gly Val Gly Pro Cys Gly Met Ala Ser Asp Leu
 Arg Gly Pro Gln Ala Leu Gly Gln Ser Glu Thr Ser Ile Met Gln Ser
 Leu Thr Pro Glu Lys Ile Ala Ala Ile Leu Pro Leu Gln Phe Phe Pro
 Gln Pro Ala Asp Phe Thr Gly Pro Tyr Val Met Leu Thr Ser Arg Arg
 225 Asn Asn Arg Ala Leu 230 Ser Gly Val Met Ile Asn Ala Asp Ala Gly Leu
 Ala Ile Arg Gly Ile Arg His Val Ala Ala Gly Leu Asp Leu
 260 265 270

<210> 10016
 <211> 900
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (1)..(900)

<400> 10016
 atg gcc gtg gag tcg cca ttc agg gcg gat gtg ttg agg ggc aag gcg 48
 Met Ala Val Glu Ser 5 Pro Phe Arg Ala Asp Val Leu Arg Gly Lys Ala
 1 gcg ctg gtc acc ggc ggc ggc tcc ggc atc ggg ttc gag atc gcc gcc 96
 Ala Leu Val Thr 20 Gly Gly Gly Ser 25 Ile Gly Phe Glu Ile Ala Ala
 cag ctc gcc cgc cac ggc gcg cac gtc gcc atc atg ggc cgc cgc cgc 144
 Gln Leu Ala Arg His Gly Ala His Val Ala Ile Met Gly Arg Arg Arg
 35 gag gtc ctc gac aag gcc gtc gcc gcc ctc cgc tcc cac ggc ctc cgg 192
 Glu Val Leu Asp Lys Ala Val Ala Ala Leu Arg Ser His Gly Leu Arg
 50 gct gtt ggt ttt gag gga gat gtg cgc aag cag gaa gat gcc gcg aga 240
 Ala Val Gly Phe Glu Gly 70 Asp Val Arg Lys Gln Glu Asp Ala Ala Arg
 65 gtg gtt gcc gca aca gtt caa cat ttt ggt aag cta gac att ctt gtc 288
 Val Val Ala Ala Thr 85 Val Gln His Phe Gly Lys Leu Asp Ile Leu Val
 90 aat ggg gca gct ggc aat ttc ctt gct tcc ccg gag gat ttg acg ccc 336
 Asn Gly Ala 100 Gly Asn Phe Leu 105 Ser Pro Glu Asp 110 Thr Pro
 aaa ggg ttc agg aca gtc gtt gac att gac aca gtg ggt aca tac act 384
 Lys Gly Phe Arg Thr Val Val Asp Ile Asp Thr Val 125 Thr Tyr Thr
 115 120 125

PF59083SeqList PF59083.txt

atg	tgc	tat	gaa	gct	cta	aag	tat	ctg	aaa	aag	ggg	ggc	cct	ggg	aaa	432
Met	Cys	Tyr	Glu	Ala	Leu	Lys	Tyr	Leu	Lys	Lys	Gly	Gly	Pro	Gly	Lys	
	130					135					140					
ggg	ccc	tct	act	ggg	ggc	gtc	atc	atc	aac	ata	agt	gct	act	ttg	cat	480
Gly	Pro	Ser	Thr	Gly	Gly	Val	Ile	Ile	Asn	Ile	Ser	Ala	Thr	Leu	His	
145					150					155					160	
tac	act	gcg	gcc	tgg	tac	caa	att	cat	gtc	tct	gct	gct	aag	gcg	ggc	528
Tyr	Thr	Ala	Ala	Trp	Tyr	Gln	Ile	His	Val	Ser	Ala	Ala	Lys	Ala	Gly	
				165					170					175		
gtt	gat	agt	ata	aca	aga	tca	ttg	gct	ctg	gaa	tgg	gga	aca	gat	tat	576
Val	Asp	Ser	Ile	Thr	Arg	Ser	Leu	Ala	Leu	Glu	Trp	Gly	Thr	Asp	Tyr	
				180					185					190		
gac	atc	agg	gtc	aat	gga	att	gca	cca	ggg	cca	att	gaa	ggc	act	cca	624
Asp	Ile	Arg	Val	Asn	Gly	Ile	Ala	Pro	Gly	Pro	Ile	Glu	Gly	Thr	Pro	
		195				200						205				
gga	atg	agg	aag	ctt	gca	cct	gag	gaa	atg	gcc	aag	ggg	agt	cgg	gaa	672
Gly	Met	Arg	Lys	Leu	Ala	Pro	Glu	Glu	Met	Ala	Lys	Gly	Ser	Arg	Glu	
	210					215					220					
ata	atg	cct	tta	ttt	aag	ttg	ggg	gaa	aaa	tgg	gac	ata	gct	atg	gct	720
Ile	Met	Pro	Leu	Phe	Lys	Leu	Gly	Glu	Lys	Trp	Asp	Ile	Ala	Met	Ala	
225					230					235					240	
gca	ctt	tac	ctt	gct	tct	gat	gca	gga	aaa	tat	gta	aat	ggg	act	aca	768
Ala	Leu	Tyr	Leu	Ala	Ser	Asp	Ala	Gly	Lys	Tyr	Val	Asn	Gly	Thr	Thr	
				245					250					255		
gtg	gtt	gtt	gat	gga	ggg	ctt	tgg	cta	agt	cgc	cct	cgc	cat	att	ccg	816
Val	Val	Val	Asp	Gly	Gly	Leu	Trp	Leu	Ser	Arg	Pro	Arg	His	Ile	Pro	
				260				265						270		
aag	gag	gaa	gtg	aag	gag	ctc	tca	aag	gtt	gtc	gag	aag	aag	gtt	agg	864
Lys	Glu	Glu	Val	Lys	Glu	Leu	Ser	Lys	Val	Val	Glu	Lys	Lys	Val	Arg	
		275				280						285				
gcc	tct	ggg	gtt	ggg	gtg	cca	tca	agc	aaa	ttg	tga					900
Ala	Ser	Gly	Val	Gly	Val	Pro	Ser	Ser	Lys	Leu						
	290					295										

<210> 10017

<211> 299

<212> PRT

<213> Oryza sativa

<400> 10017

Met	Ala	Val	Glu	Ser	Pro	Phe	Arg	Ala	Asp	Val	Leu	Arg	Gly	Lys	Ala	
1				5					10					15		
Ala	Leu	Val	Thr	Gly	Gly	Gly	Ser	Gly	Ile	Gly	Phe	Glu	Ile	Ala	Ala	
			20					25					30			
Gln	Leu	Ala	Arg	His	Gly	Ala	His	Val	Ala	Ile	Met	Gly	Arg	Arg	Arg	
		35				40						45				
Glu	Val	Leu	Asp	Lys	Ala	Val	Ala	Ala	Leu	Arg	Ser	His	Gly	Leu	Arg	
	50				55						60					
Ala	Val	Gly	Phe	Glu	Gly	Asp	Val	Arg	Lys	Gln	Glu	Asp	Ala	Ala	Arg	
65					70				75						80	
Val	Val	Ala	Ala	Thr	Val	Gln	His	Phe	Gly	Lys	Leu	Asp	Ile	Leu	Val	
				85				90						95		
Asn	Gly	Ala	Ala	Gly	Asn	Phe	Leu	Ala	Ser	Pro	Glu	Asp	Leu	Thr	Pro	
		100						105					110			
Lys	Gly	Phe	Arg	Thr	Val	Val	Asp	Ile	Asp	Thr	Val	Gly	Thr	Tyr	Thr	
		115					120					125				
Met	Cys	Tyr	Glu	Ala	Leu	Lys	Tyr	Leu	Lys	Lys	Gly	Gly	Pro	Gly	Lys	
	130					135					140					
Gly	Pro	Ser	Thr	Gly	Gly	Val	Ile	Ile	Asn	Ile	Ser	Ala	Thr	Leu	His	
145					150					155					160	
Tyr	Thr	Ala	Ala	Trp	Tyr	Gln	Ile	His	Val	Ser	Ala	Ala	Lys	Ala	Gly	
				165					170					175		
Val	Asp	Ser	Ile	Thr	Arg	Ser	Leu	Ala	Leu	Glu	Trp	Gly	Thr	Asp	Tyr	
			180					185					190			
Asp	Ile	Arg	Val	Asn	Gly	Ile	Ala	Pro	Gly	Pro	Ile	Glu	Gly	Thr	Pro	
		195					200					205				
Gly	Met	Arg	Lys	Leu	Ala	Pro	Glu	Glu	Met	Ala	Lys	Gly	Ser	Arg	Glu	
	210					215					220					
Ile	Met	Pro	Leu	Phe	Lys	Leu	Gly	Glu	Lys	Trp	Asp	Ile	Ala	Met	Ala	

PF59083SeqList PF59083.txt

Gly Arg Thr Ile Ser Ala
260

<210> 10019
<211> 262
<212> PRT
<213> Hordeum vulgare

<400> 10019
Met Ala Ala Gly Gly Met Ser Arg Glu Glu Arg Trp Ser Leu Ala Gly
1 5 10 15
Ala Thr Ala Leu Val Thr Gly Gly Ser Lys Gly Ile Gly Gln Ala Ile
20 25 30
Val Glu Glu Leu Ala Gly His Gly Ala Arg Val His Thr Cys Ala Arg
35 40 45
Ser Ala Ala Glu Leu Glu Glu Cys Arg Arg Arg Trp Glu Ala Lys Gly
50 55 60
Leu Pro Val Thr Val Ser Val Cys Asp Val Ser Leu Arg Ala Ser Arg
65 70 75 80
Glu Gln Leu Val Glu Thr Val Lys Gln Val Phe Gly Gly Lys Leu Asp
85 90 95
Ile Leu Val Asn Asn Ala Ala Gln Ile Leu Ala Lys Ala Ala Val Glu
100 105 110
Trp Thr Ser Glu Glu Tyr Ser His Leu Met Ala Thr Asn Leu Glu Ser
115 120 125
Cys Phe His Leu Ser Gln Leu Ala His Pro Leu Leu Leu Asn Ala Ser
130 135 140
Ile Ala Gly Gly Ser Ile Val Asn Ile Ser Ser Leu Gly Gly Thr Leu
145 150 155 160
Gly Phe Thr Gly Leu Ala Leu Tyr Ser Met Thr Lys Gly Gly Ile Asn
165 170 175
Gln Leu Thr Arg Ser Leu Ala Thr Glu Trp Ala Gln Asn Lys Ile Arg
180 185 190
Val Asn Cys Val Ala Pro Gly Ala Thr Lys Ser Asp Met Leu Ser Ser
195 200 205
Leu Pro Leu Glu Ile Arg Glu Asn Glu Leu Ala Arg Thr Pro Met Arg
210 215 220
Arg Ala Gly Glu Pro Ala Glu Val Ala Ala Met Val Ser Phe Leu Cys
225 230 235 240
Met Pro Ala Ala Ser Phe Val Thr Gly Gln Val Ile Ala Val Asp Gly
245 250 255
Gly Arg Thr Ile Ser Ala
260

<210> 10020
<211> 573
<212> DNA
<213> Escherichia coli K12

<220>
<221> CDS
<222> (1)..(573)
<223> transl_table=11

<400> 10020
atg ttc aaa tcg acc ctg gcg gcg atg gct gct gtt ttc gct ctt tct 48
Met Phe Lys Ser Thr Leu Ala Ala Met Ala Ala Val Phe Ala Leu Ser
1 5 10 15
gct ctt tct ccc gca gca atg gca gcg aaa ggg gac ccg cac gta ttg 96
Ala Leu Ser Pro Ala Ala Met Ala Lys Gly Asp Pro His Val Leu
20 25 30
ttg aca acc tca gct ggt aac atc gaa ctg gag ctg gat aaa caa aaa 144
Leu Thr Thr Ser Ala Gly Asn Ile Glu Leu Glu Leu Asp Lys Gln Lys
35 40 45
gcg cca gtg tct gtg caa aac ttt gtc gat tat gtg aac agc ggt ttt 192
Ala Pro Val Ser Val Gln Asn Phe Val Asp Tyr Val Asn Ser Gly Phe
50 55 60
tat aac aac act acc ttt cac cgc gtc att cct ggc ttt atg att cag 240
Tyr Asn Asn Thr Thr Phe His Arg Val Ile Pro Gly Phe Met Ile Gln
Seite 10614

PF59083SeqList PF59083.txt

65	70	75	80	
ggc ggc ggt ttc acc gag cag atg cag cag aaa aaa cca aac ccg cca				288
Gly Gly Gly Phe Thr Glu Gln Met Gln Gln Lys Lys Pro Asn Pro Pro				
	85	90	95	
atc aaa aat gaa gcc gat aac ggc ctg cgc aac acg cgt ggc acc atc				336
Ile Lys Asn Glu Ala Asp Asn Gly Leu Arg Asn Thr Arg Gly Thr Ile				
	100	105	110	
gcg atg gca cgt acc gct gac aaa gac agc gcc acc agc cag ttc ttt				384
Ala Met Ala Arg Thr Ala Asp Lys Asp Ser Ala Thr Ser Gln Phe Phe				
	115	120	125	
atc aac gtt gcc gat aac gcc ttc ctt gac cat ggt cag cgt gat ttc				432
Ile Asn Val Ala Asp Asn Ala Phe Leu Asp His Gly Gln Arg Asp Phe				
	130	135	140	
ggt tac gcg gta ttt ggt aaa gtg gtg aaa ggc atg gac gtt gcc gat				480
Gly Tyr Ala Val Phe Gly Lys Val Val Lys Gly Met Asp Val Ala Asp				
	145	150	155	
aag att tcc cag gtg ccg act cat gac gtt ggt ccg tac cag aat gtg				528
Lys Ile Ser Gln Val Pro Thr His Asp Val Gly Pro Tyr Gln Asn Val				
	165	170	175	
ccg tca aaa ccg gta gtt atc ctt tcc gct aaa gtc ctg ccg taa				573
Pro Ser Lys Pro Val Val Ile Leu Ser Ala Lys Val Leu Pro				
	180	185	190	

<210> 10021
 <211> 190
 <212> PRT
 <213> Escherichia coli K12

<400> 10021

Met Phe Lys Ser Thr Leu Ala Ala Met Ala Ala Val Phe Ala Leu Ser	
1 5 10 15	
Ala Leu Ser Pro Ala Ala Met Ala Ala Lys Gly Asp Pro His Val Leu	
20 25 30	
Leu Thr Thr Ser Ala Gly Asn Ile Glu Leu Glu Leu Asp Lys Gln Lys	
35 40 45	
Ala Pro Val Ser Val Gln Asn Phe Val Asp Tyr Val Asn Ser Gly Phe	
50 55 60	
Tyr Asn Asn Thr Thr Phe His Arg Val Ile Pro Gly Phe Met Ile Gln	
65 70 75 80	
Gly Gly Gly Phe Thr Glu Gln Met Gln Gln Lys Lys Pro Asn Pro Pro	
85 90 95	
Ile Lys Asn Glu Ala Asp Asn Gly Leu Arg Asn Thr Arg Gly Thr Ile	
100 105 110	
Ala Met Ala Arg Thr Ala Asp Lys Asp Ser Ala Thr Ser Gln Phe Phe	
115 120 125	
Ile Asn Val Ala Asp Asn Ala Phe Leu Asp His Gly Gln Arg Asp Phe	
130 135 140	
Gly Tyr Ala Val Phe Gly Lys Val Val Lys Gly Met Asp Val Ala Asp	
145 150 155 160	
Lys Ile Ser Gln Val Pro Thr His Asp Val Gly Pro Tyr Gln Asn Val	
165 170 175	
Pro Ser Lys Pro Val Val Ile Leu Ser Ala Lys Val Leu Pro	
180 185 190	

<210> 10022
 <211> 681
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(681)

<400> 10022

atg tgg atc caa gga ttc agt ttt tgg atc aaa ggt ttc tct ttg ctg	48
Met Trp Ile Gln Gly Phe Ser Phe Trp Ile Lys Gly Phe Ser Leu Leu	
1 5 10 15	
gcc tta ata tct gta att tcc gct ctg gaa ccc gaa ctg gga tcg acc	96
Ala Leu Ile Ser Val Ile Ser Ala Leu Glu Pro Glu Leu Gly Ser Thr	

PF59083SeqList PF59083.txt

			20				25			30							
cgc	gtc	gtc	ttt	cag	aca	aag	tat	gga	gat	att	gaa	ttt	ggt	ttc	tat		144
Arg	Val	Val	Phe	Gln	Thr	Lys	Tyr	Gly	Asp	Ile	Glu	Phe	Gly	Phe	Tyr		
		35					40				45						
cca	act	gtt	gca	cct	aaa	act	gtg	gac	cac	att	tat	aag	ctt	gtg	cga		192
Pro	Thr	Val	Ala	Pro	Lys	Thr	Val	Asp	His	Ile	Tyr	Lys	Leu	Val	Arg		
	50					55					60						
ctt	gga	ggc	tat	aac	act	aac	cat	ttc	ttt	cgg	gtg	gat	aag	gga	ttc		240
Leu	Gly	Gly	Tyr	Asn	Thr	Asn	His	Phe	Phe	Arg	Val	Asp	Lys	Gly	Phe		
65					70					75				80			
gtg	gcc	caa	gta	gca	gat	gtt	aca	aat	gga	aga	tca	gct	cca	atg	aac		288
Val	Ala	Gln	Val	Ala	Asp	Val	Thr	Asn	Gly	Arg	Ser	Ala	Pro	Met	Asn		
				85					90					95			
gag	gaa	caa	aga	agg	gaa	gct	gta	aag	act	gtt	gtt	ggt	gaa	ttt	act		336
Glu	Glu	Gln	Arg	Glu	Ala	Val	Lys	Thr	Val	Val	Gly	Glu	Phe	Thr			
			100				105					110					
gaa	gtc	aaa	cat	gtt	cgg	ggt	att	ctt	tcc	atg	gga	aga	tat	gat	gat		384
Glu	Val	Lys	His	Val	Arg	Gly	Ile	Leu	Ser	Met	Gly	Arg	Tyr	Asp	Asp		
		115					120					125					
cca	gac	agt	gct	tca	tct	tca	ttt	tca	ata	cta	ctt	gga	gat	gcc	cct		432
Pro	Asp	Ser	Ala	Ser	Ser	Ser	Phe	Ser	Ile	Leu	Leu	Gly	Asp	Ala	Pro		
	130					135					140						
cat	ctt	gat	ggc	aag	tat	gca	ata	ttt	gga	aaa	gtt	act	aaa	ggt	gat		480
His	Leu	Asp	Gly	Lys	Tyr	Ala	Ile	Phe	Gly	Lys	Val	Thr	Lys	Gly	Asp		
145					150				155					160			
gaa	acg	ttg	aca	aag	ctc	gag	caa	cta	cct	acc	cgc	aaa	gag	ggt	ata		528
Glu	Thr	Leu	Thr	Lys	Leu	Glu	Gln	Leu	Pro	Thr	Arg	Lys	Glu	Gly	Ile		
			165					170						175			
ttt	gta	atg	ccg	atg	gaa	cgc	atc	act	atc	ctg	tcg	tca	tat	tac	tat		576
Phe	Val	Met	Pro	Met	Glu	Arg	Ile	Thr	Ile	Leu	Ser	Ser	Tyr	Tyr	Tyr		
			180				185						190				
gat	aca	gag	aca	gaa	aat	tgc	gag	gaa	gac	aga	tca	att	ttg	aag	cgc		624
Asp	Thr	Glu	Thr	Glu	Asn	Cys	Glu	Glu	Asp	Arg	Ser	Ile	Leu	Lys	Arg		
		195				200					205						
aga	cta	gcc	tca	gct	att	gaa	gtt	gaa	aga	cag	agg	atg	aaa	tgc			672
Arg	Leu	Ala	Ala	Ser	Ile	Glu	Val	Glu	Arg	Gln	Arg	Met	Lys	Cys			
	210				215					220							
ttc	ccc	tga															681
Phe	Pro																
225																	

<210> 10023
 <211> 226
 <212> PRT
 <213> Glycine max

<400> 10023
 Met Trp Ile Gln Gly Phe Ser Phe Trp Ile Lys Gly Phe Ser Leu Leu
 1 5 10 15
 Ala Leu Ile Ser Val Ile Ser Ala Leu Glu Pro Glu Leu Gly Ser Thr
 20 25 30
 Arg Val Val Phe Gln Thr Lys Tyr Gly Asp Ile Glu Phe Gly Phe Tyr
 35 40 45
 Pro Thr Val Ala Pro Lys Thr Val Asp His Ile Tyr Lys Leu Val Arg
 50 55 60
 Leu Gly Gly Tyr Asn Thr Asn His Phe Phe Arg Val Asp Lys Gly Phe
 65 70 75 80
 Val Ala Gln Val Ala Asp Val Thr Asn Gly Arg Ser Ala Pro Met Asn
 85 90 95
 Glu Glu Gln Arg Glu Ala Val Lys Thr Val Val Gly Glu Phe Thr
 100 105 110
 Glu Val Lys His Val Arg Gly Ile Leu Ser Met Gly Arg Tyr Asp Asp
 115 120 125
 Pro Asp Ser Ala Ser Ser Ser Phe Ser Ile Leu Leu Gly Asp Ala Pro
 130 135 140
 His Leu Asp Gly Lys Tyr Ala Ile Phe Gly Lys Val Thr Lys Gly Asp
 145 150 155 160
 Glu Thr Leu Thr Lys Leu Glu Gln Leu Pro Thr Arg Lys Glu Gly Ile
 165 170 175

PF59083SeqList PF59083.txt

Phe Val Met Pro Met Glu Arg Ile Thr Ile Leu Ser Ser Tyr Tyr
 180 185 190
 Asp Thr Glu Thr Glu Asn Cys Glu Glu Asp Arg Ser Ile Leu Lys Arg
 195 200 205
 Arg Leu Ala Ala Ser Ala Ile Glu Val Glu Arg Gln Arg Met Lys Cys
 210 215 220
 Phe Pro
 225

<210> 10024
 <211> 615
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(615)

<400> 10024
 atg gcg aaa acg acg tcg ttg ctg ctc ttt aca ctg ctc ctc ttc gga 48
 Met Ala Lys Thr Thr Ser Leu Leu Leu Phe Thr Leu Leu Phe Gly
 1 5 10 15
 acc cta gct ctc atc cag gcg aag aaa tcg aag gag gat ttg aag gag 96
 Thr Leu Ala Leu Ile Gln Ala Lys Lys Ser Lys Glu Asp Leu Lys Glu
 20 25 30
 gtg acc cac aag gtt tac ttt gat gtt gag att aat gga aaa gaa gca 144
 Val Thr His Lys Val Tyr Phe Asp Val Glu Ile Asn Gly Lys Glu Ala
 35 40 45
 ggt cgt att gta atg ggt ctt tat ggg aag gct gtt cca aaa act gca 192
 Gly Arg Ile Val Met Gly Leu Tyr Gly Lys Ala Val Pro Lys Thr Ala
 50 55 60
 gaa aac ttc cga gca ctt tgc aca ggg gaa aag gga act ggt aaa agt 240
 Glu Asn Phe Arg Ala Leu Cys Thr Gly Glu Lys Gly Thr Gly Lys Ser
 65 70 75 80
 gga aag cct ctc cat tac aaa ggt agc tca ttc cat aga att att cct 288
 Gly Lys Pro Leu His Tyr Lys Gly Ser Ser Phe His Arg Ile Ile Pro
 85 90 95
 agc ttt atg ctt caa gga ggt gat ttt aca caa gga aat gga atg ggt 336
 Ser Phe Met Leu Gln Gly Gly Asp Phe Thr Gln Gly Asn Gly Met Gly
 100 105 110
 gga gaa tca att tac gga gag aag ttt gct gat gag aac ttc aag tta 384
 Gly Glu Ser Ile Tyr Gly Glu Lys Phe Ala Asp Glu Asn Phe Lys Leu
 115 120 125
 aag cat act gga cca gga ctt cta tca atg gca aat gct ggt cct aat 432
 Lys His Thr Gly Pro Gly Leu Ser Met Ala Asn Ala Gly Pro Asn
 130 135 140
 acc aat ggt tca caa ttt ttc att aca act gtg aca act agc tgg ttg 480
 Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Thr Thr Ser Trp Leu
 145 150 155 160
 gac gga agg cat gtt gtt ttt ggt aaa gtt ctt tct gga atg gat gtt 528
 Asp Gly Arg His Val Val Phe Gly Lys Val Leu Ser Gly Met Asp Val
 165 170 175
 gtt tac aag att gaa gct gaa gga aca caa agt ggc act ccc aag agc 576
 Val Tyr Lys Ile Glu Ala Glu Gly Thr Gln Ser Gly Thr Pro Lys Ser
 180 185 190
 aag gtt gtg att gtt gac agt ggt gaa ctc cct cta taa 615
 Lys Val Val Ile Val Asp Ser Gly Glu Leu Pro Leu
 195 200

<210> 10025
 <211> 204
 <212> PRT
 <213> Glycine max

<400> 10025
 Met Ala Lys Thr Thr Ser Leu Leu Leu Phe Thr Leu Leu Leu Phe Gly
 1 5 10 15
 Thr Leu Ala Leu Ile Gln Ala Lys Lys Ser Lys Glu Asp Leu Lys Glu
 20 25 30

PF59083SeqList PF59083.txt

Val Thr His Lys Val Tyr Phe Asp Val Glu Ile Asn Gly Lys Glu Ala
 35 40 45
 Gly Arg Ile Val Met Gly Leu Tyr Gly Lys Ala Val Pro Lys Thr Ala
 50 55 60
 Glu Asn Phe Arg Ala Leu Cys Thr Gly Glu Lys Gly Thr Gly Lys Ser
 65 70 75 80
 Gly Lys Pro Leu His Tyr Lys Gly Ser Ser Phe His Arg Ile Ile Pro
 85 90 95
 Ser Phe Met Leu Gln Gly Gly Asp Phe Thr Gln Gly Asn Gly Met Gly
 100 105 110
 Gly Glu Ser Ile Tyr Gly Glu Lys Phe Ala Asp Glu Asn Phe Lys Leu
 115 120 125
 Lys His Thr Gly Pro Gly Leu Leu Ser Met Ala Asn Ala Gly Pro Asn
 130 135 140
 Thr Asn Gly Ser Gln Phe Ile Thr Thr Val Thr Thr Ser Trp Leu
 145 150 155 160
 Asp Gly Arg His Val Val Phe Gly Lys Val Leu Ser Gly Met Asp Val
 165 170 175
 Val Tyr Lys Ile Glu Ala Glu Gly Thr Gln Ser Gly Thr Pro Lys Ser
 180 185 190
 Lys Val Val Ile Val Asp Ser Gly Glu Leu Pro Leu
 195 200

<210> 10026

<211> 621

<212> DNA

<213> Linum usitatissimum

<220>

<221> CDS

<222> (1)..(621)

<400> 10026

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

PF59083SeqList PF59083.txt

aag agc aag gtc gtc att gtt gac agc ggc gaa cta cct cta taa
Lys Ser Lys Val Val Ile Val Asp Ser Gly Glu Leu Pro Leu
195 200 205

621

<210> 10027
<211> 206
<212> PRT
<213> Linum usitatissimum

<400> 10027
Met Asn Ser Lys Ser Leu Ala Val Ala Leu Leu Trp Gly Ala Leu Leu
1 5 10 15
Phe Gly Thr Leu Ala Leu Ile Gln Ala Lys Lys Ser Asp Glu Lys Leu
20 25 30
Lys Glu Ile Thr His Lys Val Tyr Phe Asp Val Glu Ile Asp Gly Lys
35 40 45
Pro Ala Gly Arg Ile Thr Met Gly Leu Tyr Gly Lys Ala Val Pro Lys
50 55 60
Thr Ala Glu Asn Phe Arg Ala Leu Cys Thr Gly Glu Lys Gly Val Gly
65 70 75
Lys Ser Gly Lys Pro Leu His Tyr Lys Gly Ser Ser Phe His Arg Ile
85 90 95
Ile Pro Ser Phe Met Leu Gln Gly Gly Asp Phe Thr His Gly Asp Gly
100 105 110
Arg Gly Gly Glu Ser Ile Tyr Gly Glu Lys Phe Ala Asp Glu Asn Phe
115 120 125
Lys Leu Lys His Thr Gly Pro Gly Leu Leu Ser Met Ala Asn Ala Gly
130 135 140
Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Thr Thr Ser
145 150 155 160
Trp Leu Asp Gly Arg His Val Val Phe Gly Lys Val Leu Ser Gly Met
165 170 175
Asp Val Val Tyr Lys Val Glu Ala Glu Gly Lys Gln Ser Gly Thr Pro
180 185 190
Lys Ser Lys Val Val Ile Val Asp Ser Gly Glu Leu Pro Leu
195 200 205

<210> 10028
<211> 672
<212> DNA
<213> Linum usitatissimum

<220>
<221> CDS
<222> (1)..(672)

<400> 10028
atg acg aga atg tgg atc tta gtc gcc ggt ttg gca att gca gcg gcg 48
Met Thr Arg Met Trp Ile Leu Val Ala Gly Leu Ala Ile Ala Ala Ala
1 5 10 15
gcc ggc gtc tca ttt gcg gag cct gag ctc agc tca gct cgt gtt gtc 96
Ala Gly Val Ser Phe Ala Glu Pro Glu Leu Ser Ser Ala Arg Val Val
20 25 30
ttc cag acc aat tac ggg gat atc gag ttc gga ttc tac cca tcg gtg 144
Phe Gln Thr Asn Tyr Gly Asp Ile Glu Phe Gly Phe Tyr Pro Ser Val
35 40 45
gcg ccg ata acg gtc cag cac att ttc aag ctt gtt cgg ctt gga gga 192
Ala Pro Ile Thr Val Gln His Ile Phe Lys Leu Val Arg Leu Gly Gly
50 55 60
tac aac act aat cat ttc ttc agg gtt gac aag gga ttt gtg gct caa 240
Tyr Asn Thr Asn His Phe Phe Arg Val Asp Lys Gly Phe Val Ala Gln
65 70 75 80
gtg gcg gat gtg gct ggt ggg cga tcg gct ccg atg aat gaa gag caa 288
Val Ala Asp Val Ala Gly Gly Arg Ser Ala Pro Met Asn Glu Glu Gln
85 90 95
aga ctg gag gca gag aag act gtg att ggt gaa ttt agt gac gtt aag 336
Arg Leu Glu Ala Glu Lys Thr Val Ile Gly Glu Phe Ser Asp Val Lys
100 105 110
cat gtt cga ggc atc ctg tcc atg ggg agg tat gct gat cca aac agt 384
Seite 10619

PF59083SeqList PF59083.txt

His	Val	Arg	Gly	Ile	Leu	Ser	Met	Gly	Arg	Tyr	Ala	Asp	Pro	Asn	Ser		
		115					120					125					
gga	tct	tcc	tcg	ttt	tca	atc	cta	ctt	ggg	aat	gca	cct	cat	ctg	gac		432
Gly	Ser	Ser	Ser	Phe	Ser	Ile	Leu	Leu	Gly	Asn	Ala	Pro	His	Leu	Asp		
		130				135					140						
ggc	caa	tat	gca	ata	ttt	ggt	aaa	gtt	act	aaa	ggt	gat	gac	aca	tta		480
Gly	Gln	Tyr	Ala	Ile	Phe	Gly	Lys	Val	Thr	Lys	Gly	Asp	Asp	Thr	Leu		
					150					155					160		
acg	aag	ctg	gag	cag	ctt	cct	acc	cgg	act	gag	gga	atc	ttt	gtg	atg		528
Thr	Lys	Leu	Glu	Gln	Leu	Pro	Thr	Arg	Thr	Glu	Gly	Ile	Phe	Val	Met		
				165					170					175			
cca	aca	gaa	cgg	atc	act	att	ttg	tca	tca	tat	tac	tac	gat	act	aac		576
Pro	Thr	Glu	Arg	Ile	Thr	Ile	Leu	Ser	Ser	Tyr	Tyr	Tyr	Asp	Thr	Asn		
				180				185					190				
atg	gag	aag	tgc	gac	gag	gag	agg	tca	att	ttg	aaa	cgc	aga	ctc	gct		624
Met	Glu	Lys	Cys	Asp	Glu	Glu	Arg	Ser	Ile	Leu	Lys	Arg	Arg	Leu	Ala		
		195					200					205					
gcg	tct	gct	att	gaa	atc	gaa	aga	cag	aga	atg	aaa	tgc	ttc	cca	tga		672
Ala	Ser	Ala	Ile	Glu	Ile	Glu	Arg	Gln	Arg	Met	Lys	Cys	Phe	Pro			
		210				215					220						

<210> 10029
 <211> 223
 <212> PRT
 <213> Linum usitatissimum

<400> 10029

Met	Thr	Arg	Met	Trp	Ile	Leu	Val	Ala	Gly	Leu	Ala	Ile	Ala	Ala	Ala		
1				5					10				15				
Ala	Gly	Val	Ser	Phe	Ala	Glu	Pro	Glu	Leu	Ser	Ser	Ala	Arg	Val	Val		
			20					25					30				
Phe	Gln	Thr	Asn	Tyr	Gly	Asp	Ile	Glu	Phe	Gly	Phe	Tyr	Pro	Ser	Val		
		35				40						45					
Ala	Pro	Ile	Thr	Val	Gln	His	Ile	Phe	Lys	Leu	Val	Arg	Leu	Gly	Gly		
		50				55					60						
Tyr	Asn	Thr	Asn	His	Phe	Phe	Arg	Val	Asp	Lys	Gly	Phe	Val	Ala	Gln		
65					70				75						80		
Val	Ala	Asp	Val	Ala	Gly	Gly	Arg	Ser	Ala	Pro	Met	Asn	Glu	Glu	Gln		
				85					90					95			
Arg	Leu	Glu	Ala	Glu	Lys	Thr	Val	Ile	Gly	Glu	Phe	Ser	Asp	Val	Lys		
			100					105					110				
His	Val	Arg	Gly	Ile	Leu	Ser	Met	Gly	Arg	Tyr	Ala	Asp	Pro	Asn	Ser		
		115				120						125					
Gly	Ser	Ser	Ser	Phe	Ser	Ile	Leu	Leu	Gly	Asn	Ala	Pro	His	Leu	Asp		
		130				135					140						
Gly	Gln	Tyr	Ala	Ile	Phe	Gly	Lys	Val	Thr	Lys	Gly	Asp	Asp	Thr	Leu		
					150					155					160		
Thr	Lys	Leu	Glu	Gln	Leu	Pro	Thr	Arg	Thr	Glu	Gly	Ile	Phe	Val	Met		
				165					170					175			
Pro	Thr	Glu	Arg	Ile	Thr	Ile	Leu	Ser	Tyr	Tyr	Tyr	Asp	Thr	Asn			
			180					185				190					
Met	Glu	Lys	Cys	Asp	Glu	Glu	Arg	Ser	Ile	Leu	Lys	Arg	Arg	Leu	Ala		
		195					200					205					
Ala	Ser	Ala	Ile	Glu	Ile	Glu	Arg	Gln	Arg	Met	Lys	Cys	Phe	Pro			
		210				215					220						

<210> 10030
 <211> 630
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(630)

<400> 10030

atg	ttt	ata	aac	tac	cga	tca	ccg	cta	tca	att	ata	tta	gcc	ctt	gca		48
Met	Phe	Ile	Asn	Tyr	Arg	Ser	Pro	Leu	Ser	Ile	Ile	Leu	Ala	Leu	Ala		
	1			5				10						15			

PF59083SeqList PF59083.txt

att	ggg	cta	gta	ttc	tg	tcc	cga	tct	ggt	aac	gca	ctc	aaa	gga	ccc	96
Ile	Gly	Leu	Val	Phe	Trp	Ser	Arg	Ser	Val	Asn	Ala	Leu	Lys	Gly	Pro	
			20					25					30			
aaa	att	act	agc	aaa	gta	tat	ttt	gat	att	ctc	cat	ggg	gaa	aaa	gag	144
Lys	Ile	Thr	Ser	Lys	Val	Tyr	Phe	Asp	Ile	Leu	His	Gly	Glu	Lys	Glu	
		35					40					45				
cta	gga	cgc	ata	ggt	att	ggc	ctc	tac	ggc	ggt	act	gtc	ccg	att	aca	192
Leu	Gly	Arg	Ile	Val	Ile	Gly	Leu	Tyr	Gly	Gly	Thr	Val	Pro	Ile	Thr	
	50					55				60						
gca	gag	aac	ttt	cga	gct	ttg	gca	acc	ggc	gaa	aaa	gga	gga	gac	tta	240
Ala	Glu	Asn	Phe	Arg	Ala	Leu	Ala	Thr	Gly	Glu	Lys	Gly	Gly	Asp	Leu	
65					70				75						80	
aca	ttt	gaa	gga	tca	acc	ttt	cac	cgt	gta	atc	aag	aac	ttc	atg	ata	288
Thr	Phe	Glu	Gly	Ser	Thr	Phe	His	Arg	Val	Ile	Lys	Asn	Phe	Met	Ile	
				85					90					95		
caa	gga	gga	gat	ttt	aca	aag	ggt	gat	ggt	aca	ggt	gga	aag	tca	ata	336
Gln	Gly	Gly	Asp	Phe	Thr	Lys	Gly	Asp	Gly	Thr	Gly	Gly	Lys	Ser	Ile	
			100					105					110			
tac	ggt	gat	aaa	ttt	gcc	gac	gag	aac	ttc	aag	ttg	aaa	cac	tct	cga	384
Tyr	Gly	Asp	Lys	Phe	Ala	Asp	Glu	Asn	Phe	Lys	Leu	Lys	His	Ser	Arg	
		115					120					125				
aag	ggt	ctt	ctc	tct	atg	gcc	aac	gcg	gga	aaa	gat	acc	aat	ggc	tct	432
Lys	Gly	Leu	Leu	Ser	Met	Ala	Asn	Ala	Gly	Lys	Asp	Thr	Asn	Gly	Ser	
	130					135					140					
caa	ttc	ttt	att	acc	acc	tcc	aca	cct	ggt	tat	ctc	gac	ggc	aga	cac	480
Gln	Phe	Phe	Ile	Thr	Thr	Ser	Thr	Pro	Gly	Tyr	Leu	Asp	Gly	Arg	His	
145					150					155					160	
gtc	gtt	ttt	gga	gaa	gtc	atg	gaa	ggc	tac	gaa	ata	gtt	gaa	aaa	atc	528
Val	Val	Phe	Gly	Glu	Val	Met	Glu	Gly	Tyr	Glu	Ile	Val	Glu	Lys	Ile	
			165						170					175		
gag	gat	gtt	ccc	aaa	aat	ggt	gaa	aag	cca	aaa	gaa	gct	gtc	aag	ata	576
Glu	Asp	Val	Pro	Lys	Asn	Gly	Glu	Lys	Pro	Lys	Glu	Ala	Val	Lys	Ile	
			180					185					190			
gct	aaa	tgt	gga	gaa	ttg	cct	gta	gct	gaa	gaa	ggt	att	cac	gtc	gaa	624
Ala	Lys	Cys	Gly	Glu	Leu	Pro	Val	Ala	Glu	Glu	Gly	Ile	His	Val	Glu	
		195					200					205				
ctc	taa															630
Leu																

<210> 10031
 <211> 209
 <212> PRT
 <213> Hordeum vulgare

<400> 10031
 Met Phe Ile Asn Tyr Arg Ser Pro Leu Ser Ile Ile Leu Ala Leu Ala
 1 5 10 15
 Ile Gly Leu Val Phe Trp Ser Arg Ser Val Asn Ala Leu Lys Gly Pro
 20 25 30
 Lys Ile Thr Ser Lys Val Tyr Phe Asp Ile Leu His Gly Glu Lys Glu
 35 40 45
 Leu Gly Arg Ile Val Ile Gly Leu Tyr Gly Gly Thr Val Pro Ile Thr
 50 55 60
 Ala Glu Asn Phe Arg Ala Leu Ala Thr Gly Glu Lys Gly Gly Asp Leu
 65 70 75 80
 Thr Phe Glu Gly Ser Thr Phe His Arg Val Ile Lys Asn Phe Met Ile
 85 90 95
 Gln Gly Gly Asp Phe Thr Lys Gly Asp Gly Thr Gly Gly Lys Ser Ile
 100 105 110
 Tyr Gly Asp Lys Phe Ala Asp Glu Asn Phe Lys Leu Lys His Ser Arg
 115 120 125
 Lys Gly Leu Leu Ser Met Ala Asn Ala Gly Lys Asp Thr Asn Gly Ser
 130 135 140
 Gln Phe Phe Ile Thr Thr Ser Thr Pro Gly Tyr Leu Asp Gly Arg His
 145 150 155 160
 Val Val Phe Gly Glu Val Met Glu Gly Tyr Glu Ile Val Glu Lys Ile
 165 170 175
 Glu Asp Val Pro Lys Asn Gly Glu Lys Pro Lys Glu Ala Val Lys Ile
 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

PF59083SeqList PF59083.txt

Ala Lys Cys Gly Glu Leu Pro Val Ala Glu Glu Gly Ile His Val Glu
 180 185 190
 195 200 205
 Leu

<210> 10032
 <211> 642
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(642)

<400> 10032
 atg gcg atg agg gcg tgg agg cgg agc gcg gcg gcg agg gcc ccg gcg 48
 Met Ala Met Arg Ala Trp Arg Arg Ser Ala Ala Ala Arg Ala Pro Ala
 1 5 10 15
 cac ctg tgc ctg tgg ctg gcg ctc gtc gcc acc ctg gtg ctc gcc 96
 His Leu Cys Leu Trp Leu Ala Leu Val Ala Ala Thr Leu Val Leu Ala
 20 25 30
 cag ggg aag aag tcc aac ctg tcg gag gtg acg cac aag gtc tac ttc 144
 Gln Gly Lys Lys Ser Asn Leu Ser Glu Val Thr His Lys Val Tyr Phe
 35 40 45
 gac atc gag atc gac ggc aag ccc gca ggt cgg gtt gtc atg gga ctt 192
 Asp Ile Glu Ile Asp Gly Lys Pro Ala Gly Arg Val Val Met Gly Leu
 50 55 60
 ttt ggc aag gct gtt cct aaa act gca gag aac ttc aga gca ctc tgc 240
 Phe Gly Lys Ala Val Pro Lys Thr Ala Glu Asn Phe Arg Ala Leu Cys
 65 70 75 80
 aca gga gag aaa ggt atg ggc aac agt ggc aaa cct ctc cac tac aag 288
 Thr Gly Glu Lys Gly Met Gly Asn Ser Gly Lys Pro Leu His Tyr Lys
 85 90 95
 ggg agt tca ttc cac aga att atc ccc agc ttc atg atc caa gga ggt 336
 Gly Ser Ser Phe His Arg Ile Ile Pro Ser Phe Met Ile Gln Gly Gly
 100 105 110
 gac ttc acc ctt ggc gat gga agg ggt ggt gaa tca atc tac ggc aca 384
 Asp Phe Thr Leu Gly Asp Gly Arg Gly Gly Glu Ser Ile Tyr Gly Thr
 115 120 125
 aag ttc gcc gat gag aac ttc aag ctc aag cac act gga cca ggc tac 432
 Lys Phe Ala Asp Glu Asn Phe Lys Leu Lys His Thr Gly Pro Gly Tyr
 130 135 140
 ctt tcc atg gcc aat gct ggg aga gat acc aat gga tcc cag ttt ttc 480
 Leu Ser Met Ala Asn Ala Gly Arg Asp Thr Asn Gly Ser Gln Phe Phe
 145 150 155 160
 atc acc act gtg act acg agc tgg ttg gat ggc aag cac gtc gtg ttc 528
 Ile Thr Thr Val Thr Ser Trp Leu Asp Gly Lys His Val Val Phe
 165 170 175
 ggc aag gtg ttg tct ggg atg gac gtg gta tac aag gtt gag gct gaa 576
 Gly Lys Val Leu Ser Gly Met Asp Val Val Tyr Lys Val Glu Ala Glu
 180 185 190
 ggc aag cag aac ggg aca cca aag agc aaa gtt gtc att gct gac agc 624
 Gly Lys Gln Asn Gly Thr Pro Lys Ser Lys Val Val Ile Ala Asp Ser
 195 200 205
 gga gaa gtg ccg ctg tga 642
 Gly Glu Val Pro Leu
 210

<210> 10033
 <211> 213
 <212> PRT
 <213> Hordeum vulgare

<400> 10033
 Met Ala Met Arg Ala Trp Arg Arg Ser Ala Ala Ala Arg Ala Pro Ala
 1 5 10 15
 His Leu Cys Leu Trp Leu Ala Leu Val Ala Ala Thr Leu Val Leu Ala
 20 25 30

PF59083SeqList PF59083.txt

Gln Gly Lys Lys Ser Asn Leu Ser Glu Val Thr His Lys Val Tyr Phe
 35 40 45
 Asp Ile Glu Ile Asp Gly Lys Pro Ala Gly Arg Val Val Met Gly Leu
 50 55 60
 Phe Gly Lys Ala Val Pro Lys Thr Ala Glu Asn Phe Arg Ala Leu Cys
 65 70 75 80
 Thr Gly Glu Lys Gly Met Gly Asn Ser Gly Lys Pro Leu His Tyr Lys
 85 90 95
 Gly Ser Ser Phe His Arg Ile Ile Pro Ser Phe Met Ile Gln Gly Gly
 100 105 110
 Asp Phe Thr Leu Gly Asp Gly Arg Gly Gly Glu Ser Ile Tyr Gly Thr
 115 120 125
 Lys Phe Ala Asp Glu Asn Phe Lys Leu Lys His Thr Gly Pro Gly Tyr
 130 135 140
 Leu Ser Met Ala Asn Ala Gly Arg Asp Thr Asn Gly Ser Gln Phe Phe
 145 150 155 160
 Ile Thr Thr Val Thr Thr Ser Trp Leu Asp Gly Lys His Val Val Phe
 165 170 175
 Gly Lys Val Leu Ser Gly Met Asp Val Val Tyr Lys Val Glu Ala Glu
 180 185 190
 Gly Lys Gln Asn Gly Thr Pro Lys Ser Lys Val Val Ile Ala Asp Ser
 195 200 205
 Gly Glu Val Pro Leu
 210

<210> 10034
 <211> 483
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(483)

<400> 10034
 atg tcg gtg acg ctg cac acg aac ctg ggg gac atc aag gtg gag gtt 48
 Met Ser Val Thr Leu His Thr Asn Leu Gly Asp Ile Lys Val Glu Val
 1 5 10 15
 ttc tgc gac cag gtg ccg cgg acg gcg gag aac ttc ctg gcc ctg tgc 96
 Phe Cys Asp Gln Val Pro Arg Thr Ala Glu Asn Phe Leu Ala Leu Cys
 20 25 30
 gcc agc ggc tac tac gac ggg acg gtg ttc cac cgc aac atc aag ggg 144
 Ala Ser Gly Tyr Tyr Asp Gly Thr Val Phe His Arg Asn Ile Lys Gly
 35 40 45
 ttc atg gtg cag ggc ggc gac ccg acg ggg acg ggc aag ggc ggc gcg 192
 Phe Met Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Lys Gly Gly Ala
 50 55 60
 tcc atc tgg ggc ggc aag ttc gcg gac gag ttc cgg gag gcg ctc aag 240
 Ser Ile Trp Gly Gly Lys Phe Ala Asp Glu Phe Arg Glu Ala Leu Lys
 65 70 75 80
 cac ggg gcg agg ggc acc ctg tcc atg gcc aac tcg ggg ccc aac acc 288
 His Gly Ala Arg Gly Thr Leu Ser Met Ala Asn Ser Gly Pro Asn Thr
 85 90 95
 aac ggc agc cag ttc ttc atc acc tac gcc aag cag ccc cac ctc aac 336
 Asn Gly Ser Gln Phe Phe Ile Thr Tyr Ala Lys Gln Pro His Leu Asn
 100 105 110
 ggc cac tac acc gtg ttc gcc aag gtc atc cac ggc ttc gac gtg ctc 384
 Gly His Tyr Thr Val Phe Ala Lys Val Ile His Gly Phe Asp Val Leu
 115 120 125
 gac ctc atg gag aag acc ccc acc ggc ccc gcc gac ccc ctc gcc 432
 Asp Leu Met Glu Lys Thr Pro Thr Gly Pro Ala Asp Arg Pro Leu Ala
 130 135 140
 gag atc cgc ctc aac cgc gtc acc gtc cac gcc aac ccg ctc gcc gga 480
 Glu Ile Arg Leu Asn Arg Val Thr Val His Ala Asn Pro Leu Ala Gly
 145 150 155 160
 taa 483

PF59083SeqList PF59083.txt

<210> 10035
<211> 160
<212> PRT
<213> Hordeum vulgare

<400> 10035
Met Ser Val Thr Leu His Thr Asn Leu Gly Asp Ile Lys Val Glu Val
1 5 10 15
Phe Cys Asp Gln Val Pro Arg Thr Ala Glu Asn Phe Leu Ala Leu Cys
20 25 30
Ala Ser Gly Tyr Tyr Asp Gly Thr Val Phe His Arg Asn Ile Lys Gly
35 40 45
Phe Met Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Lys Gly Gly Ala
50 55 60
Ser Ile Trp Gly Gly Lys Phe Ala Asp Glu Phe Arg Glu Ala Leu Lys
65 70 75 80
His Gly Ala Arg Gly Thr Leu Ser Met Ala Asn Ser Gly Pro Asn Thr
85 90 95
Asn Gly Ser Gln Phe Phe Ile Thr Tyr Ala Lys Gln Pro His Leu Asn
100 105 110
Gly His Tyr Thr Val Phe Ala Lys Val Ile His Gly Phe Asp Val Leu
115 120 125
Asp Leu Met Glu Lys Thr Pro Thr Gly Pro Ala Asp Arg Pro Leu Ala
130 135 140
Glu Ile Arg Leu Asn Arg Val Thr Val His Ala Asn Pro Leu Ala Gly
145 150 155 160

<210> 10036
<211> 492
<212> DNA
<213> Helianthus annuus

<220>
<221> CDS
<222> (1)..(492)

<400> 10036
atg cca ggc gca gaa gga ggt cca ccg gag gta act ctc gaa aca tcc 48
Met Pro Gly Ala Glu Gly Gly Pro Pro Glu Val Thr Leu Glu Thr Ser 15
1 5 10
atg ggc tct ttc acc gtt gag atg tac gat aag cac gca cct agg act 96
Met Gly Ser Phe Thr Val Glu Met Tyr Asp Lys His Ala Pro Arg Thr 20 25 30
tgc aaa aac ttc att gaa ctg tct cga agg ggc tac tac aac aac gtt 144
Cys Lys Asn Phe Ile Glu Leu Ser Arg Arg Gly Tyr Tyr Asn Asn Val 35 40 45
aag ttt cac aga atc att aag gat ttt att gtt caa gga ggt gat ccc 192
Lys Phe His Arg Ile Ile Lys Asp Phe Ile Val Gln Gly Gly Asp Pro 50 55 60
act ggc act ggt aga ggt gga gaa tct att tac ggt tca aag ttt gag 240
Thr Gly Thr Gly Arg Gly Gly Glu Ser Ile Tyr Gly Ser Lys Phe Glu 65 70 75 80
gat gag atc acc cca aag ttg aag cat acg gga gct ggt atc tta tct 288
Asp Glu Ile Thr Pro Lys Leu Lys His Thr Gly Ala Gly Ile Leu Ser 85 90 95
atg gct aat gct ggt ccg aat aca aat gga agt cag ttc ttt atc aca 336
Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe Phe Ile Thr 100 105 110
ttg gcc cca gcg caa tcg ctt gat gga aag cac acg ata ttt gga aga 384
Leu Ala Pro Ala Gln Ser Leu Asp Gly Lys His Thr Ile Phe Gly Arg 115 120 125
gtg tgc aga gga atg gag att gtc aag aga ctt ggt agt gtt cag act 432
Val Cys Arg Gly Met Glu Ile Val Lys Arg Leu Gly Ser Val Gln Thr 130 135 140
gat aat acc gac agg cca att cat gac gtg aag ata cta cgg aca gca 480
Asp Asn Thr Asp Arg Pro Ile His Asp Val Lys Ile Leu Arg Thr Ala 145 150 155 160
gtt aag gat tga 492
Val Lys Asp

PF59083SeqList PF59083.txt

<210> 10037
 <211> 163
 <212> PRT
 <213> Helianthus annuus

<400> 10037
 Met Pro Gly Ala Glu Gly Gly Pro Pro Glu Val Thr Leu Glu Thr Ser
 1 5 10 15
 Met Gly Ser Phe Thr Val Glu Met Tyr Asp Lys His Ala Pro Arg Thr
 20 25 30
 Cys Lys Asn Phe Ile Glu Leu Ser Arg Arg Gly Tyr Tyr Asn Asn Val
 35 40 45
 Lys Phe His Arg Ile Ile Lys Asp Phe Ile Val Gln Gly Gly Asp Pro
 50 55 60
 Thr Gly Thr Gly Arg Gly Gly Glu Ser Ile Tyr Gly Ser Lys Phe Glu
 65 70 75 80
 Asp Glu Ile Thr Pro Lys Leu Lys His Thr Gly Ala Gly Ile Leu Ser
 85 90 95
 Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe Phe Ile Thr
 100 105 110
 Leu Ala Pro Ala Gln Ser Leu Asp Gly Lys His Thr Ile Phe Gly Arg
 115 120 125
 Val Cys Arg Gly Met Glu Ile Val Lys Arg Leu Gly Ser Val Gln Thr
 130 135 140
 Asp Asn Thr Asp Arg Pro Ile His Asp Val Lys Ile Leu Arg Thr Ala
 145 150 155 160
 Val Lys Asp

<210> 10038
 <211> 1026
 <212> DNA
 <213> Escherichia coli K12

<220>
 <221> CDS
 <222> (1)..(1026)
 <223> transl_table=11

<400> 10038
 atg aaa gcg tta tcc aaa ctg aaa gcg gaa gag ggc atc tgg atg acc 48
 Met Lys Ala Leu Ser Lys Leu Lys Ala Glu Glu Gly Ile Trp Met Thr 15
 1 5 10 15
 gac gtt cct gta ccg gaa ctc ggg cat aac gat ctg ctg att aaa atc 96
 Asp Val Pro Val Pro Glu Leu Gly His Asn Asp Leu Leu Ile Lys Ile 20 25 30
 cgt aaa aca gcc atc tgc ggg act gac gtt cac atc tat aac tgg gat 144
 Arg Lys Thr Ala Ile Cys Gly Thr Asp Val His Ile Tyr Asn Trp Asp 35 40 45
 gag tgg tcg caa aaa acc atc ccg gtg ccg atg gtc gtg ggc cat gaa 192
 Glu Trp Ser Gln Lys Thr Ile Pro Val Pro Met Val Val Gly His Glu 50 55 60
 tat gtc ggt gaa gtg gta ggt att ggt cag gaa gtg aaa ggc ttc aag 240
 Tyr Val Gly Glu Val Val Gly Ile Gly Gln Glu Val Lys Gly Phe Lys 65 70 75 80
 atc ggc gat cgc gtt tct ggc gaa ggc cat atc acc tgt ggt cat tgc 288
 Ile Gly Asp Arg Val Ser Gly Glu Gly His Ile Thr Cys Gly His Cys 85 90 95
 cgc aac tgt cgt ggt ggt cgt acc cat ttg tgc cgc aac acg ata ggc 336
 Arg Asn Cys Arg Gly Gly Arg Thr His Leu Cys Arg Asn Thr Ile Gly 100 105 110
 gtt ggt gtt aat cgc ccg ggc tgc ttt gcc gaa tat ctg gtg atc ccg 384
 Val Gly Val Asn Arg Pro Gly Cys Phe Ala Glu Tyr Leu Val Ile Pro 115 120 125
 gca ttc aac gcc ttc aaa atc ccc gac aat att tcc gat gac tta gcc 432
 Ala Phe Asn Ala Phe Lys Ile Pro Asp Asn Ile Ser Asp Asp Leu Ala 130 135 140

PF59083SeqList PF59083.txt

gca att ttt gat ccc ttc ggt aac gcc gtg cat acc gcg ctg tcg ttt	480
Ala Ile Phe Asp Pro Phe Gly Asn Ala Val His Thr Ala Leu Ser Phe	
145 150 155 160	
gat ctg gtg ggc gaa gat gtg ctg gtt tct ggt gca ggc ccg att ggt	528
Asp Leu Val Gly Glu Asp Val Leu Val Ser Gly Ala Gly Pro Ile Gly	
165 170 175	
att atg gca gcg gcg gtg gcg aaa cac gtt ggt gca cgc aat gtg gtg	576
Ile Met Ala Ala Ala Val Ala Lys His Val Gly Ala Arg Asn Val Val	
180 185 190	
atc act gat gtt aac gaa tac cgc ctt gag ctg gcg cgt aaa atg ggt	624
Ile Thr Asp Val Asn Glu Tyr Arg Leu Glu Leu Ala Arg Lys Met Gly	
195 200 205	
atc acc cgt gcg gtt aac gtc gcc aaa gaa aat ctc aat gac gtg atg	672
Ile Thr Arg Ala Val Asn Val Ala Lys Glu Asn Leu Asn Asp Val Met	
210 215 220	
gcg gag tta ggc atg acc ggt ttt gat gtc ggt ctg gaa atg tcc	720
Ala Glu Leu Gly Met Thr Glu Gly Phe Asp Val Gly Leu Glu Met Ser	
225 230 235 240	
ggt gcg ccg cca gcg ttt cgt acc atg ctt gac acc atg aat cac ggc	768
Gly Ala Pro Pro Ala Phe Arg Thr Met Leu Asp Thr Met Asn His Gly	
245 250 255	
ggc cgt att gcg atg ctg ggt att ccg ccg tct gat atg tct atc gac	816
Gly Arg Ile Ala Met Leu Gly Ile Pro Pro Ser Asp Met Ser Ile Asp	
260 265 270	
tgg acc aaa gtg atc ttt aaa ggc ttg ttc att aaa ggt att tac ggt	864
Trp Thr Lys Val Ile Phe Lys Gly Leu Phe Ile Lys Gly Ile Tyr Gly	
275 280 285	
cgt gag atg ttt gaa acc tgg tac aag atg gcg gcg ctg att cag tct	912
Arg Glu Met Phe Glu Thr Trp Tyr Lys Met Ala Ala Leu Ile Gln Ser	
290 295 300	
ggc ctc gat ctt tcg ccg atc att acc cat cgt ttc tct atc gat gat	960
Gly Leu Asp Leu Ser Pro Ile Ile Thr His Arg Phe Ser Ile Asp Asp	
305 310 315 320	
ttc cag aag ggc ttt gac gct atg cgt tcg ggc cag tcc ggg aaa gtt	1008
Phe Gln Lys Gly Phe Asp Ala Met Arg Ser Gly Gln Ser Gly Lys Val	
325 330 335	
att ctg agc tgg gat taa	1026
Ile Leu Ser Trp Asp	
340	

<210> 10039

<211> 341

<212> PRT

<213> Escherichia coli K12

<400> 10039

Met Lys Ala Leu Ser Lys Leu Lys Ala Glu Glu Gly Ile Trp Met Thr	
1 5 10 15	
Asp Val Pro Val Pro Glu Leu Gly His Asn Asp Leu Leu Ile Lys Ile	
20 25 30	
Arg Lys Thr Ala Ile Cys Gly Thr Asp Val His Ile Tyr Asn Trp Asp	
35 40 45	
Glu Trp Ser Gln Lys Thr Ile Pro Val Pro Met Val Val Gly His Glu	
50 55 60	
Tyr Val Gly Glu Val Val Gly Ile Gly Gln Glu Val Lys Gly Phe Lys	
65 70 75 80	
Ile Gly Asp Arg Val Ser Gly Glu Gly His Ile Thr Cys Gly His Cys	
85 90 95	
Arg Asn Cys Arg Gly Gly Arg Thr His Leu Cys Arg Asn Thr Ile Gly	
100 105 110	
Val Gly Val Asn Arg Pro Gly Cys Phe Ala Glu Tyr Leu Val Ile Pro	
115 120 125	
Ala Phe Asn Ala Phe Lys Ile Pro Asp Asn Ile Ser Asp Asp Leu Ala	
130 135 140	
Ala Ile Phe Asp Pro Phe Gly Asn Ala Val His Thr Ala Leu Ser Phe	
145 150 155 160	
Asp Leu Val Gly Glu Asp Val Leu Val Ser Gly Ala Gly Pro Ile Gly	
165 170 175	
Ile Met Ala Ala Ala Val Ala Lys His Val Gly Ala Arg Asn Val Val	

PF59083SeqList PF59083.txt

```

      180      185      190
Ile Thr Asp Val Asn Glu Tyr Arg Leu Glu Leu Ala Arg Lys Met Gly
      195      200      205
Ile Thr Arg Ala Val Asn Val Ala Lys Glu Asn Leu Asn Asp Val Met
      210      215      220
Ala Glu Leu Gly Met Thr Glu Gly Phe Asp Val Gly Leu Glu Met Ser
      225      230      235
Gly Ala Pro Pro Ala Phe Arg Thr Met Leu Asp Thr Met Asn His Gly
      240      245      250
Gly Arg Ile Ala Met Leu Gly Ile Pro Pro Ser Asp Met Ser Ile Asp
      255      260      265
Trp Thr Lys Val Ile Phe Lys Gly Leu Phe Ile Lys Gly Ile Tyr Gly
      270      275      280
Arg Glu Met Phe Glu Thr Trp Tyr Lys Met Ala Ala Leu Ile Gln Ser
      285      290      295
Gly Leu Asp Leu Ser Pro Ile Ile Thr His Arg Phe Ser Ile Asp Asp
      300      305      310
Phe Gln Lys Gly Phe Asp Ala Met Arg Ser Gly Gln ser Gly Lys Val
      315      320      325
Ile Leu Ser Trp Asp
      330      335      340

```

<210> 10040
 <211> 1074
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(1074)

```

<400> 10040
atg ggg aaa atg gag gta gag agg aaa aca aca ggc tgg gct gcg aga      48
Met Gly Lys Met Glu Val Glu Arg Lys Thr Thr Gly Trp Ala Ala Arg
      1      5      10
gac cct tct ggg tta ctc tct cct tac act tac act ctc aga gag aca      96
Asp Pro Ser Gly Leu Leu Ser Pro Tyr Thr Tyr Thr Leu Arg Glu Thr
      15      20      25
gga cca gag gat gtt cac ata aga atc ata tgc tgt gga atc tgc cac      144
Gly Pro Glu Asp Val His Ile Arg Ile Ile Cys Cys Gly Ile Cys His
      30      35      40
aca gat ctc cat caa acc aaa aac gat ctt ggc atg tca aac tac ccc      192
Thr Asp Leu His Gln Thr Lys Asn Asp Leu Gly Met Ser Asn Tyr Pro
      45      50      55
atg gtt cct ggg cac gag gtt gtt ggg gaa gtg gag gtg gga tca      240
Met Val Pro Gly His Glu Val Val Gly Glu Val Val Glu Val Gly Ser
      60      65      70
gat gtg agc aag ttc acc gca ggg gat ata gtt gga gtt ggt tgt ctc      288
Asp Val Ser Lys Phe Thr Ala Gly Asp Ile Val Gly Val Gly Cys Leu
      75      80      85
gtt gga tgc tgc gga ggt tgt agc ccc tgc gag aga gat ctg gaa cag      336
Val Gly Cys Cys Gly Gly Cys Ser Pro Cys Glu Arg Asp Leu Glu Gln
      90      95      100
tat tgt ccc aag aag atc tgg agc tac aac gat gtt tac atc gat ggt      384
Tyr Cys Pro Lys Lys Ile Trp Ser Tyr Asn Asp Val Tyr Ile Asp Gly
      105      110      115
caa cca aca caa ggc ggt ttc gct aga gcc acc gtc gtt cac caa aag      432
Gln Pro Thr Gln Gly Gly Phe Ala Arg Ala Thr Val Val His Gln Lys
      120      125      130
ttt gtg gtg aag att cca gaa atg gct gtt gag cag gcg gca cca      480
Phe Val Val Lys Ile Pro Glu Gly Met Ala Val Glu Gln Ala Ala Pro
      135      140      145
cta ctg tgt gcc ggt gtg aca gtg tac agt cca ctg gct cac ttc ggt      528
Leu Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Ala His Phe Gly
      150      155      160
ctg aag cga cca ggc cta aga gga ggt ata cta ggg cta ggt gga gtt      576
Leu Lys Arg Pro Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly Gly Val
      165      170      175
ggg cac atg ggt gtg aaa ata gcc aaa gca atg ggt cac cat gtg act      624
      180      185      190

```

PF59083SeqList PF59083.txt

Gly	His	Met	Gly	Val	Lys	Ile	Ala	Lys	Ala	Met	Gly	His	His	Val	Thr	
gtc	ata	agc	tca	tca	aac	aag	aag	aaa	gaa	gag	gct	ttg	aaa	gat	ctt	672
Val	Ile	Ser	Ser	Ser	Asn	Lys	Lys	Lys	Glu	Glu	Ala	Leu	Lys	Asp	Leu	
210						215					220					
gga	gca	gat	gat	tac	gtg	atc	gga	tcc	gac	caa	tcg	aag	atg	aac	gaa	720
Gly	Ala	Asp	Asp	Tyr	Val	Ile	Gly	Ser	Asp	Gln	Ser	Lys	Met	Asn	Glu	
225					230					235					240	
ttg	gcg	gat	tca	atg	gat	tac	ata	atc	gac	acg	gtc	cct	ggt	cat	cat	768
Leu	Ala	Asp	Ser	Met	Asp	Tyr	Ile	Ile	Asp	Thr	Val	Pro	Val	His	His	
				245					250					255		
gca	ctt	gag	cct	tac	ttg	tct	ctg	ctt	agg	ctt	gat	ggg	aaa	ctc	ata	816
Ala	Leu	Glu	Pro	Tyr	Leu	Ser	Leu	Leu	Arg	Leu	Asp	Gly	Lys	Leu	Ile	
			260				265						270			
ctc	atg	gga	gtc	ata	agc	aat	cca	tta	caa	ttt	ctc	act	cct	atg	gtt	864
Leu	Met	Gly	Val	Ile	Ser	Asn	Pro	Leu	Gln	Phe	Leu	Thr	Pro	Met	Val	
		275					280					285				
atg	ctt	ggg	agg	aaa	gtg	ata	acg	ggg	agc	ttc	att	ggg	agc	atg	aag	912
Met	Leu	Gly	Arg	Lys	Val	Ile	Thr	Gly	Ser	Phe	Ile	Gly	Ser	Met	Lys	
290					295						300					
gaa	aca	gag	gag	atg	ctt	gag	ttc	tgt	aaa	gaa	aag	ggt	ttg	agt	tcg	960
Glu	Thr	Glu	Glu	Met	Leu	Glu	Phe	Cys	Lys	Glu	Lys	Gly	Leu	Ser	Ser	
305					310					315					320	
atc	atc	gaa	gta	gtg	aag	atg	gat	tat	gtg	aac	act	gcg	ttt	gag	aga	1008
Ile	Ile	Glu	Val	Val	Lys	Met	Asp	Tyr	Val	Asn	Thr	Ala	Phe	Glu	Arg	
				325					330					335		
ctc	gag	aag	aac	gat	gtg	cgt	tat	agg	ttc	gtg	ggt	gat	gtc	gaa	gga	1056
Leu	Glu	Lys	Asn	Asp	Val	Arg	Tyr	Arg	Phe	Val	Val	Asp	Val	Glu	Gly	
			340					345					350			
agc	aaa	ctt	gag	gct	tga											1074
Ser	Lys	Leu	Glu	Ala												
		355														

<210> 10041
 <211> 357
 <212> PRT
 <213> Brassica napus

<400> 10041

Met	Gly	Lys	Met	Glu	Val	Glu	Arg	Lys	Thr	Thr	Gly	Trp	Ala	Ala	Arg	
1				5					10					15		
Asp	Pro	Ser	Gly	Leu	Leu	Ser	Pro	Tyr	Thr	Tyr	Thr	Leu	Arg	Glu	Thr	
			20					25					30			
Gly	Pro	Glu	Asp	Val	His	Ile	Arg	Ile	Ile	Cys	Cys	Gly	Ile	Cys	His	
		35					40					45				
Thr	Asp	Leu	His	Gln	Thr	Lys	Asn	Asp	Leu	Gly	Met	Ser	Asn	Tyr	Pro	
	50					55					60					
Met	Val	Pro	Gly	His	Glu	Val	Val	Gly	Glu	Val	Val	Glu	Val	Gly	Ser	
65					70				75						80	
Asp	Val	Ser	Lys	Phe	Thr	Ala	Gly	Asp	Ile	Val	Gly	Val	Gly	Cys	Leu	
				85					90					95		
Val	Gly	Cys	Cys	Gly	Gly	Cys	Ser	Pro	Cys	Glu	Arg	Asp	Leu	Glu	Gln	
			100					105					110			
Tyr	Cys	Pro	Lys	Lys	Ile	Trp	Ser	Tyr	Asn	Asp	Val	Tyr	Ile	Asp	Gly	
		115					120					125				
Gln	Pro	Thr	Gln	Gly	Gly	Phe	Ala	Arg	Ala	Thr	Val	Val	His	Gln	Lys	
	130					135					140					
Phe	Val	Val	Lys	Ile	Pro	Glu	Gly	Met	Ala	Val	Glu	Gln	Ala	Ala	Pro	
145					150					155					160	
Leu	Leu	Cys	Ala	Gly	Val	Thr	Val	Tyr	Ser	Pro	Leu	Ala	His	Phe	Gly	
				165					170					175		
Leu	Lys	Arg	Pro	Gly	Leu	Arg	Gly	Gly	Ile	Leu	Gly	Leu	Gly	Gly	Val	
			180					185						190		
Gly	His	Met	Gly	Val	Lys	Ile	Ala	Lys	Ala	Met	Gly	His	His	Val	Thr	
		195					200					205				
Val	Ile	Ser	Ser	Ser	Asn	Lys	Lys	Lys	Glu	Glu	Ala	Leu	Lys	Asp	Leu	
	210				215						220					
Gly	Ala	Asp	Asp	Tyr	Val	Ile	Gly	Ser	Asp	Gln	Ser	Lys	Met	Asn	Glu	240
225					230					235						

PF59083SeqList PF59083.txt

Leu Ala Asp Ser Met Asp Tyr Ile Ile Asp Thr Val Pro Val His His
 245 250 255
 Ala Leu Glu Pro Tyr Leu Ser Leu Leu Arg Leu Asp Gly Lys Leu Ile
 260 265 270
 Leu Met Gly Val Ile Ser Asn Pro Leu Gln Phe Leu Thr Pro Met Val
 275 280 285
 Met Leu Gly Arg Lys Val Ile Thr Gly Ser Phe Ile Gly Ser Met Lys
 290 295 300
 Glu Thr Glu Glu Met Leu Glu Phe Cys Lys Glu Lys Gly Leu Ser Ser
 305 310 315 320
 Ile Ile Glu Val Val Lys Met Asp Tyr Val Asn Thr Ala Phe Glu Arg
 325 330 335
 Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp Val Glu Gly
 340 345 350
 Ser Lys Leu Glu Ala
 355

<210> 10042
 <211> 1074
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(1074)

<400> 10042
 atg gga gag gtc ctt aag aag gag gcg tac gga ctg gct gta aaa gac 48
 Met Gly Glu Val Leu Lys Lys Glu Ala Tyr 10 Gly Leu Ala Val Lys Asp 15
 1 5
 gaa tct gga gtt atc tcg cct ttc cgt ttc tca aga agg gag aca gga 96
 Glu Ser Gly Val Ile Ser Pro Phe Arg Phe Ser Arg Arg Glu Thr Gly 20 25 30
 gaa aat gat gtg agg tta aaa gtg ttg ttc tgt gga att tgc cac aca 144
 Glu Asn Asp Val Arg Leu Lys 40 Leu Phe Cys Gly Ile Cys His Thr 35 45
 gat tta agc atg gcc ata aac gag tgg ggg ttt act agt tac ccc ctt 192
 Asp Leu Ser Met Ala Ile Asn 55 Glu Trp Gly Phe Thr Ser Tyr Pro Leu 50 60
 gtc ccc ggg cat gaa ata gtg ggc gtg gtg act gaa gtc gga gcc aaa 240
 Val Pro Gly His Glu Ile Val Gly Val Val Thr Glu Val Gly Ala Lys 65 70 75 80
 gtg act aaa ttc aac gcc gga gac aaa gtg gga gtt ggt tat atg gtc 288
 Val Thr Lys Phe Asn Ala Gly Asp Lys Val Gly Val Gly Tyr Met Val 85 90 95
 agc tca tgc ggg tca tgt gaa acc tgc att gat gac caa gag aac tac 336
 Ser Ser Cys Gly Ser Cys Glu Thr Cys Ile Asp Asp Gln Glu Asn Tyr 100 105 110
 tgt cca aaa atg atc cta acg tcc gga ggc aag tat tac gat gac act 384
 Cys Pro Lys Met Ile Leu Thr 120 Ser Gly Gly Lys Tyr 125 Asp Asp Thr 115
 ata aca tat ggt ggt tac tcc gac cat atg gtt tgt gaa gag gac tac 432
 Ile Thr Tyr Gly Gly Tyr Ser 135 Asp His Met Val Cys Glu Glu Asp Tyr 130 140
 atc atc cgt att cca gaa aat ctt ccc tta gac gct acc gcg ccg cta 480
 Ile Ile Arg Ile Pro Glu Asn Leu Pro Leu Asp Ala Thr Ala Pro Leu 145 150 155 160
 ctc tgc gct ggg acc acc gtc tat tcc ccg atg aag tat cac ggg ctt 528
 Leu Cys Ala Gly Thr Val Tyr Ser Pro Met Lys Tyr His Gly Leu 165 170 175
 gac aag ccg ggt atg cac att ggt gtg gtg gga cta ggc ggt tta ggt 576
 Asp Lys Pro Gly Met His Ile Gly Val Val Gly Leu Gly Gly Leu Gly 180 185 190
 cat gta gct gtg aaa ttt gct aag gct atg ggt act aag gtt aca gtt 624
 His Val Ala Val Lys Phe Ala Lys 200 Ala Met Gly Thr Lys Val Thr Val 195 205
 att agt act tcg gat agg aag aga gac gag gcg tta act cgg ctt ggt 672
 Ile Ser Thr Ser Asp Arg Lys 215 Arg Asp Glu Ala Leu Thr Arg Leu Gly 210 220

PF59083SeqList PF59083.txt

gcg	gat	ctg	ttc	ttg	gtg	agc	cgt	gac	ccg	gaa	cag	atg	aag	gat	gca	720
Ala	Asp	Leu	Phe	Leu	Val	Ser	Arg	Asp	Pro	Glu	Gln	Met	Lys	Asp	Ala	
225					230					235					240	
atg	ggg	act	atg	gat	ggg	att	att	gat	acc	gta	tct	gct	tct	cat	cca	768
Met	Gly	Thr	Met	Asp	Gly	Ile	Ile	Asp	Thr	Val	Ser	Ala	Ser	His	Pro	
				245					250					255		
gtt	ctt	ccg	att	ctt	gat	ttg	ctt	aaa	tat	aag	ggg	aaa	ctt	att	atg	816
Val	Leu	Pro	Ile	Leu	Asp	Leu	Leu	Lys	Tyr	Lys	Gly	Lys	Leu	Ile	Met	
			260					265					270			
gtt	ggg	gca	cct	gat	aaa	ccg	ctt	gag	ctt	ccg	gtt	ctg	cct	ctc	atc	864
Val	Gly	Ala	Pro	Asp	Lys	Pro	Leu	Glu	Leu	Pro	Val	Leu	Pro	Leu	Ile	
		275					280					285				
ttt	ggg	aaa	aag	atg	gtg	gtg	gga	agt	atg	gta	gga	ggg	ata	aaa	gag	912
Phe	Gly	Lys	Lys	Met	Val	Val	Gly	Ser	Met	Val	Gly	Gly	Ile	Lys	Glu	
290						295					300					
act	caa	gag	atg	atg	gat	ttg	gcc	gga	aaa	cac	aac	atc	acg	gca	gat	960
Thr	Gln	Glu	Met	Met	Asp	Leu	Ala	Gly	Lys	His	Asn	Ile	Thr	Ala	Asp	
305					310					315					320	
att	gag	ctt	atc	tct	gcg	gat	tat	gtc	aac	act	gcc	atg	aaa	cgg	ctc	1008
Ile	Glu	Leu	Ile	Ser	Ala	Asp	Tyr	Val	Asn	Thr	Ala	Met	Lys	Arg	Leu	
				325					330					335		
gag	aag	gct	gac	gtt	aga	tac	cgt	ttt	gtg	att	gat	gtt	gcc	aac	acc	1056
Glu	Lys	Ala	Asp	Val	Arg	Tyr	Arg	Phe	Val	Ile	Asp	Val	Ala	Asn	Thr	
			340					345					350			
ttg	aag	cct	agt	cct	taa											1074
Leu	Lys	Pro	Ser	Pro												
		355														

<210> 10043
 <211> 357
 <212> PRT
 <213> Brassica napus

<400> 10043

Met	Gly	Glu	Val	Leu	Lys	Lys	Glu	Ala	Tyr	Gly	Leu	Ala	Val	Lys	Asp
1				5					10					15	
Glu	Ser	Gly	Val	Ile	Ser	Pro	Phe	Arg	Phe	Ser	Arg	Arg	Glu	Thr	Gly
			20					25					30		
Glu	Asn	Asp	Val	Arg	Leu	Lys	Val	Leu	Phe	Cys	Gly	Ile	Cys	His	Thr
		35					40					45			
Asp	Leu	Ser	Met	Ala	Ile	Asn	Glu	Trp	Gly	Phe	Thr	Ser	Tyr	Pro	Leu
	50					55					60				
Val	Pro	Gly	His	Glu	Ile	Val	Gly	Val	Val	Thr	Glu	Val	Gly	Ala	Lys
65					70					75					80
Val	Thr	Lys	Phe	Asn	Ala	Gly	Asp	Lys	Val	Gly	Val	Gly	Tyr	Met	Val
			85						90					95	
Ser	Ser	Cys	Gly	Ser	Cys	Glu	Thr	Cys	Ile	Asp	Asp	Gln	Glu	Asn	Tyr
		100						105					110		
Cys	Pro	Lys	Met	Ile	Leu	Thr	Ser	Gly	Gly	Lys	Tyr	Tyr	Asp	Asp	Thr
		115					120					125			
Ile	Thr	Tyr	Gly	Gly	Tyr	Ser	Asp	His	Met	Val	Cys	Glu	Glu	Asp	Tyr
	130					135					140				
Ile	Ile	Arg	Ile	Pro	Glu	Asn	Leu	Pro	Leu	Asp	Ala	Thr	Ala	Pro	Leu
145					150					155					160
Leu	Cys	Ala	Gly	Thr	Val	Tyr	Ser	Pro	Pro	Met	Lys	Tyr	His	Gly	Leu
			165					170						175	
Asp	Lys	Pro	Gly	Met	His	Ile	Gly	Val	Val	Gly	Leu	Gly	Gly	Leu	Gly
			180					185					190		
His	Val	Ala	Val	Lys	Phe	Ala	Lys	Ala	Met	Gly	Thr	Lys	Val	Thr	Val
		195					200					205			
Ile	Ser	Thr	Ser	Asp	Arg	Lys	Arg	Asp	Glu	Ala	Leu	Thr	Arg	Leu	Gly
	210					215					220				
Ala	Asp	Leu	Phe	Leu	Val	Ser	Arg	Asp	Pro	Glu	Gln	Met	Lys	Asp	Ala
225					230					235					240
Met	Gly	Thr	Met	Asp	Gly	Ile	Ile	Asp	Thr	Val	Ser	Ala	Ser	His	Pro
				245					250					255	
Val	Leu	Pro	Ile	Leu	Asp	Leu	Leu	Lys	Tyr	Lys	Gly	Lys	Leu	Ile	Met
			260					265					270		
Val	Gly	Ala	Pro	Asp	Lys	Pro	Leu	Glu	Leu	Pro	Val	Leu	Pro	Leu	Ile

PF59083SeqList PF59083.txt

275
 Phe Gly Lys Lys Met Val Val Gly Ser Met Val Gly Gly Ile Lys Glu
 290
 Thr Gln Glu Met Met Asp Leu Ala Gly Lys His Asn Ile Thr Ala Asp
 305
 Ile Glu Leu Ile Ser Ala Asp Tyr Val Asn Thr Ala Met Lys Arg
 325
 Glu Lys Ala Asp Val Arg Tyr Arg Phe Val Ile Asp Val Ala Asn Thr
 340
 Leu Lys Pro Ser Pro
 355

<210> 10044
 <211> 1074
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(1074)

<400> 10044
 atg gga aag gtg cct gcg acg gag gcg ttc gga ttg gcc gcg aaa gac 48
 Met Gly Lys Val Pro Ala Thr Glu Ala Phe Gly Leu Ala Ala Lys Asp
 1 5 10 15
 gaa tcc gga gtt ctc tcg cct ttc cgt ttc tca aga agg gag acg gga 96
 Glu Ser Gly Val Leu Ser Pro Phe Arg Phe Ser Arg Arg Glu Thr Gly
 20 25 30
 gag aag gat gtg agg tta aaa gtg ttg ttc tgt gga att tgc cac act 144
 Glu Lys Asp Val Arg Leu Lys Val Leu Phe Cys Gly Ile Cys His Thr
 35 40 45
 gat gta tgt atg gcc aga aac gag tgg gga ttt act act tac cct ctc 192
 Asp Val Cys Met Ala Arg Asn Glu Trp Gly Phe Thr Thr Tyr Pro Leu
 50 55 60
 gtc ccc ggg cat gag att gtt ggc gtg gtg act gaa gtc gga gct aaa 240
 Val Pro Gly His Glu Ile Val Gly Val Val Thr Glu Val Gly Ala Lys
 65 70 75 80
 gtg att aaa ttc aaa gcc gga gac aaa gtc gga gtt ggt tat atg ctc 288
 Val Ile Lys Phe Lys Ala Gly Asp Lys Val Gly Val Gly Tyr Met Leu
 85 90 95
 agc tcg tgc cgg tca tgt gac atc tgc acc gat gac caa gag aac cac 336
 Ser Ser Cys Arg Ser Cys Asp Ile Cys Thr Asp Asp Gln Glu Asn His
 100 105 110
 tgt cca aaa atg att atg acg tcc gga gga aag tac tac gat gac acc 384
 Cys Pro Lys Met Ile Met Thr Ser Gly Gly Lys Tyr Tyr Asp Asp Thr
 115 120 125
 atg act tat ggt ggt tac tct gac cac ctg gtt tgt gaa gag gat tac 432
 Met Thr Tyr Gly Gly Tyr Ser Asp His Leu Val Cys Glu Glu Asp Tyr
 130 135 140
 atc atc cgt att cct gaa aat ctc ccg tta gac gct gcc gcg ccg cta 480
 Ile Ile Arg Ile Pro Glu Asn Leu Pro Leu Asp Ala Ala Ala Pro Leu
 145 150 155 160
 ctc tgc gct ggg gtc acg gtt tat tca ccg ttg aag tct cac gga ctc 528
 Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys Ser His Gly Leu
 165 170 175
 gac aag ccc gga atc cac att ggt gtg gtg gga cta ggc ggt tta ggt 576
 Asp Lys Pro Gly Ile His Ile Gly Val Val Gly Leu Gly Gly Leu Gly
 180 185 190
 cac gta gca gtg aaa ttt gcc aag gct atg ggt act aag gtt acg gtt 624
 His Val Ala Val Lys Phe Ala Lys Ala Met Gly Thr Lys Val Thr Val
 195 200 205
 att agt tcg tca gat ggt aag aga gac gag gcg att aat cgg ctt ggt 672
 Ile Ser Ser Ser Asp Gly Lys Arg Asp Glu Ala Ile Asn Arg Leu Gly
 210 215 220
 gcg gat ctg ttc ttg gtg agc cgt gac ccg gaa gag atg aag gat gca 720
 Ala Asp Leu Phe Leu Val Ser Arg Asp Pro Glu Glu Met Lys Asp Ala
 225 230 235 240
 atg ggg act atg gat ggt att att gat aca gta tct gcc act cat ccg 768
 Met Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala Thr His Pro

PF59083SeqList PF59083.txt

245	250	255	
ctt ctt ccg ctt ctt ggt ttg cta aaa tat aag gga aaa ttt att atg			816
Leu Leu Pro Leu Leu Gly Leu Leu Lys Tyr Lys Gly Lys Phe Ile Met			
260	265	270	
ggt ggt gca ccc gat aaa cca ctt gac ctt cca gct tta ccg ctc atc			864
Val Gly Ala Pro Asp Lys Pro Leu Asp Leu Pro Ala Leu Pro Leu Ile			
275	280	285	
tta ggg aag aag atg gtg gtg gga agt atg aca gga ggg ata aaa gag			912
Leu Gly Lys Lys Met Val Val Gly Ser Met Thr Gly Gly Ile Lys Glu			
290	295	300	
tct caa gag atg gtt gat ttt gcc ggt aaa cac aac ata acg gca gat			960
Ser Gln Glu Met Val Asp Phe Ala Gly Lys His Asn Ile Thr Ala Asp			
305	310	315	
att gag ctt atc tct gcg gat tat gtc aac atg gct atg gaa cgg cta			1008
Ile Glu Leu Ile Ser Ala Asp Tyr Val Asn Met Ala Met Glu Arg Leu			
325	330	335	
gaa aag ggg gat gtt aga tac cgt ttt gtg att gat gtt gcc aac aca			1056
Glu Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Val Ala Asn Thr			
340	345	350	
atg aag cct act cct tag			1074
Met Lys Pro Thr Pro			
355			

<210> 10045

<211> 357

<212> PRT

<213> Brassica napus

<400> 10045

Met Gly Lys Val Pro Ala Thr Glu Ala Phe Gly Leu Ala Ala Lys Asp	
1 5 10 15	
Glu Ser Gly Val Leu Ser Pro Phe Arg Phe Ser Arg Arg Glu Thr Gly	
20 25 30	
Glu Lys Asp Val Arg Leu Lys Val Leu Phe Cys Gly Ile Cys His Thr	
35 40 45	
Asp Val Cys Met Ala Arg Asn Glu Trp Gly Phe Thr Thr Tyr Pro Leu	
50 55 60	
Val Pro Gly His Glu Ile Val Gly Val Val Thr Glu Val Gly Ala Lys	
65 70 75 80	
Val Ile Lys Phe Lys Ala Gly Asp Lys Val Gly Val Gly Tyr Met Leu	
85 90 95	
Ser Ser Cys Arg Ser Cys Asp Ile Cys Thr Asp Asp Gln Glu Asn His	
100 105 110	
Cys Pro Lys Met Ile Met Thr Ser Gly Gly Lys Tyr Tyr Asp Asp Thr	
115 120 125	
Met Thr Tyr Gly Gly Tyr Ser Asp His Leu Val Cys Glu Glu Asp Tyr	
130 135 140	
Ile Ile Arg Ile Pro Glu Asn Leu Pro Leu Asp Ala Ala Ala Pro Leu	
145 150 155 160	
Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys Ser His Gly Leu	
165 170 175	
Asp Lys Pro Gly Ile His Ile Gly Val Val Gly Leu Gly Gly Leu Gly	
180 185 190	
His Val Ala Val Lys Phe Ala Lys Ala Met Gly Thr Lys Val Thr Val	
195 200 205	
Ile Ser Ser Ser Asp Gly Lys Arg Asp Glu Ala Ile Asn Arg Leu Gly	
210 215 220	
Ala Asp Leu Phe Leu Val Ser Arg Asp Pro Glu Glu Met Lys Asp Ala	
225 230 235 240	
Met Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala Thr His Pro	
245 250 255	
Leu Leu Pro Leu Leu Gly Leu Leu Lys Tyr Lys Gly Lys Phe Ile Met	
260 265 270	
Val Gly Ala Pro Asp Lys Pro Leu Asp Leu Pro Ala Leu Pro Leu Ile	
275 280 285	
Leu Gly Lys Lys Met Val Val Gly Ser Met Thr Gly Gly Ile Lys Glu	
290 295 300	
Ser Gln Glu Met Val Asp Phe Ala Gly Lys His Asn Ile Thr Ala Asp	
305 310 315 320	

PF59083SeqList PF59083.txt

Ile Glu Leu Ile Ser Ala Asp Tyr Val Asn Met Ala Met Glu Arg Leu
 325 330 335
 Glu Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Val Ala Asn Thr
 340 345 350
 Met Lys Pro Thr Pro
 355

<210> 10046
 <211> 1083
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(1083)

<400> 10046
 atg gcg aaa tct cca gag aca gag cat ccg aac aaa gcc ttt ggt tgg 48
 Met Ala Lys Ser Pro Glu Thr Glu His Pro Asn Lys Ala Phe Gly Trp
 1 5 10 15
 gct gcc aaa gac aaa tct ggt gta ctc tct cct ttc cat ttc tcc aga 96
 Ala Ala Lys Asp Lys Ser Gly Val Leu Ser Pro Phe His Phe Ser Arg
 20 25 30
 aga gac aat ggt gac aat gat gtg aca gtg aaa atc ttg tac tgt gga 144
 Arg Asp Asn Gly Asp Asn Asp Val Thr Val Lys Ile Leu Tyr Cys Gly
 35 40 45
 gtg tgc cac act gat tta cat acc atc aaa aac gac tgg ggt ttc tcc 192
 Val Cys His Thr Asp Leu His Thr Ile Lys Asn Asp Trp Gly Phe Ser
 50 55 60
 tat tat cct gta gtt ccc ggg cat gaa ata gtt gga ata gct aca aaa 240
 Tyr Tyr Pro Val Val Pro Gly His Glu Ile Val Gly Ile Ala Thr Lys
 65 70 75 80
 gtt ggc aaa aac gtg act aaa ttc aga gaa gga gac cgt gtt gga gta 288
 Val Gly Lys Asn Val Thr Lys Phe Arg Glu Gly Asp Arg Val Gly Val
 85 90 95
 gga gtg atc act ggt tct tgc cag tct tgc gaa tct tgt aac caa gat 336
 Gly Val Ile Thr Gly Ser Cys Gln Ser Cys Glu Ser Cys Asn Gln Asp
 100 105 110
 ctt gaa aac tac tgt ccc caa atg tct ttc acc tac aac tcc ata gga 384
 Leu Glu Asn Tyr Cys Pro Gln Met Ser Phe Thr Tyr Asn Ser Ile Gly
 115 120 125
 tcc gat gga acc aag acc tac ggt gga tat tcg gag tcc att gtg gtc 432
 Ser Asp Gly Thr Lys Thr Tyr Gly Gly Tyr Ser Glu Ser Ile Val Val
 130 135 140
 gat caa cgt ttt gtc tta cag ttt ccc gag gga ttg cct agc gat tcg 480
 Asp Gln Arg Phe Val Leu Gln Phe Pro Glu Gly Leu Pro Ser Asp Ser
 145 150 155 160
 ggt gcc ccc ttg ctg tgt gct ggt atc act gtg tat agt cca atg aag 528
 Gly Ala Pro Leu Leu Cys Ala Gly Ile Thr Val Tyr Ser Pro Met Lys
 165 170 175
 tac tat ggt atg acc gag cca ggg aag cat ttg ggc gtg gct gga ctt 576
 Tyr Tyr Gly Met Thr Glu Pro Gly Lys His Leu Gly Val Ala Gly Leu
 180 185 190
 ggt ggg ctt ggt cat gtt gct gtc aag att ggt aaa gcc ttt ggt ttg 624
 Gly Gly Leu Gly His Val Ala Val Lys Ile Gly Lys Ala Phe Gly Leu
 195 200 205
 aaa gtt act gtg att agt tct tct cct agt aaa gaa gac gaa gct att 672
 Lys Val Thr Val Ile Ser Ser Ser Pro Ser Lys Glu Asp Glu Ala Ile
 210 215 220
 aat cga ctt ggt gct gat tcg ttt ctt gtc tca tct gat cct cag aag 720
 Asn Arg Leu Gly Ala Asp Ser Phe Leu Val Ser Ser Asp Pro Gln Lys
 225 230 235 240
 atg aag gct gca att gga act atg gac tat att atc gat acg gta tca 768
 Met Lys Ala Ala Ile Gly Thr Met Asp Tyr Ile Ile Asp Thr Val Ser
 245 250 255
 gca gta cat gct ctg ttt cca ttg ctt ggt tta ctc aaa gtc aat gga 816
 Ala Val His Ala Leu Phe Pro Leu Leu Gly Leu Leu Lys Val Asn Gly
 260 265 270
 aag ctt gtc acg tta ggc tta cct gag aag cct ctt gag cta cca atc 864

PF59083SeqList PF59083.txt

Lys	Leu	Val	Thr	Leu	Gly	Leu	Pro	Glu	Lys	Pro	Leu	Glu	Leu	Pro	Ile		
275							280					285					
ttc	cct	ctt	gtt	ctc	gga	aga	aaa	atg	gtg	gga	gga	agt	gac	att	gga		912
Phe	Pro	Leu	Val	Leu	Gly	Arg	Lys	Met	Val	Gly	Gly	Ser	Asp	Ile	Gly		
290						295					300						
ggg	atg	aag	gag	aca	caa	gag	atg	ctt	gag	ttc	tgc	gct	aag	cat	aac		960
Gly	Met	Lys	Glu	Thr	Gln	Glu	Met	Leu	Glu	Phe	Cys	Ala	Lys	His	Asn		
305					310					315					320		
ata	acg	gca	gat	att	gag	ctg	atc	aag	atg	gat	gag	att	aac	act	gcg		1008
Ile	Thr	Ala	Asp	Ile	Glu	Leu	Ile	Lys	Met	Asp	Glu	Ile	Asn	Thr	Ala		
				325					330					335			
atg	gag	agg	ctt	gct	aag	tct	gat	gtt	agg	tac	agg	ttc	gtg	atc	gac		1056
Met	Glu	Arg	Leu	Ala	Lys	Ser	Asp	Val	Arg	Tyr	Arg	Phe	Val	Ile	Asp		
			340					345					350				
gtg	gct	aac	tcc	ttg	agc	cct	cca	tga									1083
Val	Ala	Asn	Ser	Leu	Ser	Pro	Pro										
		355					360										

<210> 10047
 <211> 360
 <212> PRT
 <213> Brassica napus

<400> 10047

Met	Ala	Lys	Ser	Pro	Glu	Thr	Glu	His	Pro	Asn	Lys	Ala	Phe	Gly	Trp		
1				5					10					15			
Ala	Ala	Lys	Asp	Lys	Ser	Gly	Val	Leu	Ser	Pro	Phe	His	Phe	Ser	Arg		
			20					25					30				
Arg	Asp	Asn	Gly	Asp	Asn	Asp	Val	Thr	Val	Lys	Ile	Leu	Tyr	Cys	Gly		
			35				40					45					
Val	Cys	His	Thr	Asp	Leu	His	Thr	Ile	Lys	Asn	Asp	Trp	Gly	Phe	Ser		
	50					55					60						
Tyr	Tyr	Pro	Val	Val	Pro	Gly	His	Glu	Ile	Val	Gly	Ile	Ala	Thr	Lys		
65					70					75					80		
Val	Gly	Lys	Asn	Val	Thr	Lys	Phe	Arg	Glu	Gly	Asp	Arg	Val	Gly	Val		
				85					90					95			
Gly	Val	Ile	Thr	Gly	Ser	Cys	Gln	Ser	Cys	Glu	Ser	Cys	Asn	Gln	Asp		
			100				105						110				
Leu	Glu	Asn	Tyr	Cys	Pro	Gln	Met	Ser	Phe	Thr	Tyr	Asn	Ser	Ile	Gly		
		115				120						125					
Ser	Asp	Gly	Thr	Lys	Thr	Tyr	Gly	Gly	Tyr	Ser	Glu	Ser	Ile	Val	Val		
	130					135					140						
Asp	Gln	Arg	Phe	Val	Leu	Gln	Phe	Pro	Glu	Gly	Leu	Pro	Ser	Asp	Ser		
145					150					155					160		
Gly	Ala	Pro	Leu	Leu	Cys	Ala	Gly	Ile	Thr	Val	Tyr	Ser	Pro	Met	Lys		
				165					170					175			
Tyr	Tyr	Gly	Met	Thr	Glu	Pro	Gly	Lys	His	Leu	Gly	Val	Ala	Gly	Leu		
			180					185						190			
Gly	Gly	Leu	Gly	His	Val	Ala	Val	Lys	Ile	Gly	Lys	Ala	Phe	Gly	Leu		
		195					200					205					
Lys	Val	Thr	Val	Ile	Ser	Ser	Ser	Pro	Ser	Lys	Glu	Asp	Glu	Ala	Ile		
	210					215					220						
Asn	Arg	Leu	Gly	Ala	Asp	Ser	Phe	Leu	Val	Ser	Ser	Asp	Pro	Gln	Lys		
225					230					235					240		
Met	Lys	Ala	Ala	Ile	Gly	Thr	Met	Asp	Tyr	Ile	Ile	Asp	Thr	Val	Ser		
				245					250					255			
Ala	Val	His	Ala	Leu	Phe	Pro	Leu	Leu	Gly	Leu	Leu	Lys	Val	Asn	Gly		
			260						265					270			
Lys	Leu	Val	Thr	Leu	Gly	Leu	Pro	Glu	Lys	Pro	Leu	Glu	Leu	Pro	Ile		
		275					280					285					
Phe	Pro	Leu	Val	Leu	Gly	Arg	Lys	Met	Val	Gly	Gly	Ser	Asp	Ile	Gly		
	290					295					300						
Gly	Met	Lys	Glu	Thr	Gln	Glu	Met	Leu	Glu	Phe	Cys	Ala	Lys	His	Asn		
305					310					315					320		
Ile	Thr	Ala	Asp	Ile	Glu	Leu	Ile	Lys	Met	Asp	Glu	Ile	Asn	Thr	Ala		
				325					330					335			
Met	Glu	Arg	Leu	Ala	Lys	Ser	Asp	Val	Arg	Tyr	Arg	Phe	Val	Ile	Asp		
			340					345					350				
Val	Ala	Asn	Ser	Leu	Ser	Pro	Pro										

355

<210> 10048
<211> 1110
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(1110)

```

<400> 10048
atg gcg cct acg gca acg acg acg acg acg gcg gcg gag cag cag cag      48
Met Ala Pro Thr Ala Thr Thr Thr Thr Thr Ala Ala Glu Gln Gln Gln
1 5 10 15
cac ccg agg aag gcg gtg ggg ctc gcg gcg cac gac gca tcc ggc cac      96
His Pro Arg Lys Ala Val Gly Leu Ala Ala His Asp Ala Ser Gly His
20 25 30
ctc tcg ccc atc cgc atc ccc cga agg agc act ggt gac gac gac gtg      144
Leu Ser Pro Ile Arg Ile Pro Arg Arg Ser Thr Gly Asp Asp Asp Val
35 40 45
gcc ata aag gtg ctc tac tgc ggc atc tgc cac tcc gac ctg cac acc      192
Ala Ile Lys Val Leu Tyr Cys Gly Ile Cys His Ser Asp Leu His Thr
50 55 60
atc aag aac gac tgg agg aac gcc atc tac ccc gtc ccc ggc cac      240
Ile Lys Asn Asp Trp Arg Asn Ala Ile Tyr Pro Val Val Pro Gly His
65 70 75 80
gag att gcc ggg gtg gtg acg gag gtc ggc aag aac gtg gcg ggg ttc      288
Glu Ile Ala Gly Val Val Thr Glu Val Gly Lys Asn Val Ala Gly Phe
85 90 95
gcg gcc ggc gac agg gtg ggc gtg ggc tgc atg gtg aac acc tgc cgg      336
Ala Ala Gly Asp Arg Val Gly Val Gly Cys Met Val Asn Thr Cys Arg
100 105
gcc tgc gag agc tgc gag gag ggc gcc gag aac tac tgc gcc agg gtc      384
Ala Cys Glu Ser Cys Glu Glu Gly Ala Glu Asn Tyr Cys Ala Arg Val
115 120 125
gtc ctc acc tac aac tcc cgc gac agg gac ggc gcc gtc acc cgc ggc      432
Val Leu Thr Tyr Asn Ser Arg Asp Arg Asp Gly Ala Val Thr Arg Gly
130 135 140
ggc tac tcc gac ctg gtc gtc gcc gac gcg cgc ttc gtc gtc cgc ttc      480
Gly Tyr Ser Asp Leu Val Val Ala Asp Ala Arg Phe Val Val Arg Phe
145 150 155 160
ccc gac gcc ctg ccg ctc gac gtc gcc gcg ccg ctg ctc tgc gcg ggc      528
Pro Asp Ala Leu Pro Leu Asp Val Ala Ala Pro Leu Leu Cys Ala Gly
165 170 175
gcc acc gtg tac gcc ccc atg cgg cgc cac ggc ctg ggc gcg ccc ggc      576
Ala Thr Val Tyr Ala Pro Met Arg Arg His Gly Leu Gly Ala Pro Gly
180 185 190
agc cac gtg ggc gtg atc ggc ctc ggc ggc ctc ggc cac gtc gcc gtc      624
Ser His Val Gly Val Ile Gly Leu Gly Gly Leu Gly His Val Ala Val
195 200 205
aag ttc gcc agg gcg ttc ggc gcg gcg aag gtg acg gtg atc agc acg      672
Lys Phe Ala Arg Ala Phe Gly Ala Ala Lys Val Thr Val Ile Ser Thr
210 215 220
tcg ccc ggg aag ccg gag gag gcg ctg gag ccg ctg ggc gcg gac gcg      720
Ser Pro Gly Lys Arg Glu Glu Ala Leu Glu Arg Leu Gly Ala Asp Ala
225 230 235 240
ttc gtc ctc agc acc gac gcg gcg gag atg aag gcc gcc gcg ggc acc      768
Phe Val Leu Ser Thr Asp Ala Ala Glu Met Lys Ala Ala Ala Gly Thr
245 250 255
atg cac ggc atc gtc aac acg gcg tcc gcc gcc gcg tcc ctg cac ccg      816
Met His Gly Ile Val Asn Thr Ala Ser Ala Ala Ala Ser Leu His Pro
260 265 270
tac ctg gcg ctc ctc aaa ccc cac ggc aag atg atc ctg ctc ggc atc      864
Tyr Leu Ala Leu Leu Lys Pro His Gly Lys Met Ile Leu Leu Gly Ile
275 280 285
ccc gat aag ccc ctg caa gtc tcc gca ttc gct ctc atc ggc ggc ggc      912
Pro Asp Lys Pro Leu Gln Val Ser Ala Phe Ala Leu Ile Gly Gly Gly
290 295 300

```

PF59083SeqList PF59083.txt

aag	act	ctt	gcc	ggg	agc	tgc	atg	gcg	agc	atc	agc	gag	acg	cag	gag	960
Lys	Thr	Leu	Ala	Gly	Ser	Cys	Met	Ala	Ser	Ile	Ser	Glu	Thr	Gln	Glu	
305					310					315					320	
atg	cta	gac	ttc	gcc	gcc	gag	cat	ggc	gtg	gcg	gcg	gac	gtc	gag	gtg	1008
Met	Leu	Asp	Phe	Ala	Ala	Glu	His	Gly	Val	Ala	Ala	Asp	Val	Glu	Val	
				325					330					335		
atc	ggc	gcc	ggg	gag	gtg	aac	gcg	gcc	atg	gag	cgc	ctg	gcc	aag	ggc	1056
Ile	Gly	Ala	Gly	Glu	Val	Asn	Ala	Ala	Met	Glu	Arg	Leu	Ala	Lys	Gly	
			340					345					350			
gac	gtc	agg	tac	cgc	ttc	gtc	atc	gac	gtc	ggc	aac	acc	ctc	aag	gcg	1104
Asp	Val	Arg	Tyr	Arg	Phe	Val	Ile	Asp	Val	Gly	Asn	Thr	Leu	Lys	Ala	
		355					360					365				
gat	tga															1110
Asp																

<210> 10049
 <211> 369
 <212> PRT
 <213> Triticum aestivum

<400> 10049
 Met Ala Pro Thr Ala Thr Thr Thr Thr Thr Ala Ala Glu Gln Gln Gln
 1 5 10 15
 His Pro Arg Lys Ala Val Gly Leu Ala His Asp Ala Ser Gly His
 20 25 30
 Leu Ser Pro Ile Arg Ile Pro Arg Arg Ser Thr Gly Asp Asp Asp Val
 35 40 45
 Ala Ile Lys Val Leu Tyr Cys Gly Ile Cys His Ser Asp Leu His Thr
 50 55 60
 Ile Lys Asn Asp Trp Arg Asn Ala Ile Tyr Pro Val Val Pro Gly His
 65 70 75 80
 Glu Ile Ala Gly Val Val Thr Glu Val Gly Lys Asn Val Ala Gly Phe
 85 90 95
 Ala Ala Gly Asp Arg Val Gly Val Gly Cys Met Val Asn Thr Cys Arg
 100 105 110
 Ala Cys Glu Ser Cys Glu Glu Gly Ala Glu Asn Tyr Cys Ala Arg Val
 115 120 125
 Val Leu Thr Tyr Asn Ser Arg Asp Arg Asp Gly Ala Val Thr Arg Gly
 130 135 140
 Gly Tyr Ser Asp Leu Val Val Ala Asp Ala Arg Phe Val Val Arg Phe
 145 150 155 160
 Pro Asp Ala Leu Pro Leu Asp Val Ala Ala Pro Leu Leu Cys Ala Gly
 165 170 175
 Ala Thr Val Tyr Ala Pro Met Arg Arg His Gly Leu Gly Ala Pro Gly
 180 185 190
 Ser His Val Gly Val Ile Gly Leu Gly Gly Leu Gly His Val Ala Val
 195 200 205
 Lys Phe Ala Arg Ala Phe Gly Ala Ala Lys Val Thr Val Ile Ser Thr
 210 215 220
 Ser Pro Gly Lys Arg Glu Glu Ala Leu Glu Arg Leu Gly Ala Asp Ala
 225 230 235 240
 Phe Val Leu Ser Thr Asp Ala Ala Glu Met Lys Ala Ala Ala Gly Thr
 245 250 255
 Met His Gly Ile Val Asn Thr Ala Ser Ala Ala Ser Leu His Pro
 260 265 270
 Tyr Leu Ala Leu Leu Lys Pro His Gly Lys Met Ile Leu Leu Gly Ile
 275 280 285
 Pro Asp Lys Pro Leu Gln Val Ser Ala Phe Ala Leu Ile Gly Gly Gly
 290 295 300
 Lys Thr Leu Ala Gly Ser Cys Met Ala Ser Ile Ser Glu Thr Gln Glu
 305 310 315 320
 Met Leu Asp Phe Ala Ala Glu His Gly Val Ala Ala Asp Val Glu Val
 325 330 335
 Ile Gly Ala Gly Val Asn Ala Ala Met Glu Arg Leu Ala Lys Gly
 340 345 350
 Asp Val Arg Tyr Arg Phe Val Ile Asp Val Gly Asn Thr Leu Lys Ala
 355 360 365
 Asp

PF59083SeqList PF59083.txt

<210> 10050
 <211> 1074
 <212> DNA
 <213> Linum usitatissimum

<220>
 <221> CDS
 <222> (1)..(1074)

```

<400> 10050
atg gca gag aaa caa cat ccg gtg ccg gcc tac gga ttg gct gcc aga      48
Met Ala Glu Lys Gln His Pro Val Pro Ala Tyr Gly Leu Ala Ala Arg
  1      5      10
gac cag tct gga ctt gtt tct cct ttc aac ttc tcc aga aga gaa aca      96
Asp Gln Ser Gly Leu Val Ser Pro Phe Asn Phe Ser Arg Arg Glu Thr
      20      25      30
ggg gaa acc gat gtg aaa ttt aag gtt ctc tac tgt ggg att tgc cat     144
Gly Glu Thr Asp Val Lys Phe Lys Val Leu Tyr Cys Gly Ile Cys His
      35      40      45
tcc gat ctt cat atg ctc aag aat gaa tgg ggc tcc tcc acc tat ccc     192
Ser Asp Leu His Met Leu Lys Asn Glu Trp Gly Ser Ser Thr Tyr Pro
      50      55      60
att gtc cct ggg cat gag ata gtg gga caa gtg aca gag gtt gga agc     240
Ile Val Pro Gly His Glu Ile Val Gly Gln Val Thr Glu Val Gly Ser
      65      70      75      80
aaa gtg gag aaa tac aga gtt gga gac aga gta ggc gtt gga tgc atg     288
Lys Val Glu Lys Tyr Arg Val Gly Asp Arg Val Gly Val Gly Cys Met
      85      90      95
gtt ggg tcg tgc cga tct tgc aac aac tgc tcc caa agc atc gaa aat     336
Val Gly Ser Cys Arg Ser Cys Asn Asn Cys Ser Gln Ser Ile Glu Asn
      100      105      110
tac tgc ccc aag atg atc caa acc tat gga gga acc tac cat gat ggc     384
Tyr Cys Pro Lys Met Ile Gln Thr Tyr Gly Gly Thr Tyr His Asp Gly
      115      120      125
acc cct acc tac gga ggc tac tcc gac gtc atg gtc tgc gac gag cat     432
Thr Pro Thr Tyr Gly Gly Tyr Ser Asp Val Met Val Cys Asp Glu His
      130      135      140
ttc gtg gtc cga gtc ccc gac tcc ctg ccc tta gac gtt gcc gca cct     480
Phe Val Val Arg Val Pro Asp Ser Leu Pro Leu Asp Val Ala Ala Pro
      145      150      155      160
ctg ctc tgc gct ggt atc aca ctt tac agc cct tta aag ttc tat gga     528
Leu Leu Cys Ala Gly Ile Thr Leu Tyr Ser Pro Leu Lys Phe Tyr Gly
      165      170      175
ctg gac aag ccg ggc ctc cac gtc ggc att gtc ggg ctc ggt gga ctg     576
Leu Asp Lys Pro Gly Leu His Val Gly Ile Val Gly Leu Gly Gly Leu
      180      185      190
ggc cac gtg ggt gtc aag ttt gct aaa gcc atg ggt gtg aaa gtc acc     624
Gly His Val Gly Val Lys Phe Ala Lys Ala Met Gly Val Lys Val Thr
      195      200      205
gtg att agt acc tcc cct ggc aag aag cag gag gca atc gag cga cat     672
Val Ile Ser Thr Ser Pro Gly Lys Lys Gln Glu Ala Ile Glu Arg His
      210      215      220
ggt gct gat gcc ttc ttg gtg agc ctt gac cag gaa atg aag gct     720
Gly Ala Asp Ala Phe Leu Val Ser Leu Asp Gln Glu Gln Met Lys Ala
      225      230      235      240
gca atg ggg acg atg gat ggt att atc gac acg gta tca gct gtt cac     768
Ala Met Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala Val His
      245      250      255
cca ata atg cca ttg att ggg ctg tta aag aca caa ggc aag ttg gtg     816
Pro Ile Met Pro Leu Ile Gly Leu Leu Lys Thr Gln Gly Lys Leu Val
      260      265      270
ttg gtt ggt gct cca gag aag cct ctt gag ttg cca gtt ttc cct ctg     864
Leu Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Pro Leu
      275      280      285
ctc atg gga agg aag ata gta gga ggg agt tgc att gga gga atg aag     912
Leu Met Gly Arg Lys Ile Val Gly Gly Ser Cys Ile Gly Gly Met Lys
      290      295      300
    
```

PF59083SeqList PF59083.txt

gag	acg	caa	gag	atg	ctt	gat	ttc	gca	gca	aag	cac	aac	atc	act	gcg	960
Glu	Thr	Gln	Glu	Met	Leu	Asp	Phe	Ala	Ala	Lys	His	Asn	Ile	Thr	Ala	
305					310					315					320	
gac	att	gag	gtt	ata	tca	gca	gac	tat	gtg	aac	act	gca	atg	gag	agg	1008
Asp	Ile	Glu	Val	Ile	Ser	Ala	Asp	Tyr	Val	Asn	Thr	Ala	Met	Glu	Arg	
				325					330					335		
ctt	gcc	aag	aat	gat	gtt	aaa	tac	aga	ttc	gtc	atc	gat	gtt	gcc	aac	1056
Leu	Ala	Lys	Asn	Asp	Val	Lys	Tyr	Arg	Phe	Val	Ile	Asp	Val	Ala	Asn	
			340					345					350			
act	atg	caa	gct	cct	tga											1074
Thr	Met	Gln	Ala	Pro												
		355														

<210> 10051

<211> 357

<212> PRT

<213> Linum usitatissimum

<400> 10051

Met	Ala	Glu	Lys	Gln	His	Pro	Val	Pro	Ala	Tyr	Gly	Leu	Ala	Ala	Arg	
1				5					10					15		
Asp	Gln	Ser	Gly	Leu	Val	Ser	Pro	Phe	Asn	Phe	Ser	Arg	Arg	Glu	Thr	
			20					25					30			
Gly	Glu	Thr	Asp	Val	Lys	Phe	Lys	Val	Leu	Tyr	Cys	Gly	Ile	Cys	His	
		35					40					45				
Ser	Asp	Leu	His	Met	Leu	Lys	Asn	Glu	Trp	Gly	Ser	Ser	Thr	Tyr	Pro	
	50					55				60						
Ile	Val	Pro	Gly	His	Glu	Ile	Val	Gly	Gln	Val	Thr	Glu	Val	Gly	Ser	
65					70				75						80	
Lys	Val	Glu	Lys	Tyr	Arg	Val	Gly	Asp	Arg	Val	Gly	Val	Gly	Cys	Met	
			85					90						95		
Val	Gly	Ser	Cys	Arg	Ser	Cys	Asn	Asn	Cys	Ser	Gln	Ser	Ile	Glu	Asn	
		100					105						110			
Tyr	Cys	Pro	Lys	Met	Ile	Gln	Thr	Tyr	Gly	Gly	Thr	Tyr	His	Asp	Gly	
		115					120					125				
Thr	Pro	Thr	Tyr	Gly	Gly	Tyr	Ser	Asp	Val	Met	Val	Cys	Asp	Glu	His	
	130					135					140					
Phe	Val	Val	Arg	Val	Pro	Asp	Ser	Leu	Pro	Leu	Asp	Val	Ala	Ala	Pro	
145					150					155					160	
Leu	Leu	Cys	Ala	Gly	Ile	Thr	Leu	Tyr	Ser	Pro	Leu	Lys	Phe	Tyr	Gly	
			165					170						175		
Leu	Asp	Lys	Pro	Gly	Leu	His	Val	Gly	Ile	Val	Gly	Leu	Gly	Gly	Leu	
		180						185					190			
Gly	His	Val	Gly	Val	Lys	Phe	Ala	Lys	Ala	Met	Gly	Val	Lys	Val	Thr	
		195					200					205				
Val	Ile	Ser	Thr	Ser	Pro	Gly	Lys	Lys	Gln	Glu	Ala	Ile	Glu	Arg	His	
	210					215					220					
Gly	Ala	Asp	Ala	Phe	Leu	Val	Ser	Leu	Asp	Gln	Glu	Gln	Met	Lys	Ala	
225					230					235					240	
Ala	Met	Gly	Thr	Met	Asp	Gly	Ile	Ile	Asp	Thr	Val	Ser	Ala	Val	His	
			245						250					255		
Pro	Ile	Met	Pro	Leu	Ile	Gly	Leu	Leu	Lys	Thr	Gln	Gly	Lys	Leu	Val	
		260					265						270			
Leu	Val	Gly	Ala	Pro	Glu	Lys	Pro	Leu	Glu	Leu	Pro	Val	Phe	Pro	Leu	
	275						280					285				
Leu	Met	Gly	Arg	Lys	Ile	Val	Gly	Gly	Ser	Cys	Ile	Gly	Gly	Met	Lys	
	290					295					300					
Glu	Thr	Gln	Glu	Met	Leu	Asp	Phe	Ala	Ala	Lys	His	Asn	Ile	Thr	Ala	
305					310					315					320	
Asp	Ile	Glu	Val	Ile	Ser	Ala	Asp	Tyr	Val	Asn	Thr	Ala	Met	Glu	Arg	
			325						330					335		
Leu	Ala	Lys	Asn	Asp	Val	Lys	Tyr	Arg	Phe	Val	Ile	Asp	Val	Ala	Asn	
			340					345					350			
Thr	Met	Gln	Ala	Pro												
		355														

<210> 10052

<211> 1101

<212> DNA

<213> Linum usitatissimum

<220>

<221> CDS

<222> (1)..(1101)

<400> 10052

atg	gcg	aat	aat	gat	ggt	gaa	atc	gca	gtg	gga	aag	aga	gat	gga	gga	48
Met	Ala	Asn	Asn	Asp	Gly	Glu	Ile	Ala	Val	Gly	Lys	Arg	Asp	Gly	Gly	
1				5					10					15		
gag	gaa	gag	aac	atg	gct	gct	tgg	ctt	ctg	ggt	atc	caa	acc	ctc	aag	96
Glu	Glu	Glu	Asn	Met	Ala	Ala	Trp	Leu	Leu	Gly	Ile	Gln	Thr	Leu	Lys	
			20					25					30			
att	cag	cct	tac	caa	ctc	cct	act	ctt	ggt	cct	cat	gat	gtc	aag	gtc	144
Ile	Gln	Pro	Tyr	Gln	Leu	Pro	Thr	Leu	Gly	Pro	His	Asp	Val	Lys	Val	
			35				40					45				
cgg	att	aag	gct	cta	ggc	att	tgc	gga	agt	gat	ggt	cat	cat	ttc	aag	192
Arg	Ile	Lys	Ala	Leu	Gly	Ile	Cys	Gly	Ser	Asp	Val	His	His	Phe	Lys	
	50					55				60						
act	atg	aga	tgt	gct	aat	ttc	ata	gtg	aag	aaa	cca	atg	gtg	atc	ggc	240
Thr	Met	Arg	Cys	Ala	Asn	Phe	Ile	Val	Lys	Lys	Pro	Met	Val	Ile	Gly	
	65				70				75					80		
cat	gaa	tgt	gct	ggc	atc	att	gaa	gag	att	ggc	agt	gaa	gtc	aag	agc	288
His	Glu	Cys	Ala	Gly	Ile	Ile	Glu	Glu	Ile	Gly	Ser	Glu	Val	Lys	Ser	
				85					90					95		
ctc	tca	aca	ggt	gac	cgt	gta	gcc	tta	gag	cct	ggc	atc	agt	tgc	tca	336
Leu	Ser	Thr	Gly	Asp	Arg	Val	Ala	Leu	Glu	Pro	Gly	Ile	Ser	Cys	Ser	
			100				105						110			
agg	tgt	aac	ctt	tgc	aag	aat	ggc	cgc	tac	aac	ttg	tgc	tcc	gaa	atg	384
Arg	Cys	Asn	Leu	Cys	Lys	Asn	Gly	Arg	Tyr	Asn	Leu	Cys	Ser	Glu	Met	
		115					120					125				
cga	ttc	ttc	ggc	tct	cca	cct	acc	aac	ggc	tct	ctt	gcc	aac	aag	gtg	432
Arg	Phe	Phe	Gly	Ser	Pro	Pro	Thr	Asn	Gly	Ser	Leu	Ala	Asn	Lys	Val	
	130				135					140						
gtg	cat	ccc	gca	agc	cta	tgc	tac	aag	ctc	ccc	gag	aac	gtg	agc	ttg	480
Val	His	Pro	Ala	Ser	Leu	Cys	Tyr	Lys	Leu	Pro	Glu	Asn	Val	Ser	Leu	
	145				150					155					160	
gag	gaa	gga	gcg	atg	tgc	gag	ccc	cta	agt	gta	ggg	gtc	cac	gct	tgt	528
Glu	Glu	Gly	Ala	Met	Cys	Glu	Pro	Leu	Ser	Val	Gly	Val	His	Ala	Cys	
			165						170					175		
cgt	aga	gca	cag	ggt	ggc	ccc	gag	act	agt	gtc	ctg	atc	ttg	gga	gct	576
Arg	Arg	Ala	Gln	Val	Gly	Pro	Glu	Thr	Ser	Val	Leu	Ile	Leu	Gly	Ala	
			180				185						190			
gga	cca	atc	ggg	ctc	atc	acc	ttg	ctg	gtt	gct	cga	gca	ttc	gga	tcc	624
Gly	Pro	Ile	Gly	Leu	Ile	Thr	Leu	Leu	Val	Ala	Arg	Ala	Phe	Gly	Ser	
		195					200					205				
cct	cgc	gtt	gtg	atg	acc	gat	gtt	gat	gag	acc	cgt	cta	tcc	att	gct	672
Pro	Arg	Val	Val	Met	Thr	Asp	Val	Asp	Glu	Thr	Arg	Leu	Ser	Ile	Ala	
	210				215					220						
aag	agc	ctc	ggt	gct	gat	gag	act	atc	caa	gtc	tcg	aca	gat	ccg	aag	720
Lys	Ser	Leu	Gly	Ala	Asp	Glu	Thr	Ile	Gln	Val	Ser	Thr	Asp	Pro	Lys	
	225				230					235					240	
gat	gtt	agt	gag	gaa	gtg	atg	aaa	gtg	cag	aat	gct	atg	gga	tca	ggg	768
Asp	Val	Ser	Glu	Val	Met	Lys	Val	Gln	Val	Asn	Ala	Met	Gly	Ser	Gly	
			245					250						255		
att	gat	gtt	acc	ttg	gac	tgt	gtt	gga	tat	aac	aag	acc	atg	act	act	816
Ile	Asp	Val	Thr	Leu	Asp	Cys	Val	Gly	Tyr	Asn	Lys	Thr	Met	Thr	Thr	
			260				265						270			
gct	ctg	aat	gcc	aca	cgt	tct	ggt	ggc	aaa	gtt	tgc	cta	ata	gga	tta	864
Ala	Leu	Asn	Ala	Thr	Arg	Ser	Gly	Gly	Lys	Val	Cys	Leu	Ile	Gly	Leu	
		275					280					285				
gct	ctt	agt	gag	atg	act	gtc	cct	ctt	act	cct	gct	gct	gcc	agg	gaa	912
Ala	Leu	Ser	Glu	Met	Thr	Val	Pro	Leu	Thr	Pro	Ala	Ala	Ala	Arg	Glu	
	290				295					300						
gta	gat	gtg	att	ggc	ata	ttt	cgg	tac	cgg	aac	aca	tgg	cca	ctc	tgc	960
Val	Asp	Val	Ile	Gly	Ile	Phe	Arg	Tyr	Arg	Asn	Thr	Trp	Pro	Leu	Cys	
	305				310					315					320	
ctt	gat	ttc	ttg	aag	act	ggc	aag	att	tat	gtg	aag	cca	ttg	ata	act	1008
Leu	Asp	Phe	Leu	Lys	Thr	Gly	Lys	Ile	Tyr	Val	Lys	Pro	Leu	Ile	Thr	

PF59083SeqList PF59083.txt

															325						330						335					
cac	agg	ttt	aag	ttc	aca	cag	gag	gat	att	gac	tcg	gcg	ttc	gag	acc											1056						
His	Arg	Phe	Lys	Phe	Thr	Gln	Glu	Asp	Ile	Asp	Ser	Ala	Phe	Glu	Thr																	
															340						345						350					
agt	gct	cgt	ggg	aac	gcg	atc	aag	gtt	atg	ttt	aac	ctg	taa											1101								
Ser	Ala	Arg	Gly	Gly	Asn	Ala	Ile	Lys	Val	Met	Phe	Asn	Leu																			
															355						360						365					

<210> 10053
<211> 366
<212> PRT
<213> *Linum usitatissimum*

<400>	100	53														
Met	Ala	Asn	Asn	Asp	Gly	Glu	Ile	Ala	Val	Gly	Lys	Arg	Asp	Gly	Gly	
1				5					10					15		
Glu	Glu	Glu	Asn	Met	Ala	Ala	Trp	Leu	Leu	Gly	Ile	Gln	Thr	Leu	Lys	
			20					25					30			
Ile	Gln	Pro	Tyr	Gln	Leu	Pro	Thr	Leu	Gly	Pro	His	Asp	Val	Lys	Val	
		35					40					45				
Arg	Ile	Lys	Ala	Leu	Gly	Ile	Cys	Gly	Ser	Asp	Val	His	His	Phe	Lys	
	50					55					60					
Thr	Met	Arg	Cys	Ala	Asn	Phe	Ile	Val	Lys	Lys	Pro	Met	Val	Ile	Gly	
65					70					75					80	
His	Glu	Cys	Ala	Gly	Ile	Ile	Glu	Glu	Ile	Gly	Ser	Glu	Val	Lys	Ser	
				85					90					95		
Leu	Ser	Thr	Gly	Asp	Arg	Val	Ala	Leu	Glu	Pro	Gly	Ile	Ser	Cys	Ser	
			100					105					110			
Arg	Cys	Asn	Leu	Cys	Lys	Asn	Gly	Arg	Tyr	Asn	Leu	Cys	Ser	Glu	Met	
		115					120					125				
Arg	Phe	Phe	Gly	Ser	Pro	Pro	Thr	Asn	Gly	Ser	Leu	Ala	Asn	Lys	Val	
	130					135					140					
Val	His	Pro	Ala	Ser	Leu	Cys	Tyr	Lys	Leu	Pro	Glu	Asn	Val	Ser	Leu	
145					150					155					160	
Glu	Glu	Gly	Ala	Met	Cys	Glu	Pro	Leu	Ser	Val	Gly	Val	His	Ala	Cys	
				165					170					175		
Arg	Arg	Ala	Gln	Val	Gly	Pro	Glu	Thr	Ser	Val	Leu	Ile	Leu	Gly	Ala	
			180					185					190			
Gly	Pro	Ile	Gly	Leu	Ile	Thr	Leu	Leu	Val	Ala	Arg	Ala	Phe	Gly	Ser	
		195					200					205				
Pro	Arg	Val	Val	Met	Thr	Asp	Val	Asp	Glu	Thr	Arg	Leu	Ser	Ile	Ala	
	210					215					220					
Lys	Ser	Leu	Gly	Ala	Asp	Glu	Thr	Ile	Gln	Val	Ser	Thr	Asp	Pro	Lys	
225					230					235					240	
Asp	Val	Ser	Glu	Glu	Val	Met	Lys	Val	Gln	Asn	Ala	Met	Gly	Ser	Gly	
				245					250					255		
Ile	Asp	Val	Thr	Leu	Asp	Cys	Val	Gly	Tyr	Asn	Lys	Thr	Met	Thr	Thr	
			260					265					270			
Ala	Leu	Asn	Ala	Thr	Arg	Ser	Gly	Gly	Lys	Val	Cys	Leu	Ile	Gly	Leu	
		275					280					285				
Ala	Leu	Ser	Glu	Met	Thr	Val	Pro	Leu	Thr	Pro	Ala	Ala	Ala	Arg	Glu	
	290					295					300					
Val	Asp	Val	Ile	Gly	Ile	Phe	Arg	Tyr	Arg	Asn	Thr	Trp	Pro	Leu	Cys	
305					310					315					320	
Leu	Asp	Phe	Leu	Lys	Thr	Gly	Lys	Ile	Tyr	Val	Lys	Pro	Leu	Ile	Thr	
				325					330							

<210> 10054
<211> 1071
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (1)..(1071)

PF59083SeqList PF59083.txt

```

<400> 10054
atg gct gct gaa tcc ggg aca gag agt ggc aac tgc agt gct tgg gca      48
Met Ala Ala Glu Ser Gly Thr Glu Ser Gly Asn Cys Ser Ala Trp Ala
1      5      10      15
gca aaa gat cct tct gga cta ctc tcc ccg cac act ttc aac cgt agg      96
Ala Lys Asp Pro Ser Gly Leu Leu Ser Pro His Thr Phe Asn Arg Arg
20      25      30
act gta cga cat gat gat gtt tct ttg agg atc aca cat tgt ggt gtc      144
Thr Val Arg His Asp Asp Val Ser Leu Arg Ile Thr His Cys Gly Val
35      40      45
tgt tat gcc gat gtt atc tgg aca aaa aat agg cac aat gac tcg gtg      192
Cys Tyr Ala Asp Val Ile Trp Thr Lys Asn Arg His Asn Asp Ser Val
50      55      60
tac cct tta gtc cct ggg cat gag att gct gga gtt gta acc gag gtt      240
Tyr Pro Leu Val Pro Gly His Glu Ile Ala Gly Val Val Thr Glu Val
65      70      75      80
ggt tca gac gtc aag ggc ttc aag ctg ggt gac cat gtg gct gtg ggg      288
Gly Ser Asp Val Lys Gly Phe Lys Leu Gly Asp His Val Ala Val Gly
85      90      95
aca tat gtc aac tca tgc cgt gac tgt gac aac tgc aat agc ttc ctc      336
Thr Tyr Val Asn Ser Cys Arg Asp Cys Asp Asn Cys Asn Ser Phe Leu
100      105      110
gag aac cac tgc tca aaa ttt gtt ttc act ttc aat ggt gtt gat acg      384
Glu Asn His Cys Ser Lys Phe Val Phe Thr Phe Asn Gly Val Asp Thr
115      120      125
gat ggt act gtc aca aag gga gga tat tcc agt cac gtt gta gtt cat      432
Asp Gly Thr Val Thr Lys Gly Gly Tyr Ser Ser His Val Val Val His
130      135      140
gaa cgg tac tgc tat aaa ata cct gat ggc tac cca ctg gaa aag gcc      480
Glu Arg Tyr Cys Tyr Lys Ile Pro Asp Gly Tyr Pro Leu Glu Lys Ala
145      150      155      160
gca cct tta gtt tgt gct gga atc act gtg tac act ccg atg acg cga      528
Ala Pro Leu Val Cys Ala Gly Ile Thr Val Tyr Thr Pro Met Thr Arg
165      170      175
cat aac atg aac cag cca ggg aag tca ctt ggt gtt gtc ggt ctt ggt      576
His Asn Met Asn Gln Pro Gly Lys Ser Leu Gly Val Val Gly Leu Gly
180      185      190
ggg ttg ggt cac atg gca gtg aaa ttt ggg aaa gcc ttt gga ctg aag      624
Gly Leu Gly His Met Ala Val Lys Phe Gly Lys Ala Phe Gly Leu Lys
195      200      205
gtg act gtt ttg agt aca agt gaa tcg aaa aga gat gaa gca atc aac      672
Val Thr Val Leu Ser Thr Ser Glu Ser Lys Arg Asp Glu Ala Ile Asn
210      215      220
ctt ctt ggt gca gat aat ttt gtg gtt tca tca gat aaa aaa cag atg      720
Leu Leu Gly Ala Asp Asn Phe Val Val Ser Ser Asp Lys Lys Gln Met
225      230      235      240
gag tcc ctg aaa agt tcc ctg gac ttc att gtc gat act gcc tct ggt      768
Glu Ser Leu Lys Ser Ser Leu Asp Phe Ile Val Asp Thr Ala Ser Gly
245      250      255
gac cac cca ttt gac ccg tat ctt gcg ctt ctg aaa gtt ggt ggc ctg      816
Asp His Pro Phe Asp Pro Tyr Leu Ala Leu Leu Lys Val Gly Gly Leu
260      265      270
atg gca cta gtt ggc ttc cct gga gaa atc aga gtg cat cca gca aca      864
Met Ala Leu Val Gly Phe Pro Gly Glu Ile Arg Val His Pro Ala Thr
275      280      285
ctt aat ctg ggt gca cgg act tta tct ggg agt gta acc gga ggc acg      912
Leu Asn Leu Gly Ala Arg Thr Leu Ser Gly Ser Val Thr Gly Gly Thr
290      300
aag gac aca cag gag atg ata aac ttc tgt gcg gca aac aaa atc tac      960
Lys Asp Thr Gln Glu Met Ile Asn Phe Cys Ala Ala Asn Lys Ile Tyr
305      310      315      320
cca gac att gag ttg ata aag ata gac tac atc aac cag gct ctc gag      1008
Pro Asp Ile Glu Leu Ile Lys Ile Asp Tyr Ile Asn Gln Ala Leu Glu
325      330      335
agg ctt gtc aac cgg gat gtg agg tac cgg ttt gta atc gac ata gag      1056
Arg Leu Val Asn Arg Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Glu
340      345      350
agc tct tta aag tga
1071

```

PF59083SeqList PF59083.txt

Ser Ser Leu Lys
355

<210> 10055
<211> 356
<212> PRT
<213> Hordeum vulgare

<400> 10055
Met Ala Ala Glu Ser Gly Thr Glu Ser Gly Asn Cys Ser Ala Trp Ala
1 5 10 15
Ala Lys Asp Pro Ser Gly Leu Leu Ser Pro His Thr Phe Asn Arg Arg
20 25 30
Thr Val Arg His Asp Asp Val Ser Leu Arg Ile Thr His Cys Gly Val
35 40 45
Cys Tyr Ala Asp Val Ile Trp Thr Lys Asn Arg His Asn Asp Ser Val
50 55 60
Tyr Pro Leu Val Pro Gly His Glu Ile Ala Gly Val Val Thr Glu Val
65 70 75 80
Gly Ser Asp Val Lys Gly Phe Lys Leu Gly Asp His Val Ala Val Gly
85 90 95
Thr Tyr Val Asn Ser Cys Arg Asp Cys Asp Asn Cys Asn Ser Phe Leu
100 105 110
Glu Asn His Cys Ser Lys Phe Val Phe Thr Phe Asn Gly Val Asp Thr
115 120 125
Asp Gly Thr Val Thr Lys Gly Tyr Ser Ser His Val Val Val His
130 135 140
Glu Arg Tyr Cys Tyr Lys Ile Pro Asp Gly Tyr Pro Leu Glu Lys Ala
145 150 155 160
Ala Pro Leu Val Cys Ala Gly Ile Thr Val Tyr Thr Pro Met Thr Arg
165 170 175
His Asn Met Asn Gln Pro Gly Lys Ser Leu Gly Val Val Gly Leu Gly
180 185 190
Gly Leu Gly His Met Ala Val Lys Phe Gly Lys Ala Phe Gly Leu Lys
195 200 205
Val Thr Val Leu Ser Thr Ser Glu Ser Lys Arg Asp Glu Ala Ile Asn
210 215 220
Leu Leu Gly Ala Asp Asn Phe Val Val Ser Ser Asp Lys Lys Gln Met
225 230 235 240
Glu Ser Leu Lys Ser Leu Asp Phe Ile Val Asp Thr Ala Ser Gly
245 250 255
Asp His Pro Phe Asp Pro Tyr Leu Ala Leu Leu Lys Val Gly Gly Leu
260 265 270
Met Ala Leu Val Gly Phe Pro Gly Glu Ile Arg Val His Pro Ala Thr
275 280 285
Leu Asn Leu Gly Ala Arg Thr Leu Ser Gly Ser Val Thr Gly Gly Thr
290 295 300
Lys Asp Thr Gln Glu Met Ile Asn Phe Cys Ala Ala Asn Lys Ile Tyr
305 310 315 320
Pro Asp Ile Glu Leu Ile Lys Ile Asp Tyr Ile Asn Gln Ala Leu Glu
325 330 335
Arg Leu Val Asn Arg Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Glu
340 345 350
Ser Ser Leu Lys
355

<210> 10056
<211> 1083
<212> DNA
<213> Helianthus annuus

<220>
<221> CDS
<222> (1)..(1083)

<400> 10056
atg gca acc tca ccg gaa tcc gag cat ccg atc aag gcg tat ggt tat
Met Ala Thr Ser Pro Glu Ser Glu His Pro Ile Lys Ala Tyr Gly Tyr
1 5 10 15

PF59083SeqList PF59083.txt

gcg	gcc	cg	gac	acg	tct	gga	tta	ctt	tcc	cct	ctc	acc	ttc	tcc	aga	96
Ala	Ala	Arg	Asp	Thr	Ser	Gly	Leu	Leu	Ser	Pro	Leu	Thr	Phe	Ser	Arg	
		20						25					30			
agg	gct	act	gga	gag	aaa	gat	gtg	agg	ttc	aaa	gtt	ctt	tac	tgc	gga	144
Arg	Ala	Thr	Gly	Glu	Lys	Asp	Val	Arg	Phe	Lys	Val	Leu	Tyr	Cys	Gly	
		35					40					45				
atc	tgt	cat	tcc	gat	ctt	cac	gtt	gtc	aaa	aac	gaa	tgg	gga	ttt	acc	192
Ile	Cys	His	Ser	Asp	Leu	His	Val	Val	Lys	Asn	Glu	Trp	Gly	Phe	Thr	
	50					55					60					
aag	tac	ccg	att	act	cca	ggg	cat	gag	att	gtt	ggt	gtg	gtg	aca	gaa	240
Lys	Tyr	Pro	Ile	Thr	Pro	Gly	His	Glu	Ile	Val	Gly	Val	Val	Thr	Glu	
	65				70					75					80	
gta	gga	agc	aaa	gtg	gag	aat	ttc	aag	att	gga	gac	aaa	gtt	ggg	gtt	288
Val	Gly	Ser	Lys	Val	Glu	Asn	Phe	Lys	Ile	Gly	Asp	Lys	Val	Gly	Val	
			85						90					95		
ggg	tgc	ttg	gtg	tca	tgt	aga	tca	tgt	caa	agt	tgt	gct	tct	gac		336
Gly	Cys	Leu	Val	Gly	Ser	Cys	Arg	Ser	Cys	Gln	Ser	Cys	Ala	Ser	Asp	
		100					105						110			
tat	gaa	cag	tat	tgc	gat	aag	cag	gta	caa	act	tat	ggt	ttc	acc	aac	384
Tyr	Glu	Gln	Tyr	Cys	Asp	Lys	Gln	Val	Gln	Thr	Tyr	Gly	Phe	Thr	Asn	
		115					120					125				
ttt	gat	ggc	aca	cag	acg	tac	ggt	gga	tac	tcc	gat	cac	atg	gtt	tca	432
Phe	Asp	Gly	Thr	Gln	Thr	Tyr	Gly	Gly	Tyr	Ser	Asp	His	Met	Val	Ser	
	130					135					140					
gat	gag	cat	ttt	gta	ctc	cgt	tgg	ccg	gag	aac	tta	cca	ctt	gat	tct	480
Asp	Glu	His	Phe	Val	Leu	Arg	Trp	Pro	Glu	Asn	Leu	Pro	Leu	Asp	Ser	
	145				150					155					160	
ggt	gca	ccg	ttg	cta	tgt	gct	ggg	atc	aca	act	tac	agc	cct	ctc	aag	528
Gly	Ala	Pro	Leu	Leu	Cys	Ala	Gly	Ile	Thr	Thr	Tyr	Ser	Pro	Leu	Lys	
			165					170						175		
tac	ttt	gga	ttg	gac	aag	cct	ggt	acg	aaa	gtg	ggc	gtg	gtt	ggg	ctc	576
Tyr	Phe	Gly	Leu	Asp	Lys	Pro	Gly	Thr	Lys	Val	Gly	Val	Val	Gly	Leu	
		180						185					190			
ggt	ggg	ctc	ggt	cat	gtt	gct	gtg	aag	atg	gct	aag	gca	ttt	ggg	gct	624
Gly	Gly	Leu	Gly	His	Val	Ala	Val	Lys	Met	Ala	Lys	Ala	Phe	Gly	Ala	
		195					200					205				
gaa	gtt	act	gtt	ttt	agt	act	tcc	cct	gct	aag	gag	aaa	gaa	gca	att	672
Glu	Val	Thr	Val	Phe	Ser	Thr	Ser	Pro	Ala	Lys	Glu	Lys	Glu	Ala	Ile	
	210					215					220					
cag	gga	ctt	aaa	gct	gac	cat	ttc	gta	aac	agt	aaa	gat	gga	ctt	caa	720
Gln	Gly	Leu	Lys	Ala	Asp	His	Phe	Val	Asn	Ser	Lys	Asp	Gly	Leu	Gln	
	225				230					235					240	
atg	cag	gct	gct	aag	ggc	aca	ctc	gat	ggc	atc	atc	gac	aca	gtg	tcc	768
Met	Gln	Ala	Ala	Lys	Gly	Thr	Leu	Asp	Gly	Ile	Ile	Asp	Thr	Val	Ser	
		245							250					255		
gca	aat	cat	cca	att	gcg	cca	ttg	ctt	aat	gca	ctt	aca	ccc	cat	gga	816
Ala	Asn	His	Pro	Ile	Ala	Pro	Leu	Leu	Asn	Ala	Leu	Thr	Pro	His	Gly	
		260					265						270			
aag	ctt	gtt	ctt	gtt	ggt	gca	cct	gag	aag	cca	ctt	gaa	gta	gca	gca	864
Lys	Leu	Val	Leu	Val	Gly	Ala	Pro	Glu	Lys	Pro	Leu	Glu	Val	Ala	Ala	
		275					280					285				
ttt	tcg	ttg	atc	atg	gga	agg	aag	ctt	gtt	gcg	ggt	agt	aac	att	ggt	912
Phe	Ser	Leu	Ile	Met	Gly	Arg	Lys	Leu	Val	Ala	Gly	Ser	Asn	Ile	Gly	
	290					295					300					
gga	att	aaa	gag	act	cag	gaa	atg	ctt	gac	ttt	gca	aag	cat	ggg		960
Gly	Ile	Lys	Glu	Thr	Gln	Glu	Met	Leu	Asp	Phe	Ala	Ala	Lys	His	Gly	
	305				310					315					320	
ata	act	gca	gat	ata	gag	gtt	ata	ccg	ata	gac	tat	gtg	aac	aca	gcg	1008
Ile	Thr	Ala	Asp	Ile	Glu	Val	Ile	Pro	Ile	Asp	Tyr	Val	Asn	Thr	Ala	
			325						330					335		
atg	gaa	agg	ctg	ttg	aaa	tcc	gat	gtg	agg	tac	cga	ttt	gtg	atc	gat	1056
Met	Glu	Arg	Leu	Leu	Lys	Ser	Asp	Val	Arg	Tyr	Arg	Phe	Val	Ile	Asp	
		340						345					350			
gtg	gcg	aac	tcg	atc	aag	gct	gaa	tag								1083
Val	Ala	Asn	Ser	Ile	Lys	Ala	Glu									
		355					360									

<210> 10057

<211> 360

PF59083SeqList PF59083.txt

<212> PRT

<213> Helianthus annuus

<400> 10057

```

Met Ala Thr Ser Pro Glu Ser Glu His Pro Ile Lys Ala Tyr Gly Tyr
1      5      10      15
Ala Ala Arg Asp Thr Ser Gly Leu Leu Ser Pro Leu Thr Phe Ser Arg
      20      25      30
Arg Ala Thr Gly Glu Lys Asp Val Arg Phe Lys Val Leu Tyr Cys Gly
      35      40      45
Ile Cys His Ser Asp Leu His Val Val Lys Asn Glu Trp Gly Phe Thr
      50      55      60
Lys Tyr Pro Ile Thr Pro Gly His Glu Ile Val Gly Val Val Thr Glu
65      70      75      80
Val Gly Ser Lys Val Glu Asn Phe Lys Ile Gly Asp Lys Val Gly Val
      85      90      95
Gly Cys Leu Val Gly Ser Cys Arg Ser Cys Gln Ser Cys Ala Ser Asp
      100      105      110
Tyr Glu Gln Tyr Cys Asp Lys Gln Val Gln Thr Tyr Gly Phe Thr Asn
      115      120      125
Phe Asp Gly Thr Gln Thr Tyr Gly Tyr Ser Asp His Met Val Ser
130      135      140
Asp Glu His Phe Val Leu Arg Trp Pro Glu Asn Leu Pro Leu Asp Ser
145      150      155      160
Gly Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Lys
      165      170      175
Tyr Phe Gly Leu Asp Lys Pro Gly Thr Lys Val Gly Val Val Gly Leu
      180      185      190
Gly Gly Leu Gly His Val Ala Val Lys Met Ala Lys Ala Phe Gly Ala
      195      200      205
Glu Val Thr Val Phe Ser Thr Ser Pro Ala Lys Glu Lys Glu Ala Ile
210      215      220
Gln Gly Leu Lys Ala Asp His Phe Val Asn Ser Lys Asp Gly Leu Gln
225      230      235      240
Met Gln Ala Ala Lys Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser
      245      250      255
Ala Asn His Pro Ile Ala Pro Leu Leu Asn Ala Leu Thr Pro His Gly
      260      265      270
Lys Leu Val Leu Val Gly Ala Pro Glu Lys Pro Leu Glu Val Ala Ala
      275      280      285
Phe Ser Leu Ile Met Gly Arg Lys Leu Val Ala Gly Ser Asn Ile Gly
290      295      300
Gly Ile Lys Glu Thr Gln Glu Met Leu Asp Phe Ala Ala Lys His Gly
305      310      315      320
Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Val Asn Thr Ala
      325      330      335
Met Glu Arg Leu Leu Lys Ser Asp Val Arg Tyr Arg Phe Val Ile Asp
      340      345      350
Val Ala Asn Ser Ile Lys Ala Glu
355      360

```

<210> 10058

<211> 486

<212> DNA

<213> Escherichia coli K12

<220>

<221> CDS

<222> (1)..(486)

<223> transl_table=11

<400> 10058

```

atg aaa tac gat act tcc gag ctt tgt gac atc tat caa gaa gat gtt      48
Met Lys Tyr Asp Thr Ser Glu Leu Cys Asp Ile Tyr Gln Glu Asp Val
1      5      10      15
aac gtc gtg gaa ccg ctg ttc tcc aac ttt ggc gga cgg gcg tcg ttt      96
Asn Val Val Glu Pro Leu Phe Ser Asn Phe Gly Gly Arg Ala Ser Phe
      20      25      30
ggc gga caa ata atc acg gta aaa tgt ttc gag gac aac ggg ttg ctg      144

```

PF59083SeqList PF59083.txt

Gly	Gly	Gln	Ile	Ile	Thr	Val	Lys	Cys	Phe	Glu	Asp	Asn	Gly	Leu	Leu		
		35					40					45					
tac	gat	ctg	ctc	gaa	cag	aat	ggc	cgt	ggg	cgt	ggt	ctt	gtc	gtc	gat	192	
Tyr	Asp	Leu	Leu	Glu	Gln	Asn	Gly	Arg	Gly	Arg	Val	Leu	Val	Val	Asp		
	50					55					60						
ggc	ggt	ggt	tct	ggt	cgt	cgc	gca	ctg	gtc	gat	gct	gaa	ctg	gcg	cgt	240	
Gly	Gly	Gly	Ser	Val	Arg	Arg	Ala	Leu	Val	Asp	Ala	Glu	Leu	Ala	Arg		
65					70					75					80		
ctg	gca	gta	caa	aat	gaa	tgg	gaa	ggg	ctg	gtc	att	tac	ggc	gcg	gtg	288	
Leu	Ala	Val	Gln	Asn	Glu	Trp	Glu	Gly	Leu	Val	Ile	Tyr	Gly	Ala	Val		
				85					90					95			
cgt	cag	gta	gat	gac	ctg	gaa	gag	ttg	gat	atc	ggc	atc	cag	gcg	atg	336	
Arg	Gln	Val	Asp	Asp	Leu	Glu	Glu	Leu	Asp	Ile	Gly	Ile	Gln	Ala	Met		
			100					105				110					
gcg	gca	att	ccg	ggt	ggg	gcc	gct	ggc	gaa	ggc	att	ggc	gaa	agc	gat	384	
Ala	Ala	Ile	Pro	Val	Gly	Ala	Ala	Gly	Glu	Gly	Ile	Gly	Glu	Ser	Asp		
		115				120						125					
gtc	cgc	gtc	aat	ttt	ggc	ggg	gtc	acc	ttc	ttc	tcc	ggc	gac	cat	ctt	432	
Val	Arg	Val	Asn	Phe	Gly	Gly	Val	Thr	Phe	Phe	Ser	Gly	Asp	His	Leu		
	130				135						140						
tat	gcc	gac	aat	acc	ggg	att	att	ctt	tca	gaa	gat	ccg	ctg	gat	att	480	
Tyr	Ala	Asp	Asn	Thr	Gly	Ile	Ile	Leu	Ser	Glu	Asp	Pro	Leu	Asp	Ile		
145					150					155					160		
gaa	tga															486	
Glu																	

<210> 10059
 <211> 161
 <212> PRT
 <213> Escherichia coli K12

<400> 10059

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

<210> 10060
 <211> 507
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(507)

<400> 10060

atg	gcg	gcc	ttg	cca	ttg	gcc	acg	gcg	gaa	gtc	tgt	gac	gcc	aac	tcg	48	
Met	Ala	Ala	Leu	Pro	Leu	Ala	Thr	Ala	Glu	Val	Cys	Asp	Ala	Asn	Ser		
1				5				10						15			

PF59083SeqList PF59083.txt

cac	ctg	atc	acc	ggc	ggc	gag	ctc	cgg	gcg	ctc	cag	cca	atc	ttc	cag	96
His	Leu	Ile	Thr	Gly	Gly	Glu	Leu	Arg	Ala	Leu	Gln	Pro	Ile	Phe	Gln	
			20					25					30			
atc	tac	ggg	agg	cgg	cag	gtc	ttc	gca	ggg	ccc	atc	gtg	acg	ctc	aag	144
Ile	Tyr	Gly	Arg	Arg	Gln	Val	Phe	Ala	Gly	Pro	Ile	Val	Thr	Leu	Lys	
		35					40					45				
gtg	ttt	gag	gac	aac	gtt	ctc	gtg	cgc	gag	ttc	ctg	gag	gag	aag	ggc	192
Val	Phe	Glu	Asp	Asn	Val	Leu	Val	Arg	Glu	Phe	Leu	Glu	Glu	Lys	Gly	
	50					55					60					
cag	ggc	agg	gtg	ctg	gtg	gtg	gac	ggc	ggc	ggc	agc	ctg	cgg	tgc	gcc	240
Gln	Gly	Arg	Val	Leu	Val	Val	Asp	Gly	Gly	Gly	Ser	Leu	Arg	Cys	Ala	
	65				70				75						80	
atc	ctg	ggc	ggc	aac	ccc	gtc	cag	cag	gcg	cag	aac	aac	ggg	tg	gcg	288
Ile	Leu	Gly	Gly	Asn	Pro	Val	Gln	Gln	Ala	Gln	Asn	Asn	Gly	Trp	Ala	
				85				90						95		
ggc	atc	gtc	gtg	aac	ggc	tgc	atc	cgg	gac	gtg	gac	gag	atc	aac	ggg	336
Gly	Ile	Val	Val	Asn	Gly	Cys	Ile	Arg	Asp	Val	Asp	Glu	Ile	Asn	Gly	
		100						105					110			
tgc	gac	atc	ggc	gtg	cgc	gcc	ctc	aac	tca	cac	ccg	atg	aag	gcc	aac	384
Cys	Asp	Ile	Gly	Val	Arg	Ala	Leu	Asn	Ser	His	Pro	Met	Lys	Ala	Asn	
		115					120					125				
aag	aag	ggc	atg	ggc	gag	aag	cac	gtc	ccc	atc	acc	atc	gcg	ggc	acc	432
Lys	Lys	Gly	Met	Gly	Glu	Lys	His	Val	Pro	Ile	Thr	Ile	Ala	Gly	Thr	
	130					135					140					
cgg	atc	tgc	gac	ggc	gag	tgg	ctc	tac	gcc	gac	acc	gat	ggc	atc	ctg	480
Arg	Ile	Cys	Asp	Gly	Glu	Trp	Leu	Tyr	Ala	Asp	Thr	Asp	Gly	Ile	Leu	
	145				150					155					160	
gtc	tcc	agg	acc	gag	ctg	att	gtg	tag								507
Val	Ser	Arg	Thr	Glu	Leu	Ile	Val									
				165												

<210> 10061
 <211> 168
 <212> PRT
 <213> Hordeum vulgare

<400> 10061
 Met Ala Ala Leu Pro Leu Ala Thr Ala Glu Val Cys Asp Ala Asn Ser
 1 5 10 15
 His Leu Ile Thr Gly Gly Glu Leu Arg Ala Leu Gln Pro Ile Phe Gln
 20 25 30
 Ile Tyr Gly Arg Arg Gln Val Phe Ala Gly Pro Ile Val Thr Leu Lys
 35 40 45
 Val Phe Glu Asp Asn Val Leu Val Arg Glu Phe Leu Glu Glu Lys Gly
 50 55 60
 Gln Gly Arg Val Leu Val Val Asp Gly Gly Gly Ser Leu Arg Cys Ala
 65 70 75 80
 Ile Leu Gly Gly Asn Pro Val Gln Gln Ala Gln Asn Asn Gly Trp Ala
 85 90 95
 Gly Ile Val Val Asn Gly Cys Ile Arg Asp Val Asp Glu Ile Asn Gly
 100 105 110
 Cys Asp Ile Gly Val Arg Ala Leu Asn Ser His Pro Met Lys Ala Asn
 115 120 125
 Lys Lys Gly Met Gly Glu Lys His Val Pro Ile Thr Ile Ala Gly Thr
 130 135 140
 Arg Ile Cys Asp Gly Glu Trp Leu Tyr Ala Asp Thr Asp Gly Ile Leu
 145 150 155 160
 Val Ser Arg Thr Glu Leu Ile Val
 165

<210> 10062
 <211> 1482
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1482)
 <223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 10062
atg tgt tta aag caa atc att ggc agc ttg aaa aag aag gtt cac atg      48
Met Cys Leu Lys Gln Ile Ile Gly Ser Leu Lys Lys Lys Val His Met
1 5 10 15
tca aac aac att cgt atc gaa gaa gat ctg ttg ggt acc agg gaa gtt      96
Ser Asn Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Thr Arg Glu Val
20 25 30
cca gct gat gcc tac tat ggt gtt cac act ctg aga gcg att gaa aac      144
Pro Ala Asp Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Ile Glu Asn
35 40 45
ttc tat atc agc aac aac aaa atc agt gat att cct gaa ttt gtt cgc      192
Phe Tyr Ile Ser Asn Asn Lys Ile Ser Asp Ile Pro Glu Phe Val Arg
50 55 60
ggg atg gta atg gtt aaa aaa gcc gca gct atg gca aac aaa gag ctg      240
Gly Met Val Met Val Lys Lys Ala Ala Ala Met Ala Asn Lys Glu Leu
65 70 75 80
caa acc att cct aaa agt gta gcg aat gcc atc att gcc gca tgt gat      288
Gln Thr Ile Pro Lys Ser Val Ala Asn Ala Ile Ile Ala Ala Cys Asp
85 90 95
gaa gtc ctg aac aac gga aaa tgc atg gat cag ttc ccg gta gac gtc      336
Glu Val Leu Asn Asn Gly Lys Cys Met Asp Gln Phe Pro Val Asp Val
100 105 110
tac cag ggc ggc gca ggt act tcc gta aac atg aac acc aac gaa gtg      384
Tyr Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu Val
115 120 125
ctg gcc aat atc ggt ctg gaa ctg atg ggt cac caa aaa ggt gaa tat      432
Leu Ala Asn Ile Gly Leu Glu Leu Met Gly His Gln Lys Gly Glu Tyr
130 135 140
cag tac ctg aac ccg aac gac cat gtt aac aaa tgt cag tcc act aac      480
Gln Tyr Leu Asn Pro Asn Asp His Val Asn Lys Cys Gln Ser Thr Asn
145 150 155 160
gac gcc tac ccg acc ggt ttc cgt atc gca gtt tac tct tcc ctg att      528
Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Ser Ser Leu Ile
165 170 175
aag ctg gta gat gcg att aac caa ctg cgt gaa ggc ttt gaa cgt aaa      576
Lys Leu Val Asp Ala Ile Asn Gln Leu Arg Glu Gly Phe Glu Arg Lys
180 185 190
gct gtc gaa ttc cag gac atc ctg aaa atg ggt cgt acc cag ctg cag      624
Ala Val Glu Phe Gln Asp Ile Leu Lys Met Gly Arg Thr Gln Leu Gln
195 200 205
gac gca gta ccg atg acc ctc ggt cag gaa ttc cgc gct ttc agc atc      672
Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Arg Ala Phe Ser Ile
210 215 220
ctg ctg aaa gaa gaa gtg aaa aac atc caa cgt acc gct gaa ctg ctg      720
Leu Leu Lys Glu Glu Val Lys Asn Ile Gln Arg Thr Ala Glu Leu Leu
225 230 235 240
ctg gaa gtt aac ctt ggt gca aca gca atc ggt act ggt ctg aac acg      768
Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn Thr
245 250 255
ccg aaa gag tac tct ccg ctg gca gtg aaa aaa ctg gct gaa gtt act      816
Pro Lys Glu Tyr Ser Pro Leu Ala Val Lys Lys Leu Ala Glu Val Thr
260 265 270
ggc ttc cca tgc gta ccg gct gaa gac ctg atc gaa gcg acc tct gac      864
Gly Phe Pro Cys Val Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser Asp
275 280 285
tgc ggc gct tat gtt atg gtt cac ggc gcg ctg aaa cgc ctg gct gtg      912
Cys Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Leu Ala Val
290 295 300
aag atg tcc aaa atc tgt gac ctg cgc ttg ctc tct tca ggc cca      960
Lys Met Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro
305 310 315 320
cgt gcc ggc ctg aac gag atc aac ctg ccg gaa ctg cag gcg ggc tct      1008
Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly Ser
325 330 335
tcc atc atg cca gct aaa gta aac ccg gtt gtt ccg gaa gtg gtt aac      1056
Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val Asn
340 345 350
cag gta tgc ttc aaa gtc atc ggt aac gac acc act gtt acc atg gca      1104
350

```

PF59083SeqList PF59083.txt

Gln	Val	Cys	Phe	Lys	Val	Ile	Gly	Asn	Asp	Thr	Thr	Val	Thr	Met	Ala		
		355					360					365					
gca	gaa	gca	ggt	cag	ctg	cag	ttg	aac	gtt	atg	gag	ccg	gtc	att	ggc	1152	
Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile	Gly		
	370					375					380						
cag	gcc	atg	ttc	gaa	tcc	gtt	cac	att	ctg	acc	aac	gct	tgc	tac	aac	1200	
Gln	Ala	Met	Phe	Glu	Ser	Val	His	Ile	Leu	Thr	Asn	Ala	Cys	Tyr	Asn		
385					390					395					400		
ctg	ctg	gaa	aaa	tgc	att	aac	ggc	atc	act	gct	aac	aaa	gaa	gtg	tgc	1248	
Leu	Leu	Glu	Lys	Cys	Ile	Asn	Gly	Ile	Thr	Ala	Asn	Lys	Glu	Val	Cys		
			405						410					415			
gaa	ggt	tac	gtt	tac	aac	tct	atc	ggg	atc	gtt	act	tac	ctg	aac	ccg	1296	
Glu	Gly	Tyr	Val	Tyr	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn	Pro		
		420					425						430				
ttc	atc	ggt	cac	cac	aac	ggt	gac	atc	gtg	ggg	aaa	atc	tgt	gcc	gaa	1344	
Phe	Ile	Gly	His	His	Asn	Gly	Asp	Ile	Val	Gly	Lys	Ile	Cys	Ala	Glu		
		435					440						445				
acc	ggt	aag	agt	gta	cgt	gaa	gtc	gtt	ctg	gaa	cgc	ggg	ctg	ttg	act	1392	
Thr	Gly	Lys	Ser	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gly	Leu	Leu	Thr		
	450					455					460						
gaa	gcg	gaa	ctt	gac	gat	att	ttc	tcc	gta	cag	aat	ctg	atg	cac	ccg	1440	
Glu	Ala	Glu	Leu	Asp	Asp	Ile	Phe	Ser	Val	Gln	Asn	Leu	Met	His	Pro		
465					470					475					480		
gct	tac	aaa	gca	aaa	cgc	tat	act	gat	gaa	agc	gaa	cag	taa			1482	
Ala	Tyr	Lys	Ala	Lys	Arg	Tyr	Thr	Asp	Glu	Ser	Glu	Gln					
			485						490								

<210> 10063

<211> 493

<212> PRT

<213> Escherichia coli

<400> 10063

Met	Cys	Leu	Lys	Gln	Ile	Ile	Gly	Ser	Leu	Lys	Lys	Lys	Val	His	Met		
1				5					10					15			
Ser	Asn	Asn	Ile	Arg	Ile	Glu	Glu	Asp	Leu	Leu	Gly	Thr	Arg	Glu	Val		
			20					25					30				
Pro	Ala	Asp	Ala	Tyr	Tyr	Gly	Val	His	Thr	Leu	Arg	Ala	Ile	Glu	Asn		
		35					40					45					
Phe	Tyr	Ile	Ser	Asn	Asn	Lys	Ile	Ser	Asp	Ile	Pro	Glu	Phe	Val	Arg		
	50					55					60						
Gly	Met	Val	Met	Val	Lys	Lys	Ala	Ala	Ala	Met	Ala	Asn	Lys	Glu	Leu		
65					70				75					80			
Gln	Thr	Ile	Pro	Lys	Ser	Val	Ala	Asn	Ala	Ile	Ile	Ala	Ala	Cys	Asp		
			85					90						95			
Glu	Val	Leu	Asn	Asn	Gly	Lys	Cys	Met	Asp	Gln	Phe	Pro	Val	Asp	Val		
			100					105					110				
Tyr	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Val	Asn	Met	Asn	Thr	Asn	Glu	Val		
	115						120					125					
Leu	Ala	Asn	Ile	Gly	Leu	Glu	Leu	Met	Gly	His	Gln	Lys	Gly	Glu	Tyr		
	130					135					140						
Gln	Tyr	Leu	Asn	Pro	Asn	Asp	His	Val	Asn	Lys	Cys	Gln	Ser	Thr	Asn		
145					150				155					160			
Asp	Ala	Tyr	Pro	Thr	Gly	Phe	Arg	Ile	Ala	Val	Tyr	Ser	Ser	Leu	Ile		
			165					170						175			
Lys	Leu	Val	Asp	Ala	Ile	Asn	Gln	Leu	Arg	Glu	Gly	Phe	Glu	Arg	Lys		
			180					185					190				
Ala	Val	Glu	Phe	Gln	Asp	Ile	Leu	Lys	Met	Gly	Arg	Thr	Gln	Leu	Gln		
	195						200					205					
Asp	Ala	Val	Pro	Met	Thr	Leu	Gly	Gln	Glu	Phe	Arg	Ala	Phe	Ser	Ile		
	210					215					220						
Leu	Leu	Lys	Glu	Glu	Val	Lys	Asn	Ile	Gln	Arg	Thr	Ala	Glu	Leu	Leu		
225					230					235				240			
Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr	Gly	Leu	Asn	Thr		
			245					250						255			
Pro	Lys	Glu	Tyr	Ser	Pro	Leu	Ala	Val	Lys	Lys	Leu	Ala	Glu	Val	Thr		
			260					265					270				
Gly	Phe	Pro	Cys	Val	Pro	Ala	Glu	Asp	Leu	Ile	Glu	Ala	Thr	Ser	Asp		
		275					280					285					

PF59083SeqList PF59083.txt

Cys Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Leu Ala Val
 290 295 300
 Lys Met Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro
 305 310 315 320
 Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly Ser
 325 330 335
 Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val Asn
 340 345 350
 Gln Val Cys Phe Lys Val Ile Gly Asn Asp Thr Thr Val Thr Met Ala
 355 360 365
 Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly
 370 375 380
 Gln Ala Met Phe Glu Ser Val His Ile Leu Thr Asn Ala Cys Tyr Asn
 385 390 395 400
 Leu Leu Glu Lys Cys Ile Asn Gly Ile Thr Ala Asn Lys Glu Val Cys
 405 410 415
 Glu Gly Tyr Val Tyr Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn Pro
 420 425 430
 Phe Ile Gly His His Asn Gly Asp Ile Val Gly Lys Ile Cys Ala Glu
 435 440 445
 Thr Gly Lys Ser Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu Thr
 450 455 460
 Glu Ala Glu Leu Asp Asp Ile Phe Ser Val Gln Asn Leu Met His Pro
 465 470 475 480
 Ala Tyr Lys Ala Lys Arg Tyr Thr Asp Glu Ser Glu Gln
 485 490

<210> 10064

<211> 1485

<212> DNA

<213> Helianthus annuus

<220>

<221> CDS

<222> (1)..(1485)

<400> 10064

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

PF59083SeqList PF59083.txt

gtt	atg	cat	att	gca	gct	gca	acc	gaa	atc	aac	tct	aga	ctt	atc	cca	576
Val	Met	His	Ile	Ala	Ala	Ala	Thr	Glu	Ile	Asn	Ser	Arg	Leu	Ile	Pro	
aaa	ctt	aag	cag	ctg	cat	aca	gcc	cta	caa	gct	aag	aca	aat	gag	ttc	624
Lys	Leu	Lys	Gln	Leu	His	Thr	Ala	Leu	Gln	Ala	Lys	Thr	Asn	Glu	Phe	
tct	gat	ata	ggt	aaa	att	ggg	cgt	act	cat	act	caa	gat	gca	aca	ccc	672
Ser	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	
ttg	act	ctt	ggg	caa	gag	ttc	agc	ggc	tat	acc	aca	gtg	aag	tat		720
Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Thr	Thr	Gln	Val	Lys	Tyr	
gga	att	gat	agg	gtc	atg	tgc	act	ctc	cct	cgc	ttg	tat	cag	ctt	gca	768
Gly	Ile	Asp	Arg	Val	Met	Cys	Thr	Leu	Pro	Arg	Leu	Tyr	Gln	Leu	Ala	
caa	ggt	ggc	act	gct	gta	ggg	aca	gga	ttg	aac	aca	aag	aaa	gga	ttt	816
Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	
gat	gta	aag	att	gct	gca	gct	gtt	gct	gat	gaa	aca	agg	tta	cca	ttt	864
Asp	Val	Lys	Ile	Ala	Ala	Ala	Val	Ala	Asp	Glu	Thr	Arg	Leu	Pro	Phe	
ata	aca	gcc	gaa	aat	aag	ttc	gag	gcg	ctg	gct	gcg	cat	gac	gcc	ttt	912
Ile	Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Phe	
gtt	gaa	gct	agt	gga	gcg	tta	aac	aca	att	gcc	act	tct	ctt	atg	aag	960
Val	Glu	Ala	Ser	Gly	Ala	Leu	Asn	Thr	Ile	Ala	Thr	Ser	Leu	Met	Lys	
att	gct	aat	gat	ata	cgg	ttt	cta	gga	agt	ggg	cca	cgt	tgc	ggg	ctt	1008
Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	
ggg	gaa	ctt	att	ctt	cct	gag	aac	gaa	cct	ggg	agc	agc	atc	atg	cct	1056
Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
ggg	aaa	gtg	aat	cct	acg	cag	tgt	gaa	gct	cta	act	atg	gtt	tgt	gct	1104
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	
cag	gca	att	gga	aac	cat	gta	gcc	ctt	aca	gtg	ggc	ggg	tca	aat	gga	1152
Gln	Ala	Ile	Gly	Asn	His	Val	Ala	Leu	Thr	Val	Gly	Gly	Ser	Asn	Gly	
cat	ttt	gag	ctt	aat	gtt	ttc	aag	ccg	atg	att	gct	agt	act	ctt	tta	1200
His	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Met	Ile	Ala	Ser	Thr	Leu	Leu	
cac	tca	atc	aga	ctt	cta	gcc	gat	gca	tct	gct	tct	ttt	gaa	aag	aat	1248
His	Ser	Ile	Arg	Leu	Ala	Ala	Asp	Ala	Ser	Ala	Ser	Phe	Glu	Lys	Asn	
tgt	gtg	agt	ggc	att	caa	gca	aat	agg	gaa	agg	ata	tca	aag	cta	ttg	1296
Cys	Val	Ser	Gly	Ile	Gln	Ala	Asn	Arg	Glu	Arg	Ile	Ser	Lys	Leu	Leu	
cac	gag	tca	ctt	atg	ctt	gtg	aca	tcc	tta	aat	cct	aaa	att	ggc	tat	1344
His	Glu	Ser	Leu	Met	Leu	Val	Thr	Ser	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	
gac	aat	gct	gca	gcg	gtt	gcc	aaa	act	gcc	cac	aag	cag	gga	tgc	aca	1392
Asp	Asn	Ala	Ala	Ala	Val	Ala	Lys	Thr	Ala	His	Lys	Gln	Gly	Cys	Thr	
ctc	aag	gaa	gct	gct	ctt	aaa	ctg	gga	gtg	ttg	aat	agt	gaa	gaa	ttc	1440
Leu	Lys	Glu	Ala	Ala	Leu	Lys	Leu	Gly	Val	Leu	Asn	Ser	Glu	Glu	Phe	
gat	cag	ctt	gta	gtg	ccg	gaa	aag	atg	att	ggc	ccc	agt	gat	tga		1485
Asp	Gln	Leu	Val	Val	Pro	Glu	Lys	Met	Ile	Gly	Pro	Ser	Asp			

<210> 10065

<211> 494

<212> PRT

<213> Helianthus annuus

<400> 10065

Met Ala Met Val Gln Ala Phe Arg Arg Thr Pro Gly Gly Ser Ala Ile

PF59083SeqList PF59083.txt

```

1          5          10          15
Val Ala Asp Ser Val Arg Phe Ile Thr Cys Trp Arg His Phe Ser Thr
                20
Ala Phe Arg Glu Glu Arg Asp Thr Phe Gly Pro Ile Gln Val Pro Ser
                35
Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn Phe Glu
                50
Ile Gly Gly Asp Arg Glu Arg Met Pro Glu Pro Ile Ile Arg Ser Phe
        65                70                75
Gly Ile Leu Lys Lys Cys Ala Ala Lys Val Asn Met Glu Tyr Gly Leu
                85                90                95
Asp Pro Ser Ile Gly Lys Ala Ile Met Glu Ala Ala Gln Glu Val Ala
                100                105                110
Glu Gly Lys Leu Asn Asp His Phe Pro Leu Val Ile Trp Gln Thr Gly
                115                120                125
Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ala Asn Arg
        130                135                140
Ala Ala Glu Ile Leu Gly His Lys Arg Gly Asp Lys Phe Val His Pro
        145                150                155
Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr
                165                170                175
Val Met His Ile Ala Ala Ala Thr Glu Ile Asn Ser Arg Leu Ile Pro
                180                185                190
Lys Leu Lys Gln Leu His Thr Ala Leu Gln Ala Lys Thr Asn Glu Phe
        195                200                205
Ser Asp Ile Val Lys Ile Gly Arg Thr His Thr Gln Asp Ala Thr Pro
        210                215                220
Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Thr Thr Gln Val Lys Tyr
        225                230                235
Gly Ile Asp Arg Val Met Cys Thr Leu Pro Arg Leu Tyr Gln Leu Ala
                245                250                255
Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Lys Lys Gly Phe
                260                265                270
Asp Val Lys Ile Ala Ala Ala Val Ala Asp Glu Thr Arg Leu Pro Phe
                275                280                285
Ile Thr Ala Glu Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Phe
        290                295                300
Val Glu Ala Ser Gly Ala Leu Asn Thr Ile Ala Thr Ser Leu Met Lys
        305                310                315
Ile Ala Asn Asp Ile Arg Phe Leu Gly Ser Gly Pro Arg Cys Gly Leu
                325                330                335
Gly Glu Leu Ile Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro
                340                345                350
Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys Ala
                355                360                365
Gln Ala Ile Gly Asn His Val Ala Leu Thr Val Gly Gly Ser Asn Gly
        370                375                380
His Phe Glu Leu Asn Val Phe Lys Pro Met Ile Ala Ser Thr Leu Leu
        385                390                395
His Ser Ile Arg Leu Leu Ala Asp Ala Ser Ala Ser Phe Glu Lys Asn
                405                410                415
Cys Val Ser Gly Ile Gln Ala Asn Arg Glu Arg Ile Ser Lys Leu Leu
                420                425                430
His Glu Ser Leu Met Leu Val Thr Ser Leu Asn Pro Lys Ile Gly Tyr
                435                440                445
Asp Asn Ala Ala Ala Val Ala Lys Thr Ala His Lys Gln Gly Cys Thr
        450                455                460
Leu Lys Glu Ala Ala Leu Lys Leu Gly Val Leu Asn Ser Glu Glu Phe
        465                470                475
Asp Gln Leu Val Val Pro Glu Lys Met Ile Gly Pro Ser Asp
                485                490

```

<210> 10066

<211> 1437

<212> DNA

<213> Escherichia coli K12

<220>

<221> CDS

PF59083SeqList PF59083.txt

<222> (1)..(1437)

<223> transl_table=11

<400> 10066

atg tca aac aac att cgt atc gaa gaa gat ctg ttg ggt acc agg gaa	48
Met Ser Asn Asn Ile Arg Ile Glu Glu Asp Leu Leu Gly Thr Arg Glu	
1 5 10 15	
gtt cca gct gat gcc tac tat ggt gtt cac act ctg aga gcg att gaa	96
Val Pro Ala Asp Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Ile Glu	
20 25 30	
aac ttc tat atc agc aac aac aaa atc agt gat att cct gaa ttt gtt	144
Asn Phe Tyr Ile Ser Asn Asn Lys Ile Ser Asp Ile Pro Glu Phe Val	
35 40 45	
cgc ggt atg gta atg gtt aaa aaa gcc gca gct atg gca aac aaa gag	192
Arg Gly Met Val Met Val Lys Lys Ala Ala Ala Met Ala Asn Lys Glu	
50 55 60	
ctg caa acc att cct aaa agt gta gcg aat gcc atc att gcc gca tgt	240
Leu Gln Thr Ile Pro Lys Ser Val Ala Asn Ala Ile Ile Ala Ala Cys	
65 70 75 80	
gat gaa gtc ctg aac aac gga aaa tgc atg gat cag ttc ccg gta gac	288
Asp Glu Val Leu Asn Asn Gly Lys Cys Met Asp Gln Phe Pro Val Asp	
85 90 95	
gtc tac cag ggc ggc gca ggt act tcc gta aac atg aac acc aac gaa	336
Val Tyr Gln Gly Gly Ala Gly Thr Ser Val Asn Met Asn Thr Asn Glu	
100 105 110	
gtg ctg gcc aat atc ggt ctg gaa ctg atg ggt cac caa aaa ggt gaa	384
Val Leu Ala Asn Ile Gly Leu Glu Leu Met Gly His Gln Lys Gly Glu	
115 120 125	
tat cag tac ctg aac ccg aac gac cat gtt aac aaa tgt cag tcc act	432
Tyr Gln Tyr Leu Asn Pro Asp His Val Asn Lys Cys Gln Ser Thr	
130 135 140	
aac gac gcc tac ccg acc ggt ttc cgt atc gca gtt tac tct tcc ctg	480
Asn Asp Ala Tyr Pro Thr Gly Phe Arg Ile Ala Val Tyr Ser Ser Leu	
145 150 155 160	
att aag ctg gta gat gcg att aac caa ctg cgt gaa ggc ttt gaa cgt	528
Ile Lys Leu Val Asp Ala Ile Asn Gln Leu Arg Glu Gly Phe Glu Arg	
165 170 175	
aaa gct gtc gaa ttc cag gac atc ctg aaa atg ggt cgt acc cag ctg	576
Lys Ala Val Glu Phe Gln Asp Ile Leu Lys Met Gly Arg Thr Gln Leu	
180 185 190	
cag gac gca gta ccg atg acc ctc ggt cag gaa ttc cgc gct ttc agc	624
Gln Asp Ala Val Pro Met Thr Leu Gly Gln Glu Phe Arg Ala Phe Ser	
195 200 205	
atc ctg ctg aaa gaa gaa gtg aaa aac atc caa cgt acc gct gaa ctg	672
Ile Leu Leu Lys Glu Glu Val Lys Asn Ile Gln Arg Thr Ala Glu Leu	
210 215 220	
ctg ctg gaa gtt aac ctt ggt gca aca gca atc ggt act ggt ctg aac	720
Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Leu Asn	
225 230 235 240	
acg ccg aaa gag tac tct ccg ctg gca gtg aaa ctg gct gaa gtt	768
Thr Pro Lys Glu Tyr Ser Pro Leu Ala Val Lys Lys Leu Ala Glu Val	
245 250 255	
act ggc ttc cca tgc gta ccg gct gaa gac ctg atc gaa gcg acc tct	816
Thr Gly Phe Pro Cys Val Pro Ala Glu Asp Leu Ile Glu Ala Thr Ser	
260 265 270	
gac tgc ggc gct tat gtt atg gtt cac ggc gcg ctg aaa cgc ctg gct	864
Asp Cys Gly Ala Tyr Val Met Val His Gly Ala Leu Lys Arg Leu Ala	
275 280 285	
gtg aag atg tcc aaa atc tgt aac gac ctg cgc ttg ctc tct tca ggc	912
Val Lys Met Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly	
290 295 300	
cca cgt gcc ggc ctg aac gag atc aac ctg ccg gaa ctg cag gcg ggc	960
Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly	
305 310 315 320	
tct tcc atc atg cca gct aaa gta aac ccg gtt gtt ccg gaa gtg gtt	1008
Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Val Pro Glu Val Val	
325 330 335	
aac cag gta tgc ttc aaa gtc atc ggt aac gac acc act gtt acc atg	1056
Asn Gln Val Cys Phe Lys Val Ile Gly Asn Asp Thr Val Thr Met	

PF59083SeqList PF59083.txt

1104															
gca	gca	gaa	gca	ggt	cag	ctg	cag	ttg	aac	gtt	atg	gag	ccg	gtc	att
Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu	Pro	Val	Ile
1152															
ggc	cag	gcc	atg	ttc	gaa	tcc	ggt	cac	att	ctg	acc	aac	gct	tgc	tac
Gly	Gln	Ala	Met	Phe	Glu	Ser	Val	His	Ile	Leu	Thr	Asn	Ala	Cys	Tyr
1200															
aac	ctg	ctg	gaa	aaa	tgc	att	aac	ggc	atc	act	gct	aac	aaa	gaa	gtg
Asn	Leu	Leu	Glu	Lys	Cys	Ile	Asn	Gly	Ile	Thr	Ala	Asn	Lys	Glu	Val
1248															
tgc	gaa	ggt	tac	gtt	tac	aac	tct	atc	ggc	atc	ggt	act	tac	ctg	aac
Cys	Glu	Gly	Tyr	Val	Tyr	Asn	Ser	Ile	Gly	Ile	Val	Thr	Tyr	Leu	Asn
1296															
ccg	ttc	atc	ggt	cac	cac	aac	ggt	gac	atc	gtg	ggt	aaa	atc	tgt	gcc
Pro	Phe	Ile	Gly	His	His	Asn	Gly	Asp	Ile	Val	Gly	Lys	Ile	Cys	Ala
1344															
gaa	acc	ggt	aag	agt	gta	cgt	gaa	gtc	ggt	ctg	gaa	cgc	ggt	ctg	ttg
Glu	Thr	Gly	Lys	Ser	Val	Arg	Glu	Val	Val	Leu	Glu	Arg	Gly	Leu	Leu
1392															
act	gaa	gcg	gaa	ctt	gac	gat	att	ttc	tcc	gta	cag	aat	ctg	atg	cac
Thr	Glu	Ala	Glu	Leu	Asp	Asp	Ile	Phe	Ser	Val	Gln	Asn	Leu	Met	His
1437															
ccg	gct	tac	aaa	gca	aaa	cgc	tat	act	gat	gaa	agc	gaa	cag	taa	
Pro	Ala	Tyr	Lys	Ala	Lys	Arg	Tyr	Thr	Asp	Glu	Ser	Glu	Gln		

<210> 10067

<211> 478

<212> PRT

<213> Escherichia coli K12

<400> 10067

Met 1	Ser 5	Asn 10	Ile 15	Arg 20	Ile 25	Glu 30	Glu 35	Asp 40	Leu 45	Leu 50	Gly 55	Thr 60	Arg 65	Glu 70	
Val	Pro	Ala	Asp 20	Ala	Tyr	Tyr	Gly 25	Val	His	Thr	Leu	Arg	Ala 30	Ile 35	Glu 40
Asn	Phe	Tyr 35	Ile	Ser	Asn	Asn	Lys 40	Ile	Ser	Asp	Ile	Pro 45	Glu	Phe	Val
Arg	Gly 50	Met	Val	Met	Val	Lys 55	Lys	Ala	Ala	Ala	Met 60	Ala	Asn	Lys	Glu
Leu 65	Gln	Thr	Ile	Pro	Lys 70	Ser	Val	Ala	Asn	Ala 75	Ile	Ile	Ala	Ala 80	Cys 85
Asp	Glu	Val	Leu	Asn 85	Asn	Gly	Lys	Cys	Met 90	Asp	Gln	Phe	Pro	Val 95	Asp 100
Val	Tyr	Gln	Gly 100	Gly	Ala	Gly	Thr	Ser 105	Val	Asn	Met	Asn	Thr 110	Asn	Glu
Val	Leu	Ala 115	Asn	Ile	Gly	Leu	Glu 120	Leu	Met	Gly	His	Gln 125	Lys	Gly	Glu
Tyr	Gln 130	Tyr	Leu	Asn	Pro	Asn 135	Asp	His	Val	Asn	Lys 140	Cys	Gln	Ser	Thr
Asn 145	Asp	Ala	Tyr	Pro	Thr 150	Gly	Phe	Arg	Ile	Ala 155	Val	Tyr	Ser	Ser	Leu 160
Ile	Lys	Leu	Val	Asp 165	Ala	Ile	Asn	Gln	Leu 170	Arg	Glu	Gly	Phe	Glu 175	Arg
Lys	Ala	Val	Glu 180	Phe	Gln	Asp	Ile	Leu 185	Lys	Met	Gly	Arg	Thr 190	Gln	Leu
Gln	Asp 195	Ala	Val	Pro	Met	Thr	Leu 200	Gly	Gln	Glu	Phe	Arg 205	Ala	Phe	Ser
Ile 210	Leu	Leu	Lys	Glu	Glu	Val 215	Lys	Asn	Ile	Gln	Arg 220	Thr	Ala	Glu	Leu
Leu 225	Leu	Glu	Val	Asn 230	Leu	Gly	Ala	Thr	Ala	Ile 235	Gly	Thr	Gly	Leu	Asn 240
Thr	Pro	Lys	Glu	Tyr 245	Ser	Pro	Leu	Ala	Val 250	Lys	Lys	Leu	Ala	Glu 255	Val
Thr	Gly	Phe	Pro 260	Cys	Val	Pro	Ala	Glu 265	Asp	Leu	Ile	Glu	Ala 270	Thr	Ser
Asp	Cys	Gly 275	Ala	Tyr	Val	Met	Val 280	His	Gly	Ala	Leu	Lys 285	Arg	Leu	Ala
Val	Lys	Met	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu	Ser	Ser	Gly

PF59083SeqList PF59083.txt

```

290          295          300
Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Glu Leu Gln Ala Gly
305 Ser Ser Ile Met Pro 310 Lys Val Asn Pro 315 Val Val Pro Glu Val Val
Asn Gln Val Cys 325 Phe Lys Val Ile Gly 330 Asn Asp Thr Thr Val Thr Met
Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile
335 340 350
Gly Gln Ala Met Phe Glu Ser Val His Ile Leu Thr Asn Ala Cys Tyr
370 375 380
Asn Leu Leu Glu Lys Cys Ile Asn Gly Ile Thr Ala Asn Lys Glu Val
385 Cys Glu Gly Tyr Val Tyr Asn Ser Ile Gly Ile Val Thr Tyr Leu Asn
405 410 415
Pro Phe Ile Gly His His Asn Gly Asp Ile Val Gly Lys Ile Cys Ala
420 425 430
Glu Thr Gly Lys Ser Val Arg Glu Val Val Leu Glu Arg Gly Leu Leu
435 440 445
Thr Glu Ala Glu Leu Asp Asp Ile Phe Ser Val Gln Asn Leu Met His
450 455 460
Pro Ala Tyr Lys Ala Lys Arg Tyr Thr Asp Glu Ser Glu Gln
465 470 475

```

<210> 10068
 <211> 1485
 <212> DNA
 <213> Helianthus annuus

<220>
 <221> CDS
 <222> (1)..(1485)

```

<400> 10068
atg gcg atg gtt cag gca ttt cgt cga aca cct ggt gga tcg gcc atc      48
Met Ala Met Val Gln Ala Phe Arg Arg Thr Pro Gly Gly Ser Ala Ile
1      5      10      15
gtt gca gat tcg gtt cgg ttt att aca tgc tgg aga cat ttc tct acg      96
Val Ala Asp Ser Val Arg Phe Ile Thr Cys Trp Arg His Phe Ser Thr
20      25      30
gct ttt aga gag gaa aga gat acg ttt gga cca att caa gtc ccg tct      144
Ala Phe Arg Glu Glu Arg Asp Thr Phe Gly Pro Ile Gln Val Pro Ser
35      40      45
gat aag tta tgg gga gct caa aca caa aga tct tta caa aat ttt gaa      192
Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn Phe Glu
50      55      60
att gga ggt gac cgt gaa aga atg cca gaa cca atc att cgt tct ttt      240
Ile Gly Gly Asp Arg Glu Arg Met Pro Glu Pro Ile Ile Arg Ser Phe
65      70      75      80
gga atc ctc aaa aag tgt gct gct aag gta aac atg gaa tac ggc ctt      288
Gly Ile Leu Lys Lys Cys Ala Ala Lys Val Asn Met Glu Tyr Gly Leu
85      90      95
gat cca tcc ata ggg aaa gca ata atg gaa gct gca caa gaa gtg gca      336
Asp Pro Ser Ile Gly Lys Ala Ile Met Glu Ala Ala Gln Glu Val Ala
100      105      110
gag ggg aaa tta aac gat cac ttt cca cta gtt ata tgg cag act ggc      384
Glu Gly Lys Leu Asn Asp His Phe Pro Leu Val Ile Trp Gln Thr Gly
115      120      125
agt ggc act caa agc aat atg aat gcc aac gag gtc att gca aat aga      432
Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ala Asn Arg
130      135      140
gca gct gaa ata ctt ggc cat aag cgc ggc gac aag ttt gtg cac cca      480
Ala Ala Glu Ile Leu Gly His Lys Arg Gly Asp Lys Phe Val His Pro
145      150      155      160
aat gac cat gtt aac aga tca cag tct tca aat gat aca ttc ccg act      528
Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr
165      170      175
gtt atg cat att gca gct gca acc gaa atc aac tct aga ctt atc cca      576
Val Met His Ile Ala Ala Ala Thr Glu Ile Asn Ser Arg Leu Ile Pro

```

PF59083SeqList PF59083.txt

180																624
aaa	ctt	aag	cag	ctg	cat	aca	gcc	cta	caa	gct	aag	aca	aat	gag	ttc	624
Lys	Leu	Lys	Gln	Leu	His	Thr	Ala	Leu	Gln	Ala	Lys	Thr	Asn	Glu	Phe	
195																
tct	gat	ata	gtt	aaa	att	ggg	cgt	act	cat	act	caa	gat	gca	aca	ccc	672
Ser	Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	
210																
ttg	act	ctt	ggg	caa	gag	ttc	agc	ggc	tat	acc	aca	caa	gtg	aag	tat	720
Leu	Thr	Leu	Gly	Gln	Glu	Phe	Ser	Gly	Tyr	Thr	Thr	Gln	Val	Lys	Tyr	
225																
gga	att	gat	agg	gtc	atg	tgc	act	ctc	cct	cgc	ttg	tat	cag	ctt	gca	768
Gly	Ile	Asp	Arg	Val	Met	Cys	Thr	Leu	Pro	Arg	Leu	Tyr	Gln	Leu	Ala	
245																
caa	ggt	ggc	act	gct	gta	ggg	aca	gga	ttg	aac	aca	aag	aaa	gga	ttt	816
Gln	Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	
260																
gat	gta	aag	att	gct	gca	gct	gtt	gct	gat	gaa	aca	agg	tta	cca	ttt	864
Asp	Val	Lys	Ile	Ala	Ala	Ala	Val	Ala	Asp	Glu	Thr	Arg	Leu	Pro	Phe	
275																
ata	aca	gcc	gaa	aat	aag	ttc	gag	gcg	ctg	gct	gcg	cat	gac	gcc	ttt	912
Ile	Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Phe	
290																
gtt	gaa	gct	agt	gga	gcg	tta	aac	aca	att	gcc	act	tct	ctt	atg	aag	960
Val	Glu	Ala	Ser	Gly	Ala	Leu	Asn	Thr	Ile	Ala	Thr	Ser	Leu	Met	Lys	
305																
att	gct	aat	gat	ata	cgg	ttt	cta	gga	agt	ggg	cca	cgt	tgc	ggg	ctt	1008
Ile	Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	
325																
ggg	gaa	ctt	att	ctt	cct	gag	aac	gaa	cct	ggg	agc	agc	atc	atg	cct	1056
Gly	Glu	Leu	Ile	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	
340																
ggg	aaa	gtg	aat	cct	acg	cag	tgt	gaa	gct	cta	act	atg	gtt	tgt	gct	1104
Gly	Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	
355																
cag	gca	att	gga	aac	cat	gta	gcc	ctt	aca	gtg	ggc	ggg	tca	aat	gga	1152
Gln	Ala	Ile	Gly	Asn	His	Val	Ala	Leu	Thr	Val	Gly	Gly	Ser	Asn	Gly	
370																
cat	ttt	gag	ctt	aat	gtt	ttc	aag	ccg	atg	att	gct	agt	act	ctt	tta	1200
His	Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Met	Ile	Ala	Ser	Thr	Leu	Leu	
385																
cac	tca	atc	aga	ctt	cta	gcc	gat	gca	tct	gct	tct	ttt	gaa	aag	aat	1248
His	Ser	Ile	Arg	Leu	Leu	Ala	Asp	Ala	Ser	Ala	Ser	Phe	Glu	Lys	Asn	
405																
tgt	gtg	agt	ggc	att	caa	gca	aat	agg	gaa	agg	ata	tca	aag	cta	ttg	1296
Cys	Val	Ser	Gly	Ile	Gln	Ala	Asn	Arg	Glu	Arg	Ile	Ser	Lys	Leu	Leu	
420																
cac	gag	tca	ctt	atg	ctt	gtg	aca	tcc	tta	aat	cct	aaa	att	ggc	tat	1344
His	Glu	Ser	Leu	Met	Leu	Val	Thr	Ser	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	
435																
gac	aat	gct	gca	gcg	gtt	gcc	aaa	act	gcc	cac	aag	cag	gga	tgc	aca	1392
Asp	Asn	Ala	Ala	Ala	Val	Ala	Lys	Thr	Ala	His	Lys	Gln	Gly	Cys	Thr	
450																

```
<210> 10069
<211> 494
<212> PRT
<213> Helianthus annuus
```

<400> 10069
Met Ala Met Val Gln Ala Phe Arg Arg Thr Pro Gly Gly Ser Ala Ile
1 5 10 15
Val Ala Asp Ser Val Arg Phe Ile Thr Cys Trp Arg His Phe Ser Thr
20 25 30

PF59083SeqList PF59083.txt

Ala Phe Arg Glu Glu Arg Asp Thr Phe Gly Pro Ile Gln Val Pro Ser
 35 40 45
 Asp Lys Leu Trp Gly Ala Gln Thr Gln Arg Ser Leu Gln Asn Phe Glu
 50 55 60
 Ile Gly Gly Asp Arg Glu Arg Met Pro Glu Pro Ile Ile Arg Ser Phe
 65 70 75 80
 Gly Ile Leu Lys Lys Cys Ala Ala Lys Val Asn Met Glu Tyr Gly Leu
 85 90 95
 Asp Pro Ser Ile Gly Lys Ala Ile Met Glu Ala Ala Gln Glu Val Ala
 100 105 110
 Glu Gly Lys Leu Asn Asp His Phe Pro Leu Val Ile Trp Gln Thr Gly
 115 120 125
 Ser Gly Thr Gln Ser Asn Met Asn Ala Asn Glu Val Ile Ala Asn Arg
 130 135 140
 Ala Ala Glu Ile Leu Gly His Lys Arg Gly Asp Lys Phe Val His Pro
 145 150 155 160
 Asn Asp His Val Asn Arg Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr
 165 170 175
 Val Met His Ile Ala Ala Ala Thr Glu Ile Asn Ser Arg Leu Ile Pro
 180 185 190
 Lys Leu Lys Gln Leu His Thr Ala Leu Gln Ala Lys Thr Asn Glu Phe
 195 200 205
 Ser Asp Ile Val Lys Ile Gly Arg Thr His Thr Gln Asp Ala Thr Pro
 210 215 220
 Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Thr Thr Gln Val Lys Tyr
 225 230 235 240
 Gly Ile Asp Arg Val Met Cys Thr Leu Pro Arg Leu Tyr Gln Leu Ala
 245 250 255
 Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn Thr Lys Lys Gly Phe
 260 265 270
 Asp Val Lys Ile Ala Ala Ala Val Ala Asp Glu Thr Arg Leu Pro Phe
 275 280 285
 Ile Thr Ala Glu Asn Lys Phe Glu Ala Leu Ala Ala His Asp Ala Phe
 290 295 300
 Val Glu Ala Ser Gly Ala Leu Asn Thr Ile Ala Thr Ser Leu Met Lys
 305 310 315 320
 Ile Ala Asn Asp Ile Arg Phe Leu Gly Ser Gly Pro Arg Cys Gly Leu
 325 330 335
 Gly Glu Leu Ile Leu Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro
 340 345 350
 Gly Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Thr Met Val Cys Ala
 355 360 365
 Gln Ala Ile Gly Asn His Val Ala Leu Thr Val Gly Gly Ser Asn Gly
 370 375 380
 His Phe Glu Leu Asn Val Phe Lys Pro Met Ile Ala Ser Thr Leu Leu
 385 390 395 400
 His Ser Ile Arg Leu Leu Ala Asp Ala Ser Ala Ser Phe Glu Lys Asn
 405 410 415
 Cys Val Ser Gly Ile Gln Ala Asn Arg Glu Arg Ile Ser Lys Leu Leu
 420 425 430
 His Glu Ser Leu Met Leu Val Thr Ser Leu Asn Pro Lys Ile Gly Tyr
 435 440 445
 Asp Asn Ala Ala Ala Val Ala Lys Thr Ala His Lys Gln Gly Cys Thr
 450 455 460
 Leu Lys Glu Ala Ala Leu Lys Leu Gly Val Leu Asn Ser Glu Glu Phe
 465 470 475 480
 Asp Gln Leu Val Val Pro Glu Lys Met Ile Gly Pro Ser Asp
 485 490

<210> 10070

<211> 741

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(741)

<400> 10070

PF59083SeqList PF59083.txt

atg	gca	tct	aat	caa	cct	ggc	aag	tgt	tgc	ttt	gaa	gga	gtt	tgt	cac	48
Met	Ala	Ser	Asn	Gln	Pro	Gly	Lys	Cys	Cys	Phe	Glu	Gly	Val	Cys	His	
1				5				10					15			
gat	gga	aca	ccc	aag	ggt	cgt	cgt	gaa	gaa	atc	ttc	ggt	tta	gat	act	96
Asp	Gly	Thr	Pro	Lys	Gly	Arg	Arg	Glu	Glu	Ile	Phe	Gly	Leu	Asp	Thr	
			20					25					30			
tat	gca	gca	ggc	tct	aca	tct	ccc	aag	gaa	aaa	gtt	ata	gtt	atc	ttg	144
Tyr	Ala	Ala	Gly	Ser	Thr	Ser	Pro	Lys	Glu	Lys	Val	Ile	Val	Ile	Leu	
			35				40				45					
aca	gat	gtg	tat	ggc	aat	aaa	ttc	aac	aat	gtt	tta	tta	acg	gcc	gac	192
Thr	Asp	Val	Tyr	Gly	Asn	Lys	Phe	Asn	Asn	Val	Leu	Leu	Thr	Ala	Asp	
			50			55					60					
aaa	ttt	gct	agt	gct	ggg	tac	atg	gtc	ttt	gtt	ccc	gat	att	tta	ttc	240
Lys	Phe	Ala	Ser	Ala	Gly	Tyr	Met	Val	Phe	Val	Pro	Asp	Ile	Leu	Phe	
					70					75					80	
ggc	gat	gct	atc	tca	tcg	gac	aaa	cca	att	gat	cgt	gat	gcc	tggt	ttt	288
Gly	Asp	Ala	Ile	Ser	Ser	Asp	Lys	Pro	Ile	Asp	Arg	Asp	Ala	Trp	Phe	
				85					90					95		
caa	aga	cat	tct	cct	gaa	gtc	acc	aag	aaa	att	gtt	gat	gga	ttc	atg	336
Gln	Arg	His	Ser	Pro	Glu	Val	Thr	Lys	Lys	Ile	Val	Asp	Gly	Phe	Met	
			100					105					110			
aag	ttg	tta	aaa	ctt	gaa	tat	gac	cca	aag	ttt	att	ggc	gtt	gtg	ggt	384
Lys	Leu	Leu	Lys	Leu	Glu	Tyr	Asp	Pro	Lys	Phe	Ile	Gly	Val	Val	Gly	
			115				120					125				
tac	tgt	ttt	ggg	gca	aag	ttt	gcc	gtc	caa	cac	att	agt	ggc	gac	ggg	432
Tyr	Cys	Phe	Gly	Ala	Lys	Phe	Ala	Val	Gln	His	Ile	Ser	Gly	Asp	Gly	
			130			135					140					
ggg	ctt	gcc	aat	gct	gca	gcc	att	gca	cat	cca	tct	ttc	gtc	agc	atc	480
Gly	Leu	Ala	Asn	Ala	Ala	Ala	Ile	Ala	His	Pro	Ser	Phe	Val	Ser	Ile	
				150						155					160	
gag	gaa	att	gaa	gca	att	gat	agc	aag	aaa	cca	ata	ttg	att	tca	gca	528
Glu	Glu	Ile	Glu	Ala	Ile	Asp	Ser	Lys	Lys	Pro	Ile	Leu	Ile	Ser	Ala	
				165					170					175		
gcg	gaa	gag	gat	cac	atc	ttt	ccg	gca	aac	tta	aga	cac	tta	acg	gag	576
Ala	Glu	Glu	Asp	His	Ile	Phe	Pro	Ala	Asn	Leu	Arg	His	Leu	Thr	Glu	
			180					185					190			
gaa	aaa	tta	aag	gat	aat	cac	gct	act	tac	cag	tta	gac	ctc	ttc	agt	624
Glu	Lys	Leu	Lys	Asp	Asn	His	Ala	Thr	Tyr	Gln	Leu	Asp	Leu	Phe	Ser	
			195				200					205				
ggg	gtg	gct	cac	ggg	ttt	gca	aga	ggc	gat	ata	tcc	ata	cct	gcc		672
Gly	Val	Ala	His	Gly	Phe	Ala	Ala	Arg	Gly	Asp	Ile	Ser	Ile	Pro	Ala	
						215				220						
gta	aaa	tat	gcg	aag	gag	aaa	gtc	ttg	ctc	gac	caa	ata	tac	tggt	ttc	720
Val	Lys	Tyr	Ala	Lys	Glu	Lys	Val	Leu	Leu	Asp	Gln	Ile	Tyr	Trp	Phe	
					230					235					240	
aat	cat	ttt	tcg	aat	gtt	taa										741
Asn	His	Phe	Ser	Asn	Val											
				245												

<210> 10071

<211> 246

<212> PRT

<213> Saccharomyces cerevisiae

<400> 10071

Met	Ala	Ser	Asn	Gln	Pro	Gly	Lys	Cys	Cys	Phe	Glu	Gly	Val	Cys	His
1				5					10					15	
Asp	Gly	Thr	Pro	Lys	Gly	Arg	Arg	Glu	Glu	Ile	Phe	Gly	Leu	Asp	Thr
			20					25					30		
Tyr	Ala	Ala	Gly	Ser	Thr	Ser	Pro	Lys	Glu	Lys	Val	Ile	Val	Ile	Leu
			35				40					45			
Thr	Asp	Val	Tyr	Gly	Asn	Lys	Phe	Asn	Asn	Val	Leu	Leu	Thr	Ala	Asp
			50			55					60				
Lys	Phe	Ala	Ser	Ala	Gly	Tyr	Met	Val	Phe	Val	Pro	Asp	Ile	Leu	Phe
					70					75					80
Gly	Asp	Ala	Ile	Ser	Ser	Asp	Lys	Pro	Ile	Asp	Arg	Asp	Ala	Trp	Phe
				85					90					95	
Gln	Arg	His	Ser	Pro	Glu	Val	Thr	Lys	Lys	Ile	Val	Asp	Gly	Phe	Met
			100					105					110		

PF59083SeqList PF59083.txt

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

<210> 10072
 <211> 720
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(720)

<400> 10072

atg	tcg	gga	cct	cag	tgc	tgc	gaa	aac	ccg	ccg	gct	ctt	aac	ccg	gtc	48
Met	Ser	Gly	Pro	Gln	Cys	Cys	Glu	Asn	Pro	Pro	Ala	Leu	Asn	Pro	Val	
1				5					10					15		
tcc	ggg	tcg	ggt	cat	gtg	gag	aag	ctg	ggt	ggg	ctc	gat	gct	tac	gtc	96
Ser	Gly	Ser	Gly	His	Val	Glu	Lys	Leu	Gly	Gly	Leu	Asp	Ala	Tyr	Val	
			20					25					30			
tct	ggc	tct	ctt	gat	tcc	aag	ttg	tgc	gtc	atc	ctc	atc	tct	gat	gtt	144
Ser	Gly	Ser	Leu	Asp	Ser	Lys	Leu	Cys	Val	Ile	Leu	Ile	Ser	Asp	Val	
		35				40				45						
ttt	ggg	tat	gaa	gct	cca	aac	ttg	agg	gcg	ctt	gcg	gat	aag	gtt	gga	192
Phe	Gly	Tyr	Glu	Ala	Pro	Asn	Leu	Arg	Ala	Leu	Ala	Asp	Lys	Val	Gly	
	50					55				60						
gct	tct	gga	ttc	tat	gtt	gtg	gtt	cct	gat	tac	ttc	tat	gga	gat	cct	240
Ala	Ser	Gly	Phe	Tyr	Val	Val	Val	Pro	Asp	Tyr	Phe	Tyr	Gly	Asp	Pro	
65				70					75					80		
ttt	gat	gcc	tct	aat	cag	gag	aga	ccc	atc	tct	ctc	tgg	atc	aaa	gac	288
Phe	Asp	Ala	Ser	Asn	Gln	Glu	Arg	Pro	Ile	Ser	Leu	Trp	Ile	Lys	Asp	
				85				90						95		
cat	ggc	gct	gat	aag	gga	ttt	gaa	gac	aca	aag	cca	gta	att	gaa	gcc	336
His	Gly	Ala	Asp	Lys	Gly	Phe	Glu	Asp	Thr	Lys	Pro	Val	Ile	Glu	Ala	
			100					105					110			
ata	aag	acc	aaa	ggc	ata	act	gct	att	gga	gct	gca	ggg	atg	tgt	tgg	384
Ile	Lys	Thr	Lys	Gly	Ile	Thr	Ala	Ile	Gly	Ala	Ala	Gly	Met	Cys	Trp	
		115				120						125				
ggt	gca	aaa	gtg	gtg	gtg	gaa	ttg	tct	aag	caa	gag	ctt	gtt	caa	gca	432
Gly	Ala	Lys	Val	Val	Val	Glu	Leu	Ser	Lys	Gln	Glu	Leu	Val	Gln	Ala	
	130					135				140						
gat	gtt	ttg	ctt	cat	cct	tct	ttt	gtc	acg	gtc	gat	gat	atc	aag	ggt	480
Asp	Val	Leu	Leu	His	Pro	Ser	Phe	Val	Thr	Val	Asp	Asp	Ile	Lys	Gly	
145					150				155						160	
ggg	aag	gta	cca	att	gct	ata	cta	gga	gct	gag	att	gat	cag	gtg	tct	528
Gly	Lys	Val	Pro	Ile	Ala	Ile	Leu	Gly	Ala	Glu	Ile	Asp	Gln	Val	Ser	
			165					170						175		
cca	cca	gca	ctc	ttg	aag	caa	ttt	gag	gag	att	ctt	gct	tcc	aaa	cct	576
Pro	Pro	Ala	Leu	Leu	Lys	Gln	Phe	Glu	Glu	Ile	Leu	Ala	Ser	Lys	Pro	
			180					185					190			
gag	gtg	aat	agt	tat	gtg	aag	ata	tac	ccg	aaa	gtg	gca	cac	ggt	tgg	624
Glu	Val	Asn	Ser	Tyr	Val	Lys	Ile	Tyr	Pro	Lys	Val	Ala	His	Gly	Trp	
		195				200						205				
aca	gtt	agg	tac	aag	acg	gat	gac	cca	gac	gcg	gtt	aaa	gct	gca	gaa	672

PF59083SeqList PF59083.txt

Thr	Val	Arg	Tyr	Lys	Thr	Asp	Asp	Pro	Asp	Ala	Val	Lys	Ala	Ala	Glu		
210						215					220						
gaa	gcg	cac	aag	gag	atg	ctt	gat	tgg	ttt	gtg	act	tac	ggt	aag	tga		720
Glu	Ala	His	Lys	Glu	Met	Leu	Asp	Trp	Phe	Val	Thr	Tyr	Val	Lys			
225					230					235							

<210> 10073
 <211> 239
 <212> PRT
 <213> Brassica napus

<400> 10073

Met	Ser	Gly	Pro	Gln	Cys	Cys	Glu	Asn	Pro	Pro	Ala	Leu	Asn	Pro	Val		
1				5					10					15			
Ser	Gly	Ser	Gly	His	Val	Glu	Lys	Leu	Gly	Gly	Leu	Asp	Ala	Tyr	Val		
			20					25					30				
Ser	Gly	Ser	Leu	Asp	Ser	Lys	Leu	Cys	Val	Ile	Leu	Ile	Ser	Asp	Val		
			35				40					45					
Phe	Gly	Tyr	Glu	Ala	Pro	Asn	Leu	Arg	Ala	Leu	Ala	Asp	Lys	Val	Gly		
	50					55					60						
Ala	Ser	Gly	Phe	Tyr	Val	Val	Val	Pro	Asp	Tyr	Phe	Tyr	Gly	Asp	Pro		
65					70					75					80		
Phe	Asp	Ala	Ser	Asn	Gln	Glu	Arg	Pro	Ile	Ser	Leu	Trp	Ile	Lys	Asp		
				85					90					95			
His	Gly	Ala	Asp	Lys	Gly	Phe	Glu	Asp	Thr	Lys	Pro	Val	Ile	Glu	Ala		
			100					105					110				
Ile	Lys	Thr	Lys	Gly	Ile	Thr	Ala	Ile	Gly	Ala	Ala	Gly	Met	Cys	Trp		
			115				120					125					
Gly	Ala	Lys	Val	Val	Val	Glu	Leu	Ser	Lys	Gln	Glu	Leu	Val	Gln	Ala		
	130					135					140						
Asp	Val	Leu	Leu	His	Pro	Ser	Phe	Val	Thr	Val	Asp	Ile	Lys	Gly			
145					150					155				160			
Gly	Lys	Val	Pro	Ile	Ala	Ile	Leu	Gly	Ala	Glu	Ile	Asp	Gln	Val	Ser		
				165					170					175			
Pro	Pro	Ala	Leu	Lys	Gln	Phe	Glu	Glu	Ile	Leu	Ala	Ser	Lys	Pro			
			180				185						190				
Glu	Val	Asn	Ser	Tyr	Val	Lys	Ile	Tyr	Pro	Lys	Val	Ala	His	Gly	Trp		
		195					200					205					
Thr	Val	Arg	Tyr	Lys	Thr	Asp	Asp	Pro	Asp	Ala	Val	Lys	Ala	Ala	Glu		
					215						220						
Glu	Ala	His	Lys	Glu	Met	Leu	Asp	Trp	Phe	Val	Thr	Tyr	Val	Lys			
225					230					235							

<210> 10074
 <211> 720
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(720)

<400> 10074

atg	tca	ggg	cct	tgc	tgt	tca	aat	cca	ccc	agc	ctg	aac	ccc	agt			48
Met	Ser	Gly	Pro	Gln	Cys	Cys	Ser	Asn	Pro	Pro	Ser	Leu	Asn	Pro	Ser		
1				5				10					15				
gga	gga	ggt	ggg	cat	gtc	aat	aaa	gtg	ggt	ggt	gtc	gat	tcc	tat	ttc		96
Gly	Gly	Gly	Gly	His	Val	Asn	Lys	Val	Gly	Gly	Val	Asp	Ser	Tyr	Phe		
			20					25					30				
agt	ggc	tct	tct	cac	tct	aaa	ctc	gcc	ctt	ctt	atg	ctc	tcc	gat	gtc		144
Ser	Gly	Ser	Ser	His	Ser	Lys	Leu	Ala	Leu	Leu	Met	Leu	Ser	Asp	Val		
			35				40					45					
ttt	ggt	tat	gaa	gca	cca	aat	tta	agg	aag	ctt	gct	gac	aaa	gtt	gca		192
Phe	Gly	Tyr	Glu	Ala	Pro	Asn	Leu	Arg	Lys	Leu	Ala	Asp	Lys	Val	Ala		
			50			55					60						
gct	gct	ggg	tat	tat	gtg	gtt	gtt	ccc	gac	ctc	ttg	gat	ggt	gaa	ccc		240
Ala	Ala	Gly	Tyr	Tyr	Val	Val	Val	Pro	Asp	Leu	Leu	Asp	Gly	Glu	Pro		
					70					75					80		
ttt	aat	tat	cag	aat	tct	aac	aga	ccc	tta	cct	gtg	tgg	cta	aaa	gat		288

PF59083SeqList PF59083.txt

Phe	Asn	Tyr	Gln	Asn	Ser	Asn	Arg	Pro	Leu	Pro	Val	Trp	Leu	Lys	Asp	
				85					90					95		
cat	gga	ccg	gac	aaa	ggt	tct	gaa	gct	aca	aaa	ccc	ata	att	gag	gcc	336
His	Gly	Pro	Asp	Lys	Gly	Ser	Glu	Ala	Thr	Lys	Pro	Ile	Ile	Glu	Ala	
			100					105					110			
ttg	aaa	agt	aaa	ggt	ggt	tct	ggt	att	gcc	gct	ggt	ggt	ttt	tgt	tg	384
Leu	Lys	Ser	Lys	Gly	Val	Ser	Val	Ile	Ala	Ala	Val	Gly	Phe	Cys	Trp	
		115					120					125				
ggt	gca	aag	ggt	gtg	ggt	gaa	ctt	gta	aag	tcc	aaa	ctt	ata	caa	act	432
Gly	Ala	Lys	Val	Val	Val	Glu	Leu	Val	Lys	Ser	Lys	Leu	Ile	Gln	Thr	
	130					135					140					
gct	gtg	cta	atg	cat	cca	tcg	ttt	gtc	tct	ctg	gac	gac	atc	aag	gct	480
Ala	Val	Leu	Met	His	Pro	Ser	Phe	Val	Ser	Leu	Asp	Asp	Ile	Lys	Ala	
	145				150				155						160	
ggt	gat	att	cca	att	gct	ata	ctc	gga	gct	gag	att	gac	caa	tat	tct	528
Val	Asp	Ile	Pro	Ile	Ala	Ile	Leu	Gly	Ala	Glu	Ile	Asp	Gln	Tyr	Ser	
				165				170						175		
cct	ccc	gag	ctt	gtg	aaa	caa	ttt	gaa	caa	gtc	cta	gct	gct	aaa	gct	576
Pro	Pro	Glu	Leu	Val	Lys	Gln	Phe	Glu	Gln	Val	Leu	Ala	Ala	Lys	Ala	
			180					185					190			
ggg	ggt	gct	agt	ttt	ggt	aaa	ata	ttt	ccc	aaa	att	tca	cac	ggt	tg	624
Gly	Val	Ala	Ser	Phe	Val	Lys	Ile	Phe	Pro	Lys	Ile	Ser	His	Gly	Trp	
		195					200				205					
gct	gtg	aga	tac	aac	gct	gaa	gat	gca	gaa	gct	gtg	aag	ggt	gca	gag	672
Ala	Val	Arg	Tyr	Asn	Ala	Glu	Asp	Ala	Glu	Ala	Val	Lys	Val	Ala	Glu	
	210					215					220					
gag	gct	cac	cgg	gac	atg	ttg	gac	tg	ctt	gct	aaa	cat	cac	aag	tga	720
Glu	Ala	His	Arg	Asp	Met	Leu	Asp	Trp	Leu	Ala	Lys	His	His	Lys		
	225				230					235						

<210> 10075
 <211> 239
 <212> PRT
 <213> Glycine max

<400> 10075																
Met	Ser	Gly	Pro	Gln	Cys	Cys	Ser	Asn	Pro	Pro	Ser	Leu	Asn	Pro	Ser	
1				5					10					15		
Gly	Gly	Gly	Gly	His	Val	Asn	Lys	Val	Gly	Gly	Val	Asp	Ser	Tyr	Phe	
			20					25					30			
Ser	Gly	Ser	Ser	His	Ser	Lys	Leu	Ala	Leu	Leu	Met	Leu	Ser	Asp	Val	
		35				40						45				
Phe	Gly	Tyr	Glu	Ala	Pro	Asn	Leu	Arg	Lys	Leu	Ala	Asp	Lys	Val	Ala	
	50					55					60					
Ala	Ala	Gly	Tyr	Tyr	Val	Val	Val	Pro	Asp	Leu	Leu	Asp	Gly	Glu	Pro	
65					70					75					80	
Phe	Asn	Tyr	Gln	Asn	Ser	Asn	Arg	Pro	Leu	Pro	Val	Trp	Leu	Lys	Asp	
				85					90					95		
His	Gly	Pro	Asp	Lys	Gly	Ser	Glu	Ala	Thr	Lys	Pro	Ile	Ile	Glu	Ala	
		100						105					110			
Leu	Lys	Ser	Lys	Gly	Val	Ser	Val	Ile	Ala	Ala	Val	Gly	Phe	Cys	Trp	
		115					120					125				
Gly	Ala	Lys	Val	Val	Val	Glu	Leu	Val	Lys	Ser	Lys	Leu	Ile	Gln	Thr	
	130					135					140					
Ala	Val	Leu	Met	His	Pro	Ser	Phe	Val	Ser	Leu	Asp	Asp	Ile	Lys	Ala	
145					150				155						160	
Val	Asp	Ile	Pro	Ile	Ala	Ile	Leu	Gly	Ala	Glu	Ile	Asp	Gln	Tyr	Ser	
				165				170						175		
Pro	Pro	Glu	Leu	Val	Lys	Gln	Phe	Glu	Gln	Val	Leu	Ala	Ala	Lys	Ala	
		180						185					190			
Gly	Val	Ala	Ser	Phe	Val	Lys	Ile	Phe	Pro	Lys	Ile	Ser	His	Gly	Trp	
		195					200					205				
Ala	Val	Arg	Tyr	Asn	Ala	Glu	Asp	Ala	Glu	Ala	Val	Lys	Val	Ala	Glu	
	210					215					220					
Glu	Ala	His	Arg	Asp	Met	Leu	Asp	Trp	Leu	Ala	Lys	His	His	Lys		
	225				230					235						

<210> 10076
 <211> 1017

PF59083SeqList PF59083.txt

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(1017)

<400> 10076

atg	aat	agc	gta	aaa	aga	gta	aag	cta	aat	tca	aaa	atg	tcc	aaa	caa	48
Met	Asn	Ser	Val	Lys	Arg	Val	Lys	Leu	Asn	Ser	Lys	Met	Ser	Lys	Gln	
1				5					10					15		
ata	tgc	acg	cat	tcc	gga	tct	ttt	cac	gcg	gac	gag	tcg	ttg	gcg	gta	96
Ile	Cys	Thr	His	Ser	Gly	Ser	Phe	His	Ala	Asp	Glu	Ser	Leu	Ala	Val	
			20					25					30			
tac	atg	tta	agg	cta	cta	ccc	gaa	ttt	aaa	gat	gct	aag	ttg	gtt	aga	144
Tyr	Met	Leu	Arg	Leu	Leu	Pro	Glu	Phe	Lys	Asp	Ala	Lys	Leu	Val	Arg	
		35					40					45				
tca	aga	aat	ccc	aag	gac	tgg	gag	gct	agt	gac	att	cta	gtg	gat	gta	192
Ser	Arg	Asn	Pro	Lys	Asp	Trp	Glu	Ala	Ser	Asp	Ile	Leu	Val	Asp	Val	
		50				55					60					
gga	gct	cag	tat	gac	ggc	gtg	aaa	ttt	ttt	gac	cac	cag	cgt	gga		240
Gly	Ala	Gln	Tyr	Asp	Gly	Val	Lys	Phe	Phe	Asp	His	His	Gln	Arg	Gly	
65				70					75					80		
ttt	ttc	gaa	act	ttc	aac	gag	aaa	tac	aag	act	aag	ctc	tca	agt	gct	288
Phe	Phe	Glu	Thr	Phe	Asn	Glu	Lys	Tyr	Lys	Thr	Lys	Leu	Ser	Ser	Ala	
				85					90					95		
ggg	ctg	atc	ttc	aaa	cac	tac	ggg	cgt	gac	att	atc	aaa	aca	att	ttg	336
Gly	Leu	Ile	Phe	Lys	His	Tyr	Gly	Arg	Asp	Ile	Ile	Lys	Thr	Ile	Leu	
			100				105					110				
aac	aac	aag	ggt	agc	agc	tct	gat	tta	gat	ctg	ctc	tat	gac	aag	gta	384
Asn	Asn	Lys	Val	Ser	Ser	Ser	Asp	Leu	Asp	Leu	Leu	Tyr	Asp	Lys	Val	
		115					120					125				
tac	aaa	caa	ttt	gtc	gag	gca	ctg	gat	gca	aac	gac	aac	ggt	att	agc	432
Tyr	Lys	Gln	Phe	Val	Glu	Ala	Leu	Asp	Ala	Asn	Asp	Asn	Gly	Ile	Ser	
	130				135				140							
aag	tac	acg	att	cct	aag	gat	tcc	aac	ttg	gaa	ccg	aat	ttc	agg	gat	480
Lys	Tyr	Thr	Ile	Pro	Lys	Asp	Ser	Asn	Leu	Glu	Pro	Asn	Phe	Arg	Asp	
145				150					155					160		
aac	gcc	atc	agc	att	ccc	ggg	att	att	tca	ggg	atg	aat	cct	aac	tgg	528
Asn	Ala	Ile	Ser	Ile	Pro	Gly	Ile	Ile	Ser	Gly	Met	Asn	Pro	Asn	Trp	
				165					170					175		
aac	gaa	gac	act	tcc	gat	gag	tct	ttt	gac	aga	tgc	ttt	gct	cgc	gca	576
Asn	Glu	Asp	Thr	Ser	Asp	Glu	Ser	Phe	Asp	Arg	Cys	Phe	Ala	Arg	Ala	
			180				185					190				
agt	gag	ttt	atc	ggg	ggg	gtc	ttt	gtc	aca	ttg	gta	aga	ggc	tac	ggg	624
Ser	Glu	Phe	Ile	Gly	Gly	Val	Phe	Val	Thr	Leu	Val	Arg	Gly	Tyr	Gly	
		195				200						205				
caa	tcg	tgg	ttg	cca	gcc	aag	gcc	ctt	gtg	gcg	caa	gcc	att	gat	gaa	672
Gln	Ser	Trp	Leu	Pro	Ala	Lys	Ala	Leu	Val	Ala	Gln	Ala	Ile	Asp	Glu	
	210				215						220					
aga	atg	gat	ggt	gat	aag	agt	ggc	aaa	atc	att	gtc	ttg	ccc	caa	ttc	720
Arg	Met	Asp	Val	Asp	Lys	Ser	Gly	Lys	Ile	Ile	Val	Leu	Pro	Gln	Phe	
225				230					235					240		
tgt	cca	tgg	aag	gag	cat	cta	tac	gag	ctg	gaa	aga	gag	aag	aac	att	768
Cys	Pro	Trp	Lys	Glu	His	Leu	Tyr	Glu	Leu	Glu	Arg	Glu	Lys	Asn	Ile	
				245				250						255		
gaa	aag	caa	atc	gag	ttt	gtt	ctc	ttc	aca	gac	tct	tct	ggg	gcc	tgg	816
Glu	Lys	Gln	Ile	Glu	Phe	Val	Leu	Phe	Thr	Asp	Ser	Ser	Gly	Ala	Trp	
		260					265						270			
agg	gta	tct	act	gta	cca	atc	aac	tcc	acc	tcc	ttc	cag	ttt	agg	aga	864
Arg	Val	Ser	Thr	Val	Pro	Ile	Asn	Ser	Thr	Ser	Phe	Gln	Phe	Arg	Arg	
		275				280						285				
ggg	ttg	ccg	gag	cca	tta	aga	ggc	ctc	aga	gac	gaa	gag	ctg	agc	acc	912
Gly	Leu	Pro	Glu	Pro	Leu	Arg	Gly	Leu	Arg	Asp	Glu	Glu	Leu	Ser	Thr	
	290				295						300					
aag	agc	ggg	gtg	cca	gga	tgt	atc	ttc	att	cat	gca	gca	ggg	ttc	att	960
Lys	Ser	Gly	Val	Pro	Gly	Cys	Ile	Phe	Ile	His	Ala	Ala	Gly	Phe	Ile	
305				310					315					320		
gga	ggg	gcc	aag	tcc	aaa	gag	gct	gta	tat	gag	ctg	gct	aag	atg	tct	1008

PF59083SeqList PF59083.txt

Gly Gly Ala Lys Ser Lys Glu Ala Val Tyr Glu Leu Ala Lys Met Ser
 325 330 335
 ttg gcc tag
 Leu Ala

1017

<210> 10077
 <211> 338
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 10077
 Met Asn Ser Val Lys Arg Val Lys Leu Asn Ser Lys Met Ser Lys Gln
 1 5 10 15
 Ile Cys Thr His Ser Gly Ser Phe His Ala Asp Glu Ser Leu Ala Val
 20 25 30
 Tyr Met Leu Arg Leu Leu Pro Glu Phe Lys Asp Ala Lys Leu Val Arg
 35 40 45
 Ser Arg Asn Pro Lys Asp Trp Glu Ala Ser Asp Ile Leu Val Asp Val
 50 55 60
 Gly Ala Gln Tyr Asp Gly Val Lys Phe Phe Asp His His Gln Arg Gly
 65 70 75 80
 Phe Phe Glu Thr Phe Asn Glu Lys Tyr Lys Thr Lys Leu Ser Ser Ala
 85 90 95
 Gly Leu Ile Phe Lys His Tyr Gly Arg Asp Ile Ile Lys Thr Ile Leu
 100 105 110
 Asn Asn Lys Val Ser Ser Ser Asp Leu Asp Leu Leu Tyr Asp Lys Val
 115 120 125
 Tyr Lys Gln Phe Val Glu Ala Leu Asp Ala Asn Asp Asn Gly Ile Ser
 130 135 140
 Lys Tyr Thr Ile Pro Lys Asp Ser Asn Leu Glu Pro Asn Phe Arg Asp
 145 150 155 160
 Asn Ala Ile Ser Ile Pro Gly Ile Ile Ser Gly Met Asn Pro Asn Trp
 165 170 175
 Asn Glu Asp Thr Ser Asp Glu Ser Phe Asp Arg Cys Phe Ala Arg Ala
 180 185 190
 Ser Glu Phe Ile Gly Gly Val Phe Val Thr Leu Val Arg Gly Tyr Gly
 195 200 205
 Gln Ser Trp Leu Pro Ala Lys Ala Leu Val Ala Gln Ala Ile Asp Glu
 210 215 220
 Arg Met Asp Val Asp Lys Ser Gly Lys Ile Ile Val Leu Pro Gln Phe
 225 230 235 240
 Cys Pro Trp Lys Glu His Leu Tyr Glu Leu Glu Arg Glu Lys Asn Ile
 245 250 255
 Glu Lys Gln Ile Glu Phe Val Leu Phe Thr Asp Ser Ser Gly Ala Trp
 260 265 270
 Arg Val Ser Thr Val Pro Ile Asn Ser Thr Ser Phe Gln Phe Arg Arg
 275 280 285
 Gly Leu Pro Glu Pro Leu Arg Gly Leu Arg Asp Glu Glu Leu Ser Thr
 290 295 300
 Lys Ser Gly Val Pro Gly Cys Ile Phe Ile His Ala Ala Gly Phe Ile
 305 310 315 320
 Gly Gly Ala Lys Ser Lys Glu Ala Val Tyr Glu Leu Ala Lys Met Ser
 325 330 335
 Leu Ala

<210> 10078
 <211> 1155
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(1155)

<400> 10078
 atg ctc gcc gcc tgc gcc tgg agg ctg tcc cag cga gcc gtc acg ttc
 Met Leu Ala Ala Cys Ala Trp Arg Leu Ser Gln Arg Ala Val Thr Phe
 Seite 10662

48

PF59083SeqList PF59083.txt

1	5	10	15	
ctt Leu	ccc Pro	cg Arg	gtg Val	96
gcc Ala	gcc Ala	ggc Ala	gcc Ala	144
gcc Ala	ggc Gly	gac Asp	gcc Ala	192
ggg Gly	acc Thr	cac His	aac Asn	240
ctc Leu	atc Ile	cg Arg	ctc Leu	288
cg Arg	gac Asp	tcc Ser	cag Gln	336
ggt Gly	gtc Val	tat Tyr	gat Asp	384
ttc Phe	aac Asn	gag Glu	gtc Val	432
ggg Gly	ctt Leu	gtt Val	tac Tyr	480
cag Gln	ctt Leu	aat Asn	gag Glu	528
tac Tyr	aaa Lys	agc Ser	ttt Phe	576
caa Gln	tat Tyr	gac Asp	acg Thr	624
tct Ser	tca Ser	cg Arg	ggt Gly	672
tca Ser	cct Pro	gag Glu	aag Lys	720
gga Gly	agt Ser	gag Glu	ttt Met	768
cct Pro	gca Ala	aga Arg	tct Ser	816
gat Asp	cca Pro	agt Ser	gga Glu	864
ctt Leu	cat His	cta Leu	gag Glu	912
aag Lys	tat Tyr	gtg Val	ctg Leu	960
gcc Ala	gtc Val	tct Ser	ggt Val	1008
gag Glu	aag Lys	tgg Trp	agg Arg	1056
atc Ile	cct Pro	ggc Gly	tgt Cys	1104
aag Lys	acc Thr	tac Tyr	gag Glu	1152

370
taa

375

380

1155

<210> 10079
<211> 384
<212> PRT
<213> Hordeum vulgare

<400> 10079
Met Leu Ala Ala Cys Ala Trp Arg Leu Ser Gln Arg Ala Val Thr Phe
1 5 10 15
Leu Pro Arg Val Arg Pro Gln Ile Leu Asn Pro Phe Pro Met Ala Ala
20 25 30
Ala Ala Gly Ala Ala Ser Pro Lys Arg Leu Arg Val Tyr Ser Ser Ala
35 40 45
Ala Gly Asp Ala Asp Pro Ser Asn Gly Ala Gly Asn Gly Arg Arg Val
50 55 60
Gly Thr His Asn Gly Ser Phe His Cys Asp Glu Ala Leu Gly Cys Phe
65 70 75 80
Leu Ile Arg Leu Thr Ser Gln Phe Ala Gly Ala Asp Val Val Arg Thr
85 90 95
Arg Asp Ser Gln Ile Leu Asp Ser Leu Glu Ala Val Leu Asp Val Gly
100 105 110
Gly Val Tyr Asp Pro Ser Arg His Arg Tyr Asp His His Gln Lys Gly
115 120 125
Phe Asn Glu Val Phe Gly Tyr Gly Phe Asn Thr Lys Leu Ser Ser Ala
130 135 140
Gly Leu Val Tyr Lys His Phe Gly Lys Glu Ile Ile Ala Lys Glu Leu
145 150 155 160
Gln Leu Asn Glu Asp His Glu Asp Val His Arg Val Tyr Leu Ala Ile
165 170 175
Tyr Lys Ser Phe Val Glu Ala Leu Asp Ala Ile Asp Asn Gly Ile Asn
180 185 190
Gln Tyr Asp Thr Glu Gln Thr Pro Lys Tyr Val Asn Asn Thr His Leu
195 200 205
Ser Ser Arg Val Gly Arg Leu Asn Pro Asp Trp Thr Asp Pro Asp Gln
210 215 220
Ser Pro Glu Lys Glu Asn Ala Ala Phe Gln Gln Ala Met Ala Leu Ala
225 230 235 240
Gly Ser Glu Phe Met Glu Ser Val Arg Phe His Val Lys Ser Trp Leu
245 250 255
Pro Ala Arg Ser Ile Val Met Glu Cys Leu Leu Ser Arg Gly Asn Val
260 265 270
Asp Pro Ser Gly Glu Ile Met Val Leu Asp Arg Phe Cys Pro Trp Lys
275 280 285
Leu His Leu Phe Glu Leu Glu Gln Glu Leu Lys Thr Asp Pro Leu Thr
290 295 300
Lys Tyr Val Leu Tyr Glu Asp Glu Arg Ser Lys Gly Trp Arg Val Gln
305 310 315 320
Ala Val Ser Val Ala Pro Asp Arg Phe Glu Ser Arg Lys Ala Leu Pro
325 330 335
Glu Lys Trp Arg Gly Met Arg Asp Asp Glu Leu Ser Lys Glu Thr Gly
340 345 350
Ile Pro Gly Cys Val Phe Ile His Met Ser Gly Phe Ile Gly Gly Asn
355 360 365
Lys Thr Tyr Glu Gly Ala Leu Glu Met Ala Arg Ala Ala Leu Lys Cys
370 375 380

<210> 10080
<211> 735
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (1)..(735)

PF59083SeqList PF59083.txt

```

<400> 10080
atg act gtg gtt gaa ata aaa agc cag gac caa ttt acg caa cta acc      48
Met Thr Val Val Glu Ile Lys Ser Gln Asp Gln Phe Thr Gln Leu Thr
1      5      10      15
act aca aac gct gct aat aaa ctc att gtc tta tat ttt aaa gct caa      96
Thr Thr Asn Ala Asn Lys Leu Ile Val Leu Tyr Phe Lys Ala Gln
20      25      30
tgg gct gat cct tgc aaa act atg agc cag gtg cta gaa gct gtt agt      144
Trp Ala Asp Pro Cys Lys Thr Met Ser Gln Val Leu Glu Ala Val Ser
35      40      45
gaa aaa gtt agg caa gag gat gtc cgg ttt tta tca ata gat gca gac      192
Glu Lys Val Arg Gln Glu Asp Val Arg Phe Leu Ser Ile Asp Ala Asp
50      55      60
gaa cat cca gaa ata tca gac ctt ttt gag att gca gcc gta cca tac      240
Glu His Pro Glu Ile Ser Asp Leu Phe Glu Ile Ala Ala Val Pro Tyr
65      70      75
ttc gtc ttc att caa aat ggt act att gta aaa gaa ata tca gcc gca      288
Phe Val Phe Ile Gln Asn Gly Thr Ile Val Lys Glu Ile Ser Ala Ala
85      90      95
gat cct aag gag gtt gtg aaa agc tta gaa att ctt tcg aat gct tct      336
Asp Pro Lys Glu Phe Val Lys Ser Leu Glu Ile Leu Ser Asn Ala Ser
100      105      110
gcc tca cta gcg aac aat gcc aag ggt cct aaa tct acg tct gat gag      384
Ala Ser Leu Ala Asn Asn Ala Lys Gly Pro Lys Ser Thr Ser Asp Glu
115      120      125
gaa agc agc ggg tct tcc gat gat gaa gag gac gaa act gaa gaa gaa      432
Glu Ser Ser Gly Ser Ser Asp Asp Glu Glu Asp Glu Thr Glu Glu Glu
130      135      140
ata aat gct agg ctg gtg aag cta gta caa gct gca cct gtg atg cta      480
Ile Asn Ala Arg Leu Val Lys Leu Val Gln Ala Ala Pro Val Met Leu
145      150      155
ttc atg aaa gga agc cca tca gaa cct aaa tgc gga ttt tct aga cag      528
Phe Met Lys Gly Ser Pro Ser Glu Pro Lys Cys Gly Phe Ser Arg Gln
165      170      175
tta gtt ggt atc ctc aga gaa cac caa ata agg ttc gga ttt ttt gat      576
Leu Val Gly Ile Leu Arg Glu His Gln Ile Arg Phe Gly Phe Phe Asp
180      185      190
ata tta aga gac gaa aac gtt aga caa agc ttg aag aag ttt tct gat      624
Ile Leu Arg Asp Glu Asn Val Arg Gln Ser Leu Lys Lys Phe Ser Asp
195      200      205
tgg cct act ttt cct cag tta tat atc aat ggg gag ttc cag gga ggt      672
Trp Pro Thr Phe Pro Gln Leu Tyr Ile Asn Gly Glu Phe Gln Gly Gly
210      215      220
ttg gat att atc aag gaa tct ata gaa gaa gat cct gaa tat ttc caa      720
Leu Asp Ile Ile Lys Glu Ser Ile Glu Glu Asp Pro Glu Tyr Phe Gln
225      230      235      240
cat gct cta cag taa
His Ala Leu Gln
735

```

```

<210> 10081
<211> 244
<212> PRT
<213> Saccharomyces cerevisiae

```

```

<400> 10081
Met Thr Val Val Glu Ile Lys Ser Gln Asp Gln Phe Thr Gln Leu Thr
1      5      10      15
Thr Thr Asn Ala Asn Lys Leu Ile Val Leu Tyr Phe Lys Ala Gln
20      25      30
Trp Ala Asp Pro Cys Lys Thr Met Ser Gln Val Leu Glu Ala Val Ser
35      40      45
Glu Lys Val Arg Gln Glu Asp Val Arg Phe Leu Ser Ile Asp Ala Asp
50      55      60
Glu His Pro Glu Ile Ser Asp Leu Phe Glu Ile Ala Ala Val Pro Tyr
65      70      75
Phe Val Phe Ile Gln Asn Gly Thr Ile Val Lys Glu Ile Ser Ala Ala
85      90      95
Asp Pro Lys Glu Phe Val Lys Ser Leu Glu Ile Leu Ser Asn Ala Ser
Seite 10665

```

PF59083SeqList PF59083.txt

```

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

```

<210> 10082
 <211> 1068
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(1068)

```

<400> 10082
atg ggt ggt gcg gtg aag gat atc gct tca aag tct gag ctt gat aac      48
Met Gly Gly Ala Val Lys Asp Ile Ala Ser Lys Ser Glu Leu Asp Asn
      1      5      10      15
ttg cgc cag agc ggc gca cca atc gcg ctt cac ttc tgg gca tcg tgg      96
Leu Arg Gln Ser Gly Ala Pro Ile Ala Leu His Phe Trp Ala Ser Trp
      20      25      30
tgt gat gct tcg aag cag atg gat caa gtc ttc tct cac ctc gct act      144
Cys Asp Ala Ser Lys Gln Met Asp Gln Val Phe Ser His Leu Ala Thr
      35      40      45
gat ttc cct cgc gcc cac ttc agg gta gaa gct gag gaa cat cct      192
Asp Phe Pro Arg Ala His Phe Phe Arg Val Glu Ala Glu Glu His Pro
      50      55      60
gag ata tct gaa gct tac tct gtt tct gct gtt ccc ttt ttc gtc ttc      240
Glu Ile Ser Glu Ala Tyr Ser Val Ser Ala Val Pro Phe Phe Val Phe
      65      70      75
ttc aag gat ggc aaa gct gtg gat acc ctt gaa ggc gca gat cca tcg      288
Phe Lys Asp Gly Lys Ala Val Asp Thr Leu Glu Gly Ala Asp Pro Ser
      80      85      90
agt tta gcc aac aag gtt gcc aaa ata gct ggt tct agt act tct tct      336
Ser Leu Ala Asn Lys Val Ala Lys Ile Ala Gly Ser Ser Thr Ser Ser
      100      105      110
gag cct gct gct ccg gca agc cta ggg tta gct gca ggg cca atg att      384
Glu Pro Ala Ala Pro Ala Ser Leu Gly Leu Ala Ala Gly Pro Met Ile
      115      120      125
ctc gaa acc gtg aag gag aat gcg aaa gct acc gtg aaa gac cga gct      432
Leu Glu Thr Val Lys Glu Asn Ala Lys Ala Thr Val Lys Asp Arg Ala
      130      135      140
cag cct gcg ccc acc act gaa aat ctc aat gac cgt ttg gag aag ctc      480
Gln Pro Ala Pro Thr Thr Glu Asn Leu Asn Asp Arg Leu Glu Lys Leu
      145      150      155
act aac tct cac cct gtc atg ttg ttc atg aaa ggc act cct gaa gag      528
Thr Asn Ser His Pro Val Met Leu Phe Met Lys Gly Thr Pro Glu Glu
      160      165      170
cct agg tgc ggg ttt agc agg caa gta gtg ggc gtt ttg aga gag gag      576
Pro Arg Cys Gly Phe Ser Arg Gln Val Val Gly Val Leu Arg Glu Glu
      175      180      185
aat gtt gat ttc gga agc ttc gat ata ctt tct gac aac gaa gtg cgt      624
Asn Val Asp Phe Gly Ser Phe Asp Ile Leu Ser Asp Asn Glu Val Arg
      190      200      205

```

PF59083SeqList PF59083.txt

gaa	ggt	ctg	aag	aaa	ttc	tca	aac	tgg	cca	acg	ttt	cct	cag	ctg	tac	672
Glu	Gly	Leu	Lys	Lys	Phe	Ser	Asn	Trp	Pro	Thr	Phe	Pro	Gln	Leu	Tyr	
	210					215					220					
tgc	aac	ggg	gag	ctt	cta	gga	gga	tca	gac	att	gtc	ctg	gag	atg	caa	720
Cys	Asn	Gly	Glu	Leu	Leu	Gly	Gly	Ser	Asp	Ile	Val	Leu	Glu	Met	Gln	
225					230					235					240	
aag	agc	ggc	gag	ctg	aga	caa	gtg	ttg	tct	gag	aaa	ggg	aaa	cag	agt	768
Lys	Ser	Gly	Glu	Leu	Arg	Gln	Val	Leu	Ser	Glu	Lys	Gly	Lys	Gln	Ser	
				245				250						255		
ctt	gaa	gat	agg	ttg	aag	acg	ttg	att	aac	tcg	gag	aag	gtt	atg	ctt	816
Leu	Glu	Asp	Arg	Leu	Lys	Thr	Leu	Ile	Asn	Ser	Glu	Lys	Val	Met	Leu	
				260				265					270			
ttc	atg	aaa	ggt	tcg	ccg	gat	gaa	cca	aag	tgt	ggg	ttt	agc	tca	aaa	864
Phe	Met	Lys	Gly	Ser	Pro	Asp	Glu	Pro	Lys	Cys	Gly	Phe	Ser	Ser	Lys	
		275					280					285				
gtg	gtg	aaa	gca	ctt	aga	gat	gag	aat	gtg	aat	ttc	ggg	tcg	ttt	gac	912
Val	Val	Lys	Ala	Leu	Arg	Asp	Glu	Asn	Val	Asn	Phe	Gly	Ser	Phe	Asp	
	290					295					300					
ata	ttg	agt	gat	gaa	gaa	gtg	aga	caa	ggg	ata	aag	agt	ttc	tca	aac	960
Ile	Leu	Ser	Asp	Glu	Glu	Val	Arg	Gln	Gly	Ile	Lys	Ser	Phe	Ser	Asn	
305					310					315					320	
tgg	cct	acg	ttt	cct	cag	ctt	tac	tat	aaa	ggt	gag	tta	gtt	gga	gga	1008
Trp	Pro	Thr	Phe	Pro	Gln	Leu	Tyr	Tyr	Lys	Gly	Glu	Leu	Val	Gly	Gly	
				325					330					335		
tgt	gat	atc	att	atg	gag	ctg	agt	aac	agt	ggt	gac	ctc	gga	gca	aca	1056
Cys	Asp	Ile	Ile	Met	Glu	Leu	Ser	Asn	Ser	Gly	Asp	Leu	Gly	Ala	Thr	
			340					345					350			
cta	tct	gag	taa													1068
Leu	Ser	Glu														
		355														

<210> 10083

<211> 355

<212> PRT

<213> Brassica napus

<400> 10083

Met	Gly	Gly	Ala	Val	Lys	Asp	Ile	Ala	Ser	Lys	Ser	Glu	Leu	Asp	Asn	
1				5					10					15		
Leu	Arg	Gln	Ser	Gly	Ala	Pro	Ile	Ala	Leu	His	Phe	Trp	Ala	Ser	Trp	
			20					25					30			
Cys	Asp	Ala	Ser	Lys	Gln	Met	Asp	Gln	Val	Phe	Ser	His	Leu	Ala	Thr	
		35					40					45				
Asp	Phe	Pro	Arg	Ala	His	Phe	Phe	Arg	Val	Glu	Ala	Glu	Glu	His	Pro	
		50				55				60						
Glu	Ile	Ser	Glu	Ala	Tyr	Ser	Val	Ser	Ala	Val	Pro	Phe	Phe	Val	Phe	
65					70				75						80	
Phe	Lys	Asp	Gly	Lys	Ala	Val	Asp	Thr	Leu	Glu	Gly	Ala	Asp	Pro	Ser	
				85					90					95		
Ser	Leu	Ala	Asn	Lys	Val	Ala	Lys	Ile	Ala	Gly	Ser	Ser	Thr	Ser	Ser	
			100					105					110			
Glu	Pro	Ala	Ala	Pro	Ala	Ser	Leu	Gly	Leu	Ala	Ala	Gly	Pro	Met	Ile	
		115					120					125				
Leu	Glu	Thr	Val	Lys	Glu	Asn	Ala	Lys	Ala	Thr	Val	Lys	Asp	Arg	Ala	
		130				135						140				
Gln	Pro	Ala	Pro	Thr	Thr	Glu	Asn	Leu	Asn	Asp	Arg	Leu	Glu	Lys	Leu	
145					150					155					160	
Thr	Asn	Ser	His	Pro	Val	Met	Leu	Phe	Met	Lys	Gly	Thr	Pro	Glu	Glu	
				165					170					175		
Pro	Arg	Cys	Gly	Phe	Ser	Arg	Gln	Val	Val	Gly	Val	Leu	Arg	Glu	Glu	
			180					185					190			
Asn	Val	Asp	Phe	Gly	Ser	Phe	Asp	Ile	Leu	Ser	Asp	Asn	Glu	Val	Arg	
		195					200					205				
Glu	Gly	Leu	Lys	Lys	Phe	Ser	Asn	Trp	Pro	Thr	Phe	Pro	Gln	Leu	Tyr	
		210					215				220					
Cys	Asn	Gly	Glu	Leu	Leu	Gly	Gly	Ser	Asp	Ile	Val	Leu	Glu	Met	Gln	
225					230					235					240	
Lys	Ser	Gly	Glu	Leu	Arg	Gln	Val	Leu	Ser	Glu	Lys	Gly	Lys	Gln	Ser	
				245					250					255		

PF59083SeqList PF59083.txt

Leu Glu Asp Arg Leu Lys Thr Leu Ile Asn Ser Glu Lys Val Met Leu
 260 265 270
 Phe Met Lys Gly Ser Pro Asp Glu Pro Lys Cys Gly Phe Ser Ser Lys
 275 280 285
 Val Val Lys Ala Leu Arg Asp Glu Asn Val Asn Phe Gly Ser Phe Asp
 290 295 300
 Ile Leu Ser Asp Glu Glu Val Arg Gln Gly Ile Lys Ser Phe Ser Asn
 305 310 315 320
 Trp Pro Thr Phe Pro Gln Leu Tyr Tyr Lys Gly Glu Leu Val Gly Gly
 325 330 335
 Cys Asp Ile Ile Met Glu Leu Ser Asn Ser Gly Asp Leu Gly Ala Thr
 340 345 350
 Leu Ser Glu
 355

<210> 10084
 <211> 360
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>
 <221> CDS
 <222> (1)..(360)

<400> 10084
 atg cca aag aag aga gct tcc aac ggt aga aac aag aaa ggt aga ggt 48
 Met Pro Lys Lys Arg Ala Ser Asn Gly Arg Asn Lys Lys Gly Arg Gly
 1 5 10 15
 cac gtc aaa cca gtc aga tgt gtc aac tgt tcc aag tct att cca aag 96
 His Val Lys Pro Val Arg Cys Val Asn Cys Ser Lys Ser Ile Pro Lys
 20 25 30
 gat aag gct atc aag aga atg gct atc aga aac att gtt gaa gcc gct 144
 Asp Lys Ala Ile Lys Arg Met Ala Ile Arg Asn Ile Val Glu Ala Ala
 35 40 45
 gcc gtc aga gat ttg tcc gaa gct tct gtc tac cct gaa tac gct ttg 192
 Ala Val Arg Asp Leu Ser Glu Ala Ser Val Tyr Pro Glu Tyr Ala Leu
 50 55 60
 cca aag act tac aac aag tta cac tac tgt gtt tct tgt gct att cac 240
 Pro Lys Thr Tyr Asn Lys Leu His Tyr Cys Val Ser Cys Ala Ile His
 65 70 75 80
 gcc aga att gtc aga gtc aga tcc aga gaa gac aga aag aac aga gct 288
 Ala Arg Ile Val Arg Val Arg Ser Arg Glu Asp Arg Lys Asn Arg Ala
 85 90 95
 cca cct caa aga cca aga ttc aac aga gaa aac aag gtt tcc cct gct 336
 Pro Pro Gln Arg Pro Arg Phe Asn Arg Glu Asn Lys Val Ser Pro Ala
 100 105 110
 gat gcc gcc aag aag gct tta taa 360
 Asp Ala Ala Lys Lys Ala Leu
 115

<210> 10085
 <211> 119
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 10085
 Met Pro Lys Lys Arg Ala Ser Asn Gly Arg Asn Lys Lys Gly Arg Gly
 1 5 10 15
 His Val Lys Pro Val Arg Cys Val Asn Cys Ser Lys Ser Ile Pro Lys
 20 25 30
 Asp Lys Ala Ile Lys Arg Met Ala Ile Arg Asn Ile Val Glu Ala Ala
 35 40 45
 Ala Val Arg Asp Leu Ser Glu Ala Ser Val Tyr Pro Glu Tyr Ala Leu
 50 55 60
 Pro Lys Thr Tyr Asn Lys Leu His Tyr Cys Val Ser Cys Ala Ile His
 65 70 75 80
 Ala Arg Ile Val Arg Val Arg Ser Arg Glu Asp Arg Lys Asn Arg Ala
 85 90 95
 Pro Pro Gln Arg Pro Arg Phe Asn Arg Glu Asn Lys Val Ser Pro Ala
 Seite 10668

100
Asp Ala Ala Lys Lys Ala Leu
115

<210> 10086
<211> 408
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(408)

<400> 10086
atg ata cgt caa tgg atg cag act ttc aaa cgc agg aac gga ggg agg 48
Met Ile Arg Gln Trp Met Gln Thr Phe Lys Arg Arg Asn Gly Gly Arg
1 5 10 15
aac aag cac aac cgt ggg cac gtg aag cca atc aga tgc tcc aac tgc 96
Asn Lys His Asn Arg Gly His Val Lys Pro Ile Arg Cys Ser Asn Cys
20 25 30
ggc aaa tgt tgc cca aag gac aag gcc atc aag agg ttt atc gtg agg 144
Gly Lys Cys Cys Pro Lys Asp Lys Ala Ile Lys Arg Phe Ile Val Arg
35 40 45
aac att gtg gag cag gct gct att aga gat gtt cag gaa gct agc gta 192
Asn Ile Val Glu Gln Ala Ala Ile Arg Asp Val Gln Glu Ala Ser Val
50 55 60
tac gat ggg tac aca ttg cct aag ctg tat gct aag acg cag tac tgt 240
Tyr Asp Gly Tyr Thr Leu Pro Lys Leu Tyr Ala Lys Thr Gln Tyr Cys
65 70 75 80
gtc tcc tgt gcg ata cac tct cac gtt gtt aga gtt cgt tcc cgc acc 288
Val Ser Cys Ala Ile His Ser His Val Val Arg Val Arg Ser Arg Thr
85 90 95
aac cgc aga gtt cgt act ccc ccg cct cgt ttt gtt aga cgc aag gag 336
Asn Arg Arg Val Arg Thr Pro Pro Pro Arg Phe Val Arg Arg Lys Glu
100 105 110
gat gct ccc aag cct gga caa cct ggt cag gct cct cgt cct gct gga 384
Asp Ala Pro Lys Pro Gly Gln Pro Gly Gln Ala Pro Arg Pro Ala Gly
115 120 125
gct gca gct gcc ccg cgt gcc tga 408
Ala Ala Ala Pro Arg Ala
130 135

<210> 10087
<211> 135
<212> PRT
<213> Brassica napus

<400> 10087
Met Ile Arg Gln Trp Met Gln Thr Phe Lys Arg Arg Asn Gly Gly Arg
1 5 10 15
Asn Lys His Asn Arg Gly His Val Lys Pro Ile Arg Cys Ser Asn Cys
20 25 30
Gly Lys Cys Cys Pro Lys Asp Lys Ala Ile Lys Arg Phe Ile Val Arg
35 40 45
Asn Ile Val Glu Gln Ala Ala Ile Arg Asp Val Gln Glu Ala Ser Val
50 55 60
Tyr Asp Gly Tyr Thr Leu Pro Lys Leu Tyr Ala Lys Thr Gln Tyr Cys
65 70 75 80
Val Ser Cys Ala Ile His Ser His Val Val Arg Val Arg Ser Arg Thr
85 90 95
Asn Arg Arg Val Arg Thr Pro Pro Pro Arg Phe Val Arg Arg Lys Glu
100 105 110
Asp Ala Pro Lys Pro Gly Gln Pro Gly Gln Ala Pro Arg Pro Ala Gly
115 120 125
Ala Ala Ala Pro Arg Ala
130 135

<210> 10088
<211> 393

PF59083SeqList PF59083.txt

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(393)

<400> 10088

```

atg act ttc aag cgc aga aac ggt ggt agg aac aag cac aac cgt ggt      48
Met Thr Phe Lys Arg Arg Asn Gly Gly Arg Asn Lys His Asn Arg Gly
 1          5          10          15
cat gtg aac cca atc agg tgt tcc aac tgc ggg aaa tgc tgc ccc aag      96
His Val Asn Pro Ile Arg Cys Ser Asn Cys Gly Lys Cys Cys Pro Lys
          20          25          30
gat aag gcg att aag aga ttc ctc gtc agg aac atc gtt gag caa gct     144
Asp Lys Ala Ile Lys Arg Phe Leu Val Arg Asn Ile Val Glu Gln Ala
          35          40          45
gcc atc aga gat gta caa gaa gct agt gtc tac gat ggt tac act cta     192
Ala Ile Arg Asp Val Gln Glu Ala Ser Val Tyr Asp Gly Tyr Thr Leu
          50          55          60
cca aag ttg tac gct aag atg cag tac tgt gtt tca tgt gct atc cac     240
Pro Lys Leu Tyr Ala Lys Met Gln Tyr Cys Val Ser Cys Ala Ile His
          65          70          75          80
tct cac gtt gtg aga gtt cga tcc agc act aac cgt aga gtt cgt acc     288
Ser His Val Val Arg Val Arg Ser Ser Thr Asn Arg Arg Val Arg Thr
          85          90          95
cca ccg ccc cgt ttt gcc aga cgc aag gag gat gcg ccc aag cct gga     336
Pro Pro Pro Arg Phe Ala Arg Arg Lys Glu Asp Ala Pro Lys Pro Gly
          100          105          110
cat cct ggt cag gcc cct cga cct gct ggt ggt gcc cca gct gct cct     384
His Pro Gly Gln Ala Pro Arg Pro Ala Gly Gly Ala Pro Ala Ala Pro
          115          120          125
cgt gcc taa
Arg Ala
130

```

<210> 10089

<211> 130

<212> PRT

<213> Brassica napus

<400> 10089

```

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

```

<210> 10090

<211> 393

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(393)

PF59083SeqList PF59083.txt

```

<400> 10090
atg act ttc aag cgc agg aac gga ggg agg aac aag cac aac cgt ggc      48
Met Thr Phe Lys Arg Arg Asn Gly Gly Arg Asn Lys His Asn Arg Gly
1      5      10      15
cac gtc aag cca atc aga tgc tcc aac tgc ggc aaa tgc tgc ccc aaa      96
His Val Lys Pro Ile Arg Cys Ser Asn Cys Gly Lys Cys Cys Pro Lys
20      25      30
gac aag gcc atc aag agg ttc ata gtg agg aac atc gtg gag cag gct      144
Asp Lys Ala Ile Lys Arg Phe Ile Val Arg Asn Ile Val Glu Gln Ala
35      40      45
gcc att aga gat gtt cag gaa gcc agc gtc tac gat ggg tac acg ttg      192
Ala Ile Arg Asp Val Gln Glu Ala Ser Val Tyr Asp Gly Tyr Thr Leu
50      55      60
cca aag ctg tat gcg aag acg cag tac tgt gtc tcg tgt gct atc cac      240
Pro Lys Leu Tyr Ala Lys Thr Gln Tyr Cys Val Ser Cys Ala Ile His
65      70      75      80
tct cac gtt gtt cgt gtc cgt tcc cgc act aac cgc agg gtt cgt act      288
Ser His Val Val Arg Val Arg Ser Arg Thr Asn Arg Arg Val Arg Thr
85      90      95
ccc cct cca cgt ttc gtc aga cgc aag gag gat gcg ccc aag cct gga      336
Pro Pro Pro Arg Phe Val Arg Arg Lys Glu Asp Ala Pro Lys Pro Gly
100      105      110
caa ctt ggt cag gct cct cgt cct gct gga gct gga gca gct gca ccg      384
Gln Leu Gly Gln Ala Pro Arg Pro Ala Gly Ala Gly Ala Ala Pro
115      120      125
cgt gcc tga
Arg Ala
130

```

```

<210> 10091
<211> 130
<212> PRT
<213> Brassica napus

```

```

<400> 10091
Met Thr Phe Lys Arg Arg Asn Gly Gly Arg Asn Lys His Asn Arg Gly
1      5      10      15
His Val Lys Pro Ile Arg Cys Ser Asn Cys Gly Lys Cys Cys Pro Lys
20      25      30
Asp Lys Ala Ile Lys Arg Phe Ile Val Arg Asn Ile Val Glu Gln Ala
35      40      45
Ala Ile Arg Asp Val Gln Glu Ala Ser Val Tyr Asp Gly Tyr Thr Leu
50      55      60
Pro Lys Leu Tyr Ala Lys Thr Gln Tyr Cys Val Ser Cys Ala Ile His
65      70      75      80
Ser His Val Val Arg Val Arg Ser Arg Thr Asn Arg Arg Val Arg Thr
85      90      95
Pro Pro Pro Arg Phe Val Arg Arg Lys Glu Asp Ala Pro Lys Pro Gly
100      105      110
Gln Leu Gly Gln Ala Pro Arg Pro Ala Gly Ala Gly Ala Ala Pro
115      120      125
Arg Ala
130

```

```

<210> 10092
<211> 1155
<212> DNA
<213> Saccharomyces cerevisiae

```

```

<220>
<221> CDS
<222> (1)..(1155)

```

```

<400> 10092
atg gtt aca tat gct gga aaa ctg gtt cta gct cca atg gta aga gcc      48
Met Val Thr Tyr Ala Gly Lys Leu Val Leu Ala Pro Met Val Arg Ala
1      5      10      15
ggc gaa ctg ccc acg aga ctg atg gcg ctg gcc cac ggt gca gat ctc      96

```

PF59083SeqList PF59083.txt

Gly	Glu	Leu	Pro	Thr	Arg	Leu	Met	Ala	Leu	Ala	His	Gly	Ala	Asp	Leu	
			20					25					30			
gtc	tgg	tcc	cca	gaa	atc	atc	gac	aaa	aag	cta	att	cag	tgc	gtc	agg	144
Val	Trp	Ser	Pro	Glu	Ile	Ile	Asp	Lys	Lys	Leu	Ile	Gln	Cys	Val	Arg	
		35					40					45				
aag	gaa	aac	act	gca	ctc	caa	act	gtc	gac	tac	gtc	gtg	ccg	tcc	aag	192
Lys	Glu	Asn	Thr	Ala	Leu	Gln	Thr	Val	Asp	Tyr	Val	Val	Pro	Ser	Lys	
	50					55					60					
gtt	caa	acg	agg	ccg	gag	acg	ctc	gtt	ttc	aga	aca	tat	cca	aaa	cta	240
Val	Gln	Thr	Arg	Pro	Glu	Thr	Leu	Val	Phe	Arg	Thr	Tyr	Pro	Lys	Leu	
	65				70					75					80	
gaa	tcc	tct	aaa	ttg	att	ttc	cag	atc	ggg	tct	gca	tcc	ccg	gct	ctg	288
Glu	Ser	Ser	Lys	Leu	Ile	Phe	Gln	Ile	Gly	Ser	Ala	Ser	Pro	Ala	Leu	
			85					90						95		
gcc	acc	cag	gct	ttg	aaa	gtg	atc	aac	gac	gtc	agc	ggg	ata	gat		336
Ala	Thr	Gln	Ala	Ala	Leu	Lys	Val	Ile	Asn	Asp	Val	Ser	Gly	Ile	Asp	
			100				105						110			
atc	aat	gca	ggc	tgc	ccc	aaa	cac	ttc	tct	ata	cac	tcc	ggc	atg	ggc	384
Ile	Asn	Ala	Gly	Cys	Pro	Lys	His	Phe	Ser	Ile	His	Ser	Gly	Met	Gly	
		115					120					125				
tct	gcc	ctc	ttg	cgc	acc	cca	cac	aca	ctg	tgt	ctc	atc	ttg	aaa	gaa	432
Ser	Ala	Leu	Leu	Arg	Thr	Pro	Asp	Thr	Leu	Cys	Leu	Ile	Leu	Lys	Glu	
	130					135					140					
ctg	gtt	aag	aac	gtg	ggt	aac	cct	cac	agc	aaa	ccc	atc	agt	gtg	aaa	480
Leu	Val	Lys	Asn	Val	Gly	Asn	Pro	His	Ser	Lys	Pro	Ile	Ser	Val	Lys	
	145				150					155					160	
ata	aga	ctc	ttg	gac	acc	aag	caa	gac	act	cta	cag	ctc	gtc	aaa	cgt	528
Ile	Arg	Leu	Leu	Asp	Thr	Lys	Gln	Asp	Thr	Leu	Gln	Leu	Val	Lys	Arg	
			165					170						175		
ctg	tgt	gcc	acg	ggc	atc	aca	aat	ctt	aca	ggt	cac	tgc	agg	aag	act	576
Leu	Cys	Ala	Thr	Gly	Ile	Thr	Asn	Leu	Thr	Val	His	Cys	Arg	Lys	Thr	
			180					185					190			
gaa	atg	aga	aac	aga	gag	cag	ccc	atc	aca	gat	tac	att	gcg	gag	atc	624
Glu	Met	Arg	Asn	Arg	Glu	Gln	Pro	Ile	Thr	Asp	Tyr	Ile	Ala	Glu	Ile	
		195					200					205				
tac	gag	ata	tgc	cag	gca	aat	aac	gtg	tcg	ttg	att	gtg	aac	ggc	gct	672
Tyr	Glu	Ile	Cys	Gln	Ala	Asn	Asn	Val	Ser	Leu	Ile	Val	Asn	Gly	Ala	
	210					215					220					
atc	cgc	gac	cgc	tct	cat	ttt	cat	gat	tta	caa	gcg	aat	cat	tgg	aaa	720
Ile	Arg	Asp	Arg	Ser	His	Phe	His	Asp	Leu	Gln	Ala	Asn	His	Trp	Lys	
	225				230				235						240	
aac	act	aac	att	ggt	ggt	atg	att	gca	gag	tgt	gct	gaa	cgg	gac	cct	768
Asn	Thr	Asn	Ile	Gly	Gly	Met	Ile	Ala	Glu	Cys	Ala	Glu	Arg	Asp	Pro	
			245					250						255		
aca	gtt	ttt	gat	cac	act	tct	aag	cct	tca	gaa	gac	ggt	cca	tct	tgg	816
Thr	Val	Phe	Asp	His	Thr	Ser	Lys	Pro	Ser	Glu	Asp	Gly	Pro	Ser	Trp	
			260					265					270			
gtc	gtt	gct	tgt	cgc	gag	ttt	att	cag	tgg	gca	acg	aag	ttt	gac	aac	864
Val	Val	Ala	Cys	Arg	Glu	Phe	Ile	Gln	Trp	Ala	Thr	Lys	Phe	Asp	Asn	
		275					280					285				
cac	atc	ggc	aat	aca	aaa	tac	atg	tta	agc	aga	att	gtc	ccc	gga	aaa	912
His	Ile	Gly	Asn	Thr	Lys	Tyr	Met	Leu	Ser	Arg	Ile	Val	Pro	Gly	Lys	
	290					295					300					
tca	gtc	ttt	ttt	cag	tac	ttt	gcc	cgt	tgc	aag	agc	ccg	gaa	gaa	gtt	960
Ser	Val	Phe	Phe	Gln	Tyr	Phe	Ala	Arg	Cys	Lys	Ser	Pro	Glu	Glu	Val	
	305				310				315						320	
agt	ttc	gta	cta	aag	caa	ttg	aac	gat	gat	gga	agc	gct	caa	aca	gat	1008
Ser	Phe	Val	Leu	Lys	Gln	Leu	Asn	Asp	Asp	Gly	Ser	Ala	Gln	Thr	Asp	
			325					330						335		
cct	tca	gag	tac	ttg	gaa	aac	tgc	aga	gct	caa	gaa	aaa	gct	ttg	aaa	1056
Pro	Ser	Glu	Tyr	Leu	Glu	Asn	Cys	Arg	Ala	Gln	Glu	Lys	Ala	Leu	Lys	
			340					345					350			
aac	gcc	aac	gcc	atc	gcc	aag	caa	aag	agg	aaa	cag	acc	gat	cac	ata	1104
Asn	Ala	Asn	Ala	Ile	Ala	Lys	Gln	Lys	Arg	Lys	Gln	Thr	Asp	His	Ile	
		355					360					365				
ggc	agt	gac	act	aaa	aag	caa	aag	gtt	gta	ccc	ctt	ccc	aca	gat	ata	1152
Gly	Ser	Asp	Thr	Lys	Lys	Gln	Lys	Val	Val	Pro	Leu	Pro	Thr	Asp	Ile	
	370					375					380					
taa																1155

PF59083SeqList PF59083.txt

<210> 10093
 <211> 384
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 10093
 Met Val Thr Tyr Ala Gly Lys Leu Val Leu Ala Pro Met Val Arg Ala
 1 5 10 15
 Gly Glu Leu Pro Thr Arg Leu Met Ala Leu Ala His Gly Ala Asp Leu
 20 25 30
 Val Trp Ser Pro Glu Ile Ile Asp Lys Lys Leu Ile Gln Cys Val Arg
 35 40 45
 Lys Glu Asn Thr Ala Leu Gln Thr Val Asp Tyr Val Val Pro Ser Lys
 50 55 60
 Val Gln Thr Arg Pro Glu Thr Leu Val Phe Arg Thr Tyr Pro Lys Leu
 65 70 75 80
 Glu Ser Ser Lys Leu Ile Phe Gln Ile Gly Ser Ala Ser Pro Ala Leu
 85 90 95
 Ala Thr Gln Ala Ala Leu Lys Val Ile Asn Asp Val Ser Gly Ile Asp
 100 105 110
 Ile Asn Ala Gly Cys Pro Lys His Phe Ser Ile His Ser Gly Met Gly
 115 120 125
 Ser Ala Leu Leu Arg Thr Pro Asp Thr Leu Cys Leu Ile Leu Lys Glu
 130 135 140
 Leu Val Lys Asn Val Gly Asn Pro His Ser Lys Pro Ile Ser Val Lys
 145 150 155 160
 Ile Arg Leu Leu Asp Thr Lys Gln Asp Thr Leu Gln Leu Val Lys Arg
 165 170 175
 Leu Cys Ala Thr Gly Ile Thr Asn Leu Thr Val His Cys Arg Lys Thr
 180 185 190
 Glu Met Arg Asn Arg Glu Gln Pro Ile Thr Asp Tyr Ile Ala Glu Ile
 195 200 205
 Tyr Glu Ile Cys Gln Ala Asn Asn Val Ser Leu Ile Val Asn Gly Ala
 210 215 220
 Ile Arg Asp Arg Ser His Phe His Asp Leu Gln Ala Asn His Trp Lys
 225 230 235 240
 Asn Thr Asn Ile Gly Met Ile Ala Glu Cys Ala Glu Arg Asp Pro
 245 250 255
 Thr Val Phe Asp His Thr Ser Lys Pro Ser Glu Asp Gly Pro Ser Trp
 260 265 270
 Val Val Ala Cys Arg Glu Phe Ile Gln Trp Ala Thr Lys Phe Asp Asn
 275 280 285
 His Ile Gly Asn Thr Lys Tyr Met Leu Ser Arg Ile Val Pro Gly Lys
 290 295 300
 Ser Val Phe Phe Gln Tyr Phe Ala Arg Cys Lys Ser Pro Glu Glu Val
 305 310 315 320
 Ser Phe Val Leu Lys Gln Leu Asn Asp Asp Gly Ser Ala Gln Thr Asp
 325 330 335
 Pro Ser Glu Tyr Leu Glu Asn Cys Arg Ala Gln Glu Lys Ala Leu Lys
 340 345 350
 Asn Ala Asn Ala Ile Ala Lys Gln Lys Arg Lys Gln Thr Asp His Ile
 355 360 365
 Gly Ser Asp Thr Lys Lys Gln Lys Val Val Pro Leu Pro Thr Asp Ile
 370 375 380

<210> 10094
 <211> 963
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(963)

<400> 10094
 atg gac tac cgc aac aag ctc gtg ctc gcg ccc atg gtc cgc gcg ggt
 Seite 10673

PF59083SeqList PF59083.txt

Met	Asp	Tyr	Arg	Asn	Lys	Leu	Val	Leu	Ala	Pro	Met	Val	Arg	Ala	Gly		
1				5					10				15				
act	ctg	ccg	ttt	agg	cta	ctg	gct	gct	gaa	tat	ggc	gcc	gat	att	acg	96	
Thr	Leu	Pro	Phe	Arg	Leu	Leu	Ala	Ala	Glu	Tyr	Gly	Ala	Asp	Ile	Thr		
			20					25				30					
tat	gga	gaa	ata	ata	gat	cat	aag	ttt	gtg	cac	tgt	caa	cgt	gtt	144		
Tyr	Gly	Glu	Glu	Ile	Ile	Asp	His	Lys	Phe	Val	His	Cys	Gln	Arg	Val		
		35				40					45						
aca	aat	gaa	tct	ctt	ggg	aca	act	gat	ttt	ttg	gaa	aga	ggg	act	gat	192	
Thr	Asn	Glu	Ser	Leu	Gly	Thr	Thr	Asp	Phe	Leu	Glu	Arg	Gly	Thr	Asp		
	50				55					60							
agt	gtt	gtt	ttc	cga	aca	tgc	ccg	caa	gaa	agg	gat	agg	gtt	gtc	ttc	240	
Ser	Val	Val	Phe	Arg	Thr	Cys	Pro	Gln	Glu	Arg	Asp	Arg	Val	Val	Phe		
65				70				75						80			
caa	atg	ggc	aca	tca	gat	gct	gtg	aga	gca	ctt	aaa	gct	gct	gag	att	288	
Gln	Met	Gly	Thr	Ser	Asp	Ala	Val	Arg	Ala	Leu	Lys	Ala	Ala	Glu	Ile		
			85					90					95				
gtg	tgc	aat	gat	gtt	gct	gct	ata	gat	atc	aac	atg	ggg	tgt	cca	aag	336	
Val	Cys	Asn	Asp	Val	Ala	Ala	Ile	Asp	Ile	Asn	Met	Gly	Cys	Pro	Lys		
			100				105					110					
gct	ttt	tct	gtc	agt	gga	gga	atg	ggg	tct	gca	tta	ctc	tcc	aaa	cct	384	
Ala	Phe	Ser	Val	Ser	Gly	Gly	Met	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Pro		
		115					120				125						
gag	ctt	ata	cat	gat	att	ttg	act	aca	ttg	cgg	agg	aac	ttg	aac	aca	432	
Glu	Leu	Ile	His	Asp	Ile	Thr	Thr	Leu	Arg	Arg	Asn	Leu	Asn	Thr			
	130				135					140							
cca	gtg	aca	tgt	aaa	atc	cgt	ctt	ttg	aac	aca	cgc	cag	gac	act	gtg	480	
Pro	Val	Thr	Cys	Lys	Ile	Arg	Leu	Leu	Asn	Thr	Arg	Gln	Asp	Thr	Val		
145				150				155						160			
gag	ctg	gca	cgc	cgg	att	gag	aag	tgt	ggg	gtt	cca	gct	ctg	gct	gtc	528	
Glu	Leu	Ala	Arg	Arg	Ile	Glu	Lys	Cys	Gly	Val	Pro	Ala	Leu	Ala	Val		
			165					170					175				
cat	gga	aga	aag	gtc	aaa	gac	agg	cca	agg	gat	ccg	gct	aag	tgg	gat	576	
His	Gly	Arg	Lys	Val	Lys	Asp	Arg	Pro	Arg	Asp	Pro	Ala	Lys	Trp	Asp		
			180				185						190				
gag	att	gct	gat	gtt	gtg	tcc	gca	ctg	tca	att	cca	gtt	ata	gct	aat	624	
Glu	Ile	Ala	Asp	Val	Val	Ser	Ala	Leu	Ser	Ile	Pro	Val	Ile	Ala	Asn		
		195				200					205						
ggg	gat	gta	ttt	gag	tac	gaa	gat	ttt	aag	aga	atc	aaa	gat	gct	aca	672	
Gly	Asp	Val	Phe	Glu	Tyr	Glu	Asp	Phe	Lys	Arg	Ile	Lys	Asp	Ala	Thr		
	210				215					220							
ggg	gcc	aca	tct	gta	atg	gct	gct	aga	ggg	gcc	ttg	tgg	aat	gcc	tcc	720	
Gly	Ala	Thr	Ser	Val	Met	Ala	Ala	Arg	Gly	Ala	Leu	Trp	Asn	Ala	Ser		
225				230				235						240			
att	ttc	tct	cct	aat	ggc	aaa	gta	cct	tgg	gat	ttc	aaa	aga	gag	768		
Ile	Phe	Ser	Pro	Asn	Gly	Lys	Val	Pro	Trp	Glu	Asp	Phe	Lys	Arg	Glu		
			245					250					255				
tat	gtg	aga	aag	act	att	ttg	tgg	gac	aat	tgt	att	aag	agc	aca	aag	816	
Tyr	Val	Arg	Lys	Thr	Ile	Leu	Trp	Asp	Asn	Cys	Ile	Lys	Ser	Thr	Lys		
			260					265					270				
acg	aca	cta	aga	gaa	ata	ata	atg	cac	tat	att	tgc	ctt	gaa	ctc	cct	864	
Thr	Thr	Leu	Arg	Glu	Ile	Ile	Met	His	Tyr	Ile	Cys	Leu	Glu	Leu	Pro		
		275					280				285						
gaa	ggg	aaa	ggg	gtg	ata	aag	tgt	ggg	tcg	tca	gca	gat	gta	gcg	aga	912	
Glu	Gly	Lys	Gly	Val	Ile	Lys	Cys	Gly	Ser	Ser	Ala	Asp	Val	Ala	Arg		
	290				295						300						
ctt	tat	ggg	gaa	gag	gat	tac	tat	aat	ttt	gtt	gtt	tca	aat	agg	aaa	960	
Leu	Tyr	Gly	Glu	Glu	Asp	Tyr	Tyr	Asn	Phe	Val	Val	Ser	Asn	Arg	Lys		
305				310						315					320		
tga																963	

<210> 10095
 <211> 320
 <212> PRT
 <213> Hordeum vulgare

<400> 10095

PF59083SeqList PF59083.txt

Met Asp Tyr Arg Asn Lys Leu Val Leu Ala Pro Met Val Arg Ala Gly
1 5 10 15
Thr Leu Pro Phe Arg Leu Leu Ala Ala Glu Tyr Gly Ala Asp Ile Thr
20 25 30
Tyr Gly Glu Ile Ile Asp His Lys Phe Val His Cys Gln Arg Val
35 40 45
Thr Asn Glu Ser Leu Gly Thr Thr Asp Phe Leu Glu Arg Gly Thr Asp
50 55 60
Ser Val Val Phe Arg Thr Cys Pro Gln Glu Arg Asp Arg Val Val Phe
65 70 75 80
Gln Met Gly Thr Ser Asp Ala Val Arg Ala Leu Lys Ala Ala Glu Ile
85 90 95
Val Cys Asn Asp Val Ala Ala Ile Asp Ile Asn Met Gly Cys Pro Lys
100 105 110
Ala Phe Ser Val Ser Gly Gly Met Gly Ser Ala Leu Leu Ser Lys Pro
115 120 125
Glu Leu Ile His Asp Ile Leu Thr Thr Leu Arg Arg Asn Leu Asn Thr
130 135 140
Pro Val Thr Cys Lys Ile Arg Leu Leu Asn Thr Arg Gln Asp Thr Val
145 150 155 160
Glu Leu Ala Arg Arg Ile Glu Lys Cys Gly Val Pro Ala Leu Ala Val
165 170 175
His Gly Arg Lys Val Lys Asp Arg Pro Arg Asp Pro Ala Lys Trp Asp
180 185 190
Glu Ile Ala Asp Val Val Ser Ala Leu Ser Ile Pro Val Ile Ala Asn
195 200 205
Gly Asp Val Phe Glu Tyr Glu Asp Phe Lys Arg Ile Lys Asp Ala Thr
210 215 220
Gly Ala Thr Ser Val Met Ala Ala Arg Gly Ala Leu Trp Asn Ala Ser
225 230 235 240
Ile Phe Ser Pro Asn Gly Lys Val Pro Trp Glu Asp Phe Lys Arg Glu
245 250 255
Tyr Val Arg Lys Thr Ile Leu Trp Asp Asn Cys Ile Lys Ser Thr Lys
260 265 270
Thr Thr Leu Arg Glu Ile Ile Met His Tyr Ile Cys Leu Glu Leu Pro
275 280 285
Glu Gly Lys Gly Val Ile Lys Cys Gly Ser Ser Ala Asp Val Ala Arg
290 295 300
Leu Tyr Gly Glu Glu Asp Tyr Tyr Asn Phe Val Val Ser Asn Arg Lys
305 310 315 320

<210> 10096
<211> 1344
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1344)
<223> transl_table=11

<400> 10096
atg cat gtg ctt aac att ctc tgg gtg gta ttc ggc att ggt ctg atg 48
Met His Val Leu Asn Ile Leu Trp Val Val Phe Gly Ile Gly Leu Met 15
1 5 10
ctg gta ctg aat ttg aag ttc aaa atc aat tca atg gtg gct ttg ttg 96
Leu Val Leu Asn Leu Lys Phe Lys Ile Asn Ser Met Val Ala Leu Leu 20 25 30
gtg gcg gcg ctg tcc gtc ggg atg ctg gcg ggc atg gat ttg atg tcg 144
Val Ala Ala Leu Ser Val Gly Met Leu Ala Gly Met Asp Leu Met Ser 35 40 45
ctg ctg cac act atg aaa gcg ggc ttc ggc aac acg ctg ggg gaa ctg 192
Leu Leu His Thr Met Lys Ala Gly Phe Gly Asn Thr Leu Gly Glu Leu 50 55 60
gct atc atc gtg gtg ttc ggt gcg gtc atc ggt aaa ttg atg gtc gac 240
Ala Ile Ile Val Val Phe Gly Ala Val Ile Gly Lys Leu Met Val Asp 65 70 75 80
tcc ggc gcg gct cac cag ata gcg cat acg ctg ctg gcg cgt ctc ggt 288
Ser Gly Ala Ala His Gln Ile Ala His Thr Leu Leu Ala Arg Leu Gly 290 295 300 305 310 315 320

PF59083SeqList PF59083.txt

															85											90											95		
ctg	cgc	tat	gta	cag	ctg	tcg	gtg	att	atc	atc	ggc	ctg	att	ttt	ggt	336																							
Leu	Arg	Tyr	Val	Gln	Leu	Ser	Val	Ile	Ile	Ile	Gly	Leu	Ile	Phe	Gly																								
																100											105											110	
ctg	gcg	atg	ttc	tat	gaa	gtg	gcc	ttt	atc	atg	tta	gcg	ccg	ctg	gtt	384																							
Leu	Ala	Met	Phe	Tyr	Glu	Val	Ala	Phe	Ile	Met	Leu	Ala	Pro	Leu	Val																								
																115											120											125	
att	gtt	att	gcc	gcc	gaa	gct	aaa	att	ccg	ttc	ctg	aaa	ctg	gcg	atc	432																							
Ile	Val	Ile	Ala	Ala	Glu	Ala	Lys	Ile	Pro	Phe	Leu	Lys	Leu	Ala	Ile																								
																130											135											140	
ccg	gca	gta	gca	gct	gcc	act	acc	gca	cat	tca	ctg	ttc	cca	ccg	cag	480																							
Pro	Ala	Val	Ala	Ala	Ala	Thr	Thr	Ala	His	Ser	Leu	Phe	Pro	Pro	Gln																								
																145											150											155	
ccg	ggt	ccg	gtg	gcg	ctg	gtg	aat	gct	tat	ggc	gcg	gat	atg	ggg	atg	528																							
Pro	Gly	Pro	Val	Ala	Leu	Val	Asn	Ala	Tyr	Gly	Ala	Asp	Met	Gly	Met																								
																165											170											175	
gtt	tat	atc	tat	ggc	gta	ctg	gtg	acg	atc	cca	agt	gta	atc	tgc	gca	576																							
Val	Tyr	Ile	Tyr	Gly	Val	Leu	Val	Thr	Ile	Pro	Ser	Val	Ile	Cys	Ala																								
																180											185											190	
ggt	ctg	atc	ctg	ccg	aag	ttc	ctc	ggc	aat	ctt	gag	cg	cca	acg	cca	624																							
Gly	Leu	Ile	Leu	Pro	Lys	Phe	Leu	Gly	Asn	Leu	Glu	Arg	Pro	Thr	Pro																								
																195											200											205	
tca	ttc	ctg	aaa	gca	gat	caa	ccg	gta	gat	atg	aat	aat	ctg	ccc	tct	672																							
Ser	Phe	Leu	Lys	Ala	Asp	Gln	Pro	Val	Asp	Met	Asn	Asn	Leu	Pro	Ser																								
																210											215											220	
ttc	ggc	gtt	tcg	att	ctg	gtg	ccg	ctg	atc	ccg	gcg	atc	att	atg	atc	720																							
Phe	Gly	Val	Ser	Ile	Leu	Val	Pro	Leu	Ile	Pro	Ala	Ile	Ile	Met	Ile																								
																225											230											235	
tct	acc	acc	atc	gcc	aat	atc	tgg	ctg	gta	aaa	gat	acc	cct	gcc	tgg	768																							
Ser	Thr	Thr	Ile	Ala	Asn	Ile	Trp	Leu	Val	Lys	Asp	Thr	Pro	Ala	Trp																								
																245											250											255	
gaa	gtg	gtt	aac	ttt	atc	ggt	tcc	tcg	ccg	att	gca	atg	ttt	att	gcg	816																							
Glu	Val	Val	Asn	Phe	Ile	Gly	Ser	Ser	Pro	Ile	Ala	Met	Phe	Ile	Ala																								
																260											265											270	
atg	gtg	gtt	gca	ttc	gta	ctc	ttt	ggc	acc	gca	cgt	ggt	cat	gac	atg	864																							
Met	Val	Val	Ala	Phe	Val	Leu	Phe	Gly	Thr	Ala	Arg	Gly	His	Asp	Met																								
																275											280											285	
cag	tgg	gtg	atg	aac	gct	ttt	gaa	agc	gcg	gtg	aag	agt	att	gca	atg	912																							
Gln	Trp	Val	Met	Asn	Ala	Phe	Glu	Ser	Ala	Val	Lys	Ser	Ile	Ala	Met																								
																290											295											300	
gtg	att	ctg	atc	atc	ggt	gcg	ggt	ggc	gtg	ctg	aag	cag	acc	atc	atc	960																							
Val	Ile	Leu	Ile	Ile	Gly	Ala	Gly	Gly	Val	Leu	Lys	Gln	Thr	Ile	Ile																								
																305											310											315	
gac	acc	ggc	att	ggc	gac	acc	atc	ggc	atg	ttg	atg	tcc	cac	ggc	aat	1008																							
Asp	Thr	Gly	Ile	Gly	Asp	Thr	Ile	Gly	Met	Leu	Met	Ser	His	Gly	Asn																								
																325											330											335	
atc	tcg	ccc	tac	atc	atg	gca	tgg	ctg	atc	act	gtg	cta	att	cgt	ctg	1056																							
Ile	Ser	Pro	Tyr	Ile	Met	Ala	Trp	Leu	Ile	Thr	Val	Leu	Ile	Arg	Leu																								
																340											345											350	
gcg	acg	ggt	cag	ggt	gtc	gtt	tcg	gcg	atg	acc	gcc	gcc	ggg	att	atc	1104																							
Ala	Thr	Gly	Gln	Gly	Val	Val	Ser	Ala	Met	Thr	Ala	Ala	Gly	Ile	Ile																								
																355											360											365	
agt	gct	gca	atc	cta	gat	cca	gca	act	ggt	cag	ctg	gtt	ggc	gtg	aat	1152																							
Ser	Ala	Ala	Ile	Leu	Asp	Pro	Ala	Thr	Gly	Gln	Leu	Val	Gly	Val	Asn																								
																370											375											380	
ccg	gcg	ctg	ctg	gta	ctg	gcg	acg	gct	gcg	ggt	tcc	aac	acc	ctc	acc	1200																							
Pro	Ala	Leu	Leu	Val	Leu	Ala	Thr	Ala	Ala	Gly	Ser	Asn	Thr	Leu	Thr																								
																385											390											395	
cac	att	aac	gat	gca	tct	ttc	tgg	ttg	ttc	aaa	ggt	tac	ttt	gac	ctg	1248																							
His	Ile	Asn	Asp	Ala	Ser	Phe	Trp	Leu	Phe	Lys	Gly	Tyr	Phe	Asp	Leu																								
																405											410											415	
tca	gta	aaa	gac	acg	ttg	aaa	acc	tgg	ggt	ctg	ctg	gag	ctg	gtc	aac	1296																							
Ser	Val	Lys	Asp	Thr	Leu	Lys	Thr	Trp	Gly	Leu	Leu	Glu	Leu	Val	Asn																								
																420											425											430	
tcc	gtg	gtt	ggg	ctg	att	att	gtg	ctg	att	att	agc	atg	gta	gcg	taa	1344																							
Ser	Val	Val	Gly	Leu	Ile	Ile	Val	Leu	Ile	Ile	Ser	Met	Val	Ala																									
																435											440											445	

<210> 10097

PF59083SeqList PF59083.txt

<211> 447

<212> PRT

<213> Escherichia coli

<400> 10097

```

Met His Val Leu Asn Ile Leu Trp Val Val Phe Gly Ile Gly Leu Met
1      5      10      15
Leu Val Leu Asn Leu Lys Phe Lys Ile Asn Ser Met Val Ala Leu Leu
      20      25      30
Val Ala Ala Leu Ser Val Gly Met Leu Ala Gly Met Asp Leu Met Ser
      35      40      45
Leu Leu His Thr Met Lys Ala Gly Phe Gly Asn Thr Leu Gly Glu Leu
      50      55      60
Ala Ile Ile Val Val Phe Gly Ala Val Ile Gly Lys Leu Met Val Asp
65      70      75      80
Ser Gly Ala Ala His Gln Ile Ala His Thr Leu Ala Arg Leu Gly
      85      90      95
Leu Arg Tyr Val Gln Leu Ser Val Ile Ile Ile Gly Leu Ile Phe Gly
      100      105      110
Leu Ala Met Phe Tyr Glu Val Ala Phe Ile Met Leu Ala Pro Leu Val
      115      120      125
Ile Val Ile Ala Ala Glu Ala Lys Ile Pro Phe Leu Lys Leu Ala Ile
      130      135      140
Pro Ala Val Ala Ala Ala Thr Thr Ala His Ser Leu Phe Pro Pro Gln
145      150      155      160
Pro Gly Pro Val Ala Leu Val Asn Ala Tyr Gly Ala Asp Met Gly Met
      165      170      175
Val Tyr Ile Tyr Gly Val Leu Val Thr Ile Pro Ser Val Ile Cys Ala
      180      185      190
Gly Leu Ile Leu Pro Lys Phe Leu Gly Asn Leu Glu Arg Pro Thr Pro
      195      200      205
Ser Phe Leu Lys Ala Asp Gln Pro Val Asp Met Asn Asn Leu Pro Ser
      210      215      220
Phe Gly Val Ser Ile Leu Val Pro Leu Ile Pro Ala Ile Ile Met Ile
225      230      235      240
Ser Thr Thr Ile Ala Asn Ile Trp Leu Val Lys Asp Thr Pro Ala Trp
      245      250      255
Glu Val Val Asn Phe Ile Gly Ser Ser Pro Ile Ala Met Phe Ile Ala
      260      265      270
Met Val Val Ala Phe Val Leu Phe Gly Thr Ala Arg Gly His Asp Met
      275      280      285
Gln Trp Val Met Asn Ala Phe Glu Ser Ala Val Lys Ser Ile Ala Met
      290      295      300
Val Ile Leu Ile Ile Gly Ala Gly Gly Val Leu Lys Gln Thr Ile Ile
305      310      315      320
Asp Thr Gly Ile Gly Asp Thr Ile Gly Met Leu Met Ser His Gly Asn
      325      330      335
Ile Ser Pro Tyr Ile Met Ala Trp Leu Ile Thr Val Leu Ile Arg Leu
      340      345      350
Ala Thr Gly Gln Gly Val Val Ser Ala Met Thr Ala Ala Gly Ile Ile
      355      360      365
Ser Ala Ala Ile Leu Asp Pro Ala Thr Gly Gln Leu Val Gly Val Asn
      370      375      380
Pro Ala Leu Leu Val Leu Ala Thr Ala Ala Gly Ser Asn Thr Leu Thr
385      390      395      400
His Ile Asn Asp Ala Ser Phe Trp Leu Phe Lys Gly Tyr Phe Asp Leu
      405      410      415
Ser Val Lys Asp Thr Leu Lys Thr Trp Gly Leu Leu Glu Leu Val Asn
      420      425      430
Ser Val Val Gly Leu Ile Ile Val Leu Ile Ile Ser Met Val Ala
      435      440      445

```

<210> 10098

<211> 1344

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

PF59083SeqList PF59083.txt

<222> (1)..(1344)

<223> transl_table=11

<400> 10098

atg gaa tgg att aat atc ctg tgg gtc atg ttg ggt att ggc tta atg	48
Met Glu Trp Ile Asn Ile Leu Trp Val Met Leu Gly Ile Gly Leu Met	
1 5 10 15	
cta gtg ctc aat atc cgc tac cag att aac tca atg gtc gca ttg ctg	96
Leu Val Leu Asn Ile Arg Tyr Gln Ile Asn Ser Met Val Ala Leu Leu	
20 25 30	
ctg gca gct ctg cta gta ggg act ctc gcg ggc atg gac ctg ctt aag	144
Leu Ala Ala Leu Leu Val Gly Thr Leu Ala Gly Met Asp Leu Leu Lys	
35 40 45	
ctg ctg cat acc att aag gct ggg ttt ggt ggc acg cta ggt gaa ctg	192
Leu Leu His Thr Ile Lys Ala Gly Phe Gly Gly Thr Leu Gly Glu Leu	
50 55 60	
gcg ata atc gtc gta ttt ggt gcg gtg atc ggc aaa ctg atg gtg gac	240
Ala Ile Ile Val Val Phe Gly Ala Val Ile Gly Lys Leu Met Val Asp	
65 70 75 80	
tct ggc gct gct cat cag ata gcc cag acg cta ttg cgc cga ttc ggg	288
Ser Gly Ala Ala His Gln Ile Ala Gln Thr Leu Leu Arg Arg Phe Gly	
85 90 95	
ctt aaa tat gtt gaa gcc gcg gta att atc atc ggc ctg atc ttt ggt	336
Leu Lys Tyr Val Glu Ala Ala Val Ile Ile Ile Gly Leu Ile Phe Gly	
100 105 110	
ctg gcg atg ttt tat gag gtt gcc ttt att att ttg gca cca ctg gtc	384
Leu Ala Met Phe Tyr Glu Val Ala Phe Ile Ile Leu Ala Pro Leu Val	
115 120 125	
att gct att gcg gtc gaa gcc aag ata ccg ttc ctc aaa ctg gcg atc	432
Ile Ala Ile Ala Val Glu Ala Lys Ile Pro Phe Leu Lys Leu Ala Ile	
130 135 140	
ccg gca gtt gct gca gcg acg acg gct cac tcc cta ttc cca cca cag	480
Pro Ala Val Ala Ala Thr Thr Ala His Ser Leu Phe Pro Pro Gln	
145 150 155 160	
ccg ggg ccg gtt gcg ctg gtt gcc gct tat ggc gca gac atg ggg atg	528
Pro Gly Pro Val Leu Val Ala Ala Tyr Gly Ala Asp Met Gly Met	
165 170 175	
gtt tat atc tat gga gtt ctg gtt gct att cct tca gtg atc tgt gcc	576
Val Tyr Ile Tyr Gly Val Leu Val Ala Ile Pro Ser Val Ile Cys Ala	
180 185 190	
ggg ctt att ttg cca aag ttc ttg ggc aat ctg gag cgg cca att ccg	624
Gly Leu Ile Leu Pro Lys Phe Leu Gly Asn Leu Glu Arg Pro Ile Pro	
195 200 205	
acg ttc ctg aag tct gac aac ccg att gat gaa aac aat ctg ccg tcg	672
Thr Phe Leu Lys Ser Asp Asn Pro Ile Asp Glu Asn Asn Leu Pro Ser	
210 215 220	
ttc agt acc tcg att ttg gta ccg tta att ccc gct ttc atc atg att	720
Phe Ser Thr Ser Ile Leu Val Pro Leu Ile Pro Ala Phe Ile Met Ile	
225 230 235 240	
ttt acc acc ata gcc aat atc tgg ttg gtt aaa ggg acc acg tcg tac	768
Phe Thr Thr Ile Ala Asn Ile Trp Leu Val Lys Gly Thr Thr Ser Tyr	
245 250 255	
acc att ctc aat ttc att ggc tca tca cct att gcc atg ttt atc gcc	816
Thr Ile Leu Asn Phe Ile Gly Ser Ser Pro Ile Ala Met Phe Ile Ala	
260 265 270	
atg ttg gtt gcc ttc gta ctt ttc ggc acc gga cgc ggt cat aaa atg	864
Met Leu Val Ala Phe Val Leu Phe Gly Thr Gly Arg Gly His Lys Met	
275 280 285	
gaa tgg gtc atg cac tca ttt gaa ggg gcg gta aaa ggc gtt gcc atg	912
Glu Trp Val Met His Ser Phe Glu Gly Ala Val Lys Gly Val Ala Met	
290 295 300	
gtc atc ctg atc atc ggt gcg ggc ggt gcg cta aag cag gtg atc att	960
Val Ile Leu Ile Ile Gly Ala Gly Gly Ala Leu Lys Gln Val Ile Ile	
305 310 315 320	
gat acc ggg atc ggc gat acg att ggc atg ctg atg tct gct ggt ggt	1008
Asp Thr Gly Ile Gly Asp Thr Ile Gly Met Leu Met Ser Ala Gly Gly	
325 330 335	
gta tca cct tat att atg gct tgg ctg att acg gtg ctg att cgt ctg	1056
Val Ser Pro Tyr Ile Met Ala Trp Leu Ile Thr Val Leu Ile Arg Leu	

PF59083SeqList PF59083.txt

			340					345				350					
aca	acg	ggc	caa	ggc	gtg	gtt	tcg	gcg	atg	acc	gcc	gca	ggg	att	atc		1104
Thr	Thr	Gly	Gln	Gly	Val	Val	Ser	Ala	Met	Thr	Ala	Ala	Gly	Ile	Ile		
		355					360				365						
ggg	gct	gcg	gta	atg	gac	ccg	gtc	act	ggg	acc	att	acc	tca	gtc	gat		1152
Gly	Ala	Ala	Val	Met	Asp	Pro	Val	Thr	Gly	Thr	Ile	Thr	Ser	Val	Asp		
		370				375					380						
ccg	gca	ctg	ttg	gtg	ctg	gcg	aca	gcg	gca	ggg	tct	aac	acc	ttt	act		1200
Pro	Ala	Leu	Leu	Val	Leu	Ala	Thr	Ala	Ala	Gly	Ser	Asn	Thr	Phe	Thr		
385					390					395					400		
cat	atc	aat	gac	gcc	tca	ttc	tgg	ctg	ttt	aaa	ggg	tat	ttt	gag	ctg		1248
His	Ile	Asn	Asp	Ala	Ser	Phe	Trp	Leu	Phe	Lys	Gly	Tyr	Phe	Glu	Leu		
			405						410					415			
tcg	att	aaa	gat	acg	ctg	aag	act	tgg	ggc	ctg	ctc	gaa	ttg	acc	aac		1296
Ser	Ile	Lys	Asp	Thr	Leu	Lys	Thr	Trp	Gly	Leu	Leu	Glu	Leu	Thr	Asn		
			420				425						430				
tcg	gtg	gtt	ggg	ttg	gcg	gtg	gta	ctg	ctg	atc	agc	atg	ttt	gtc			1341
Ser	Val	Val	Gly	Leu	Ala	Val	Val	Leu	Leu	Ile	Ser	Met	Phe	Val			
		435				440					445						
tag																	1344

<210> 10099
 <211> 447
 <212> PRT
 <213> Yersinia pestis

<400> 10099
 Met Glu Trp Ile Asn Ile Leu Trp Val Met Leu Gly Ile Gly Leu Met
 1 5 10 15
 Leu Val Leu Asn Ile Arg Tyr Gln Ile Asn Ser Met Val Ala Leu Leu
 20 25 30
 Leu Ala Ala Leu Leu Val Gly Thr Leu Ala Gly Met Asp Leu Leu Lys
 35 40 45
 Leu Leu His Thr Ile Lys Ala Gly Phe Gly Gly Thr Leu Gly Glu Leu
 50 55 60
 Ala Ile Ile Val Val Phe Gly Ala Val Ile Gly Lys Leu Met Val Asp
 65 70 75 80
 Ser Gly Ala Ala His Gln Ile Ala Gln Thr Leu Leu Arg Arg Phe Gly
 85 90 95
 Leu Lys Tyr Val Glu Ala Ala Val Ile Ile Ile Gly Leu Ile Phe Gly
 100 105 110
 Leu Ala Met Phe Tyr Glu Val Ala Phe Ile Ile Leu Ala Pro Leu Val
 115 120 125
 Ile Ala Ile Ala Val Glu Ala Lys Ile Pro Phe Leu Lys Leu Ala Ile
 130 135 140
 Pro Ala Val Ala Ala Ala Thr Thr Ala His Ser Leu Phe Pro Pro Gln
 145 150 155 160
 Pro Gly Pro Val Ala Leu Val Ala Ala Tyr Gly Ala Asp Met Gly Met
 165 170 175
 Val Tyr Ile Tyr Gly Val Leu Val Ala Ile Pro Ser Val Ile Cys Ala
 180 185 190
 Gly Leu Ile Leu Pro Lys Phe Leu Gly Asn Leu Glu Arg Pro Ile Pro
 195 200 205
 Thr Phe Leu Lys Ser Asp Asn Pro Ile Asp Glu Asn Asn Leu Pro Ser
 210 215 220
 Phe Ser Thr Ser Ile Leu Val Pro Leu Ile Pro Ala Phe Ile Met Ile
 225 230 235 240
 Phe Thr Thr Ile Ala Asn Ile Trp Leu Val Lys Gly Thr Thr Ser Tyr
 245 250 255
 Thr Ile Leu Asn Phe Ile Gly Ser Ser Pro Ile Ala Met Phe Ile Ala
 260 265 270
 Met Leu Val Ala Phe Val Leu Phe Gly Thr Gly Arg Gly His Lys Met
 275 280 285
 Glu Trp Val Met His Ser Phe Glu Gly Ala Val Lys Gly Val Ala Met
 290 295 300
 Val Ile Leu Ile Ile Gly Ala Gly Gly Ala Leu Lys Gln Val Ile Ile
 305 310 315 320

PF59083SeqList PF59083.txt

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

<210> 10100
 <211> 1320
 <212> DNA
 <213> Pantoea citrea
 <220>
 <221> CDS
 <222> (1)..(1320)
 <223> transl_table=11

<400> 10100
 atg cca att aca ata ata gcg ctc ggg gta ata ctg ctg ctg gtc ctg 48
 Met Pro Ile Thr Ile Ile Ala Leu Gly Val Ile Leu Leu Leu Val Leu
 1 5 10 15
 atg att gtt ttc aag gcc aac ggc ttt tta tct ctg att ttt gtc tcc 96
 Met Ile Val Phe Lys Ala Asn Gly Phe Leu Ser Leu Ile Phe Val Ser
 20 25 30
 atc gtc gta ggt ata gcc gaa ggg atg aca ccg ttg cag gcc ctg gct 144
 Ile Val Val Gly Ile Ala Glu Gly Met Thr Pro Leu Gln Ala Leu Ala
 35 40 45
 tct gta caa aaa ggg gtt ggc ggt act ctg ggc agc ctt gcg atg att 192
 Ser Val Gln Lys Gly Val Gly Gly Thr Leu Gly Ser Leu Ala Met Ile
 50 55 60
 ctt ggt ttt ggt gcc atg ctc ggt aag ctg gtg tca gat acc ggg gcc 240
 Leu Gly Phe Gly Ala Met Leu Gly Lys Leu Val Ser Asp Thr Gly Ala
 65 70 75 80
 gcc caa cgg gtg gcg acc acg ttg att gcg gct ttt ggt aaa cag cgg 288
 Ala Gln Arg Val Ala Thr Thr Leu Ile Ala Phe Gly Lys Gln Arg
 85 90 95
 gtg caa tgg gct ctg atg gtg aca ggg ctg att gtc ggg ctg gcc atg 336
 Val Gln Trp Ala Leu Met Val Thr Gly Leu Ile Val Gly Leu Ala Met
 100 105 110
 ttt tat gaa att ggt ttt gtc ctg ttg tta ccg ctg gtg ttt acc gtg 384
 Phe Tyr Glu Ile Gly Phe Val Leu Leu Pro Leu Val Phe Thr Val
 115 120 125
 gtg gcc gcc gcc ggt atg cca tta ctg tat gtg ggg ctg ccg atg gtg 432
 Val Ala Ala Ala Gly Met Pro Leu Leu Tyr Val Gly Leu Pro Met Val
 130 135 140
 gct gca ttg tca gtg acc cat tgc ttc ctg cct ccg cac ccg ggg ccg 480
 Ala Ala Leu Ser Val Thr His Cys Phe Leu Pro Pro His Pro Gly Pro
 145 150 155 160
 acg gcg atc gcc gct atc ttc ggg gcc aat ctg ggt acc aca ctg ttg 528
 Thr Ala Ile Ala Ala Ile Phe Gly Ala Asn Leu Gly Thr Thr Leu Leu
 165 170 175
 tat ggc ata att att acc ctg cca acg gtg att gtg gcc ggt ccg gta 576
 Tyr Gly Ile Ile Ile Thr Leu Pro Thr Val Ile Val Ala Gly Pro Val
 180 185 190
 ttt tct aag ttc cta aaa aac ttt gaa aaa gaa ccg ccg gaa ggg ctg 624
 Phe Ser Lys Phe Leu Lys Asn Phe Glu Lys Glu Pro Pro Glu Gly Leu
 195 200 205
 tat aac ccc aaa att ttc gcc gaa cat gag ttg ccc gga ttc gct att 672
 Tyr Asn Pro Lys Ile Phe Ala Glu His Glu Leu Pro Gly Phe Ala Ile

PF59083SeqList PF59083.txt

210	215	220	
agt ata ttt gct gca gtc atc ccg gtg atc ctt atg gcg att gcc gca			720
Ser Ile Phe Ala Ala Val Ile Pro Val Ile Leu Met Ala Ile Ala Ala			
225	230	235	240
gtt ttt gaa ctc aca act ccg aaa gag aat ccg ctc cgt cag ttt ttc			768
Val Phe Glu Leu Thr Pro Lys Glu Asn Pro Leu Arg Gln Phe Phe			
	245	250	255
gaa ttt att ggt aac cct gcg atc gcg ctg ttt att gcc gtg gtg atc			816
Glu Phe Ile Gly Asn Pro Ala Ile Ala Leu Phe Ile Ala Val Val Ile			
	260	265	270
gcc gta ttt acc ctc gga ttg cgc aat ggc cgg aaa atg ggc gaa gtc			864
Ala Val Phe Thr Leu Gly Leu Arg Asn Gly Arg Lys Met Gly Glu Val			
	275	280	285
atg gag atg tgc agc tcc tca att tcg tca att gcc atg att gta ttt			912
Met Glu Met Cys Ser Ser Ile Ser Ser Ile Ala Met Ile Val Phe			
	290	295	300
atc att gcc ggt ggc ggg gca ttt aaa caa gtc ctg gtg gac agt ggg			960
Ile Ile Ala Gly Gly Gly Ala Phe Lys Gln Val Leu Val Asp Ser Gly			
	305	310	315
gtg ggc gat ttt atc gca gga atg atg aaa gga tcg tca ttg tcg cca			1008
Val Gly Asp Phe Ile Ala Gly Met Met Lys Gly Ser Ser Leu Ser Pro			
	325	330	335
cta ttg atg tgc tgg acc gtg gcg gca atg ctg cga gtt gcg ttg gga			1056
Leu Leu Met Cys Trp Thr Val Ala Ala Met Leu Arg Val Ala Leu Gly			
	340	345	350
tca gcc aca gta gcg gcg att act acc gcg ggt att gtc act ccg att			1104
Ser Ala Thr Val Ala Ala Ile Thr Thr Ala Gly Ile Val Thr Pro Ile			
	355	360	365
atc gcg gtg act cac gca gac cct gca cta atg gtg ttg gcg gta ggg			1152
Ile Ala Val Thr His Ala Asp Pro Ala Leu Met Val Leu Ala Val Gly			
	370	375	380
tct ggt agc gtg atc gcc tcg cat gtt aat gac ccc ggt ttc tgg tta			1200
Ser Gly Ser Val Ile Ala Ser His Val Asn Asp Pro Gly Phe Trp Leu			
	385	390	400
ttc aaa ggc tac ttt aat ctg agc gtg act gaa aca ctg aaa acc tgg			1248
Phe Lys Gly Tyr Phe Asn Leu Ser Val Thr Glu Thr Leu Lys Thr Trp			
	405	410	415
act gtg atg gaa aca ctg att tcg gtg atg ggt ctg gcc gga gtc ctt			1296
Thr Val Met Glu Thr Leu Ile Ser Val Met Gly Leu Ala Gly Val Leu			
	420	425	430
att ctt aac tca gta ctg cac taa			1320
Ile Leu Asn Ser Val Leu His			
	435		

<210> 10101
 <211> 439
 <212> PRT
 <213> Pantoea citrea

<400> 10101
 Met Pro Ile Thr Ile Ile Ala Leu Gly Val Ile Leu Leu Leu Val Leu
 1 5 10 15
 Met Ile Val Phe Lys Ala Asn Gly Phe Leu Ser Leu Ile Phe Val Ser
 20 25 30
 Ile Val Val Gly Ile Ala Glu Gly Met Thr Pro Leu Gln Ala Leu Ala
 35 40 45
 Ser Val Gln Lys Gly Val Gly Gly Thr Leu Gly Ser Leu Ala Met Ile
 50 55 60
 Leu Gly Phe Gly Ala Met Leu Gly Lys Leu Val Ser Asp Thr Gly Ala
 65 70 75 80
 Ala Gln Arg Val Ala Thr Thr Leu Ile Ala Ala Phe Gly Lys Gln Arg
 85 90 95
 Val Gln Trp Ala Leu Met Val Thr Gly Leu Ile Val Gly Leu Ala Met
 100 105 110
 Phe Tyr Glu Ile Gly Phe Val Leu Leu Pro Leu Val Phe Thr Val
 115 120 125
 Val Ala Ala Ala Gly Met Pro Leu Leu Tyr Val Gly Leu Pro Met Val
 130 135 140
 Ala Ala Leu Ser Val Thr His Cys Phe Leu Pro Pro His Pro Gly Pro

PF59083SeqList PF59083.txt

```

145      150      155      160
Thr Ala Ile Ala Ala Ile Phe Gly Ala Asn Leu Gly Thr Thr Leu Leu
Tyr Gly Ile Ile Ile Thr Leu Pro Thr Val Ile Val Ala Gly Pro Val
Phe Ser Lys 180 Phe Leu Lys Asn Phe 185 Gly Lys Glu Pro Pro Gly Leu
Tyr Asn Pro Lys Ile Phe Ala Glu His Glu Leu Pro Gly Phe Ala Ile
Ser 210 Phe Ala Ala Val Ile Pro Val Ile Leu Met Ala Ile Ala Ala
225 Val Phe Glu Leu Thr Thr Pro Lys Glu Asn Pro Leu Arg Gln Phe Phe
Glu Phe Ile Gly Asn Pro Ala Ile Ala Leu Phe Ile Ala Val Val Ile
Ala Val Phe 260 Thr Leu Gly Leu Arg 265 Asn Gly Arg Lys Met Gly Glu Val
Met Glu Met Cys Ser Ser Ser Ile Ser Ser Ile Ala Met Ile Val Phe
Ile 290 Ala Gly Gly Gly Ala Phe Lys Gln Val Leu Val Asp Ser Gly
305 Val Gly Asp Phe Ile Ala Gly Met Met Lys Gly Ser Ser Leu Ser Pro
Leu Leu Met Cys Trp Thr Val Ala Ala Met Leu Arg Val Ala Leu Gly
Ser Ala Thr Val Ala Ala Ile Thr Thr Ala Gly Ile Val Thr Pro Ile
Ile Ala Val Thr His Ala Asp Pro Ala Leu Met Val Leu Ala Val Gly
Ser 370 Gly Ser Val Ile Ala Ser His Val Asn Asp Pro Gly Phe Trp Leu
385 Phe Lys Gly Tyr Phe Asn Leu Ser Val Thr Glu Thr Leu Lys Thr Trp
Thr Val Met Glu Thr Leu Ile Ser Val Met Gly Leu Ala Gly Val Leu
Ile Leu Asn Ser Val Leu His
435

```

<210> 10102

<211> 1464

<212> DNA

<213> Kineococcus radiotolerans SRS30216

<220>

<221> CDS

<222> (1)..(1464)

<223> transl_table=11

<400> 10102

```

atg gag acc gtc aca ccc gcc tac ggc acg agc acg ctg ctg ctc atc      48
Met Glu Thr Val Thr Pro Ala Tyr Gly Thr Ser Thr Leu Leu Leu Ile
1      5      10      15
gcc gcc gcc gcc gtg gcc ctg ctg ctg ctg ctg atc atc cgc ttc aag      96
Ala Ala Ala Ala Val Ala Leu Leu Leu Leu Leu Ile Ile Arg Phe Lys
20      25      30
ctg cac gcg ttc gtc gcg ctc gtg ctc gtc agc gcc gtc acc gcc gtc      144
Leu His Ala Phe Val Ala Leu Val Leu Val Ser Ala Val Thr Ala Val
35      40      45
gtc acc gtc ggt ccc gac ggg agc ctg ctc gac gtc gtc gac gtc ctg      192
Val Thr Val Gly Pro Asp Gly Ser Leu Leu Asp Val Val Asp Val Leu
50      55      60
acc gcc gcc ttc ggc agc acg ctg gcc agc gtc gcc ctg ctc gtc ggc      240
Thr Ala Gly Phe Gly Ser Thr Leu Ala Ser Val Ala Leu Leu Val Gly
65      70      75      80
ttc ggc gtc atg atc ggg cgc ctg ctg gag gtc acc ggc ggc gcg cag      288
Phe Gly Val Met Ile Gly Arg Leu Leu Glu Val Thr Gly Gly Ala Gln
85      90      95
gtg ctc gcc gac acc ctc gtg gcc cgc ttc ggc gag aag cgc gcc ccc      336
Val Leu Ala Asp Thr Leu Val Ala Arg Phe Gly Glu Lys Arg Ala Pro

```

PF59083SeqList PF59083.txt

100					105					110						
ctc	gcc	ctc	ggc	gtc	gcc	tcg	ctg	atc	ttc	ggg	ttc	ccg	atc	ttc	ttc	384
Leu	Ala	Leu	Gly	Val	Ala	Ser	Leu	Ile	Phe	Gly	Phe	Pro	Ile	Phe	Phe	
		115					120					125				
gac	gcc	ggg	ctc	gtg	gtc	ttc	ctg	ccg	atc	atc	ttc	tcg	gtg	gcc	cgc	432
Asp	Ala	Gly	Leu	Val	Val	Phe	Leu	Pro	Ile	Ile	Phe	Ser	Val	Ala	Arg	
	130					135					140					
cgc	ttc	ggc	ggc	tcc	gtc	ctg	acg	tac	gcc	ctg	ccc	gcc	gcg	ggc	gcc	480
Arg	Phe	Gly	Gly	Ser	Val	Leu	Thr	Tyr	Ala	Leu	Pro	Ala	Ala	Gly	Ala	
	145				150					155					160	
ttc	gcc	gtc	atg	cac	gcc	ttc	gtg	ccc	ccg	cac	ccc	ggc	ccg	gtc	gcg	528
Phe	Ala	Val	Met	His	Ala	Phe	Val	Pro	Pro	His	Pro	Gly	Pro	Val	Ala	
				165					170						175	
gcc	ggt	gag	ctg	ctc	ggc	gcc	gac	atc	ggc	gtc	ctc	atc	ctc	gtg	ggc	576
Ala	Gly	Glu	Leu	Leu	Gly	Ala	Asp	Ile	Gly	Val	Leu	Ile	Leu	Val	Gly	
			180					185						190		
ctc	gtc	ctc	ggc	gtc	ccc	acg	tgg	ttc	acc	gcc	agc	tac	ctc	ttc	ggc	624
Leu	Val	Leu	Ala	Val	Pro	Thr	Trp	Phe	Thr	Ala	Ser	Tyr	Leu	Phe	Gly	
		195				200						205				
ctg	tgg	ggc	ggg	cgc	cgc	acc	gac	gtg	ccg	ctg	ccc	gcg	gag	tgg	gcc	672
Leu	Trp	Ala	Gly	Arg	Arg	Thr	Asp	Val	Pro	Leu	Pro	Ala	Glu	Trp	Ala	
	210					215					220					
gag	cgc	ctg	ggc	gcg	aac	acg	gcc	ggg	cag	gcc	ggg	ccc	tcc	ggc	acc	720
Glu	Arg	Leu	Ala	Ala	Asn	Thr	Ala	Gly	Gln	Ala	Gly	Pro	Ser	Gly	Thr	
	225				230				235						240	
gcc	ggc	ggc	ggc	acc	ggc	ccg	ggc	gcg	acg	ggc	ggg	acg	ggc	acc	ccg	768
Ala	Gly	Ala	Ala	Thr	Ala	Pro	Gly	Ala	Thr	Gly	Gly	Thr	Gly	Thr	Pro	
				245					250					255		
ggc	ccg	ggc	ggc	ccg	cgc	ttc	agc	acc	gtc	ctc	ctc	gtg	ctg	ctg	ctg	816
Gly	Pro	Ala	Ala	Pro	Arg	Phe	Ser	Thr	Val	Leu	Leu	Val	Leu	Leu	Leu	
		260						265						270		
ccc	ctg	gtg	ctg	atc	ttc	ctc	aac	acg	ggc	ctg	aac	acg	ctg	gcc	acc	864
Pro	Leu	Val	Leu	Ile	Phe	Leu	Asn	Thr	Gly	Leu	Asn	Thr	Leu	Ala	Thr	
		275				280						285				
gcc	ggc	ggc	gtc	gac	ggc	gag	gcg	acc	tgg	gtg	cag	gtg	ctg	cgc	ctg	912
Ala	Gly	Ala	Val	Asp	Gly	Glu	Ala	Thr	Trp	Val	Gln	Val	Leu	Arg	Leu	
	290					295					300					
gtg	ggg	cag	acg	ccc	atc	gcg	ctg	ctc	atc	gcc	gtg	ctc	gtc	acc	atg	960
Val	Gly	Gln	Thr	Pro	Ile	Ala	Leu	Leu	Ile	Ala	Val	Leu	Val	Thr	Met	
				310						315					320	
gtc	gtc	ctc	agc	cgc	ggc	cgc	ctg	acg	cgc	ggc	gag	gtc	gag	gac	ctg	1008
Val	Val	Leu	Ser	Arg	Gly	Arg	Leu	Thr	Arg	Gly	Glu	Val	Glu	Asp	Leu	
			325						330					335		
gcc	aac	agc	tcc	ctc	ggg	ccg	gtc	tgc	gcc	gtc	atc	ctc	atc	acc	ggc	1056
Ala	Asn	Ser	Ser	Leu	Gly	Pro	Val	Cys	Ala	Val	Ile	Leu	Ile	Thr	Gly	
			340					345						350		
gcc	ggc	ggc	atg	ttc	ggc	ggg	gtc	ctg	cgc	gcc	agc	ggc	atc	ggc	ggc	1104
Ala	Gly	Gly	Met	Phe	Gly	Gly	Val	Leu	Arg	Ala	Ser	Gly	Ile	Gly	Gly	
		355				360						365				
gcc	ctg	ggc	gac	acc	ctg	gcc	gcg	acc	ggc	ctg	ccc	gtc	atc	gtg	gcc	1152
Ala	Leu	Ala	Asp	Thr	Leu	Ala	Ala	Thr	Gly	Leu	Pro	Val	Ile	Val	Ala	
	370					375					380					
gcg	ttc	atc	atc	tcc	ctg	ggc	ctg	cgc	gtg	gcg	cag	ggc	tcg	gcg	acg	1200
Ala	Phe	Ile	Ile	Ser	Leu	Gly	Leu	Arg	Val	Ala	Gln	Gly	Ser	Ala	Thr	
					390					395					400	
gtg	gcg	ctg	acc	acc	acc	gcc	ggg	ctg	atg	gcc	ccc	acc	gtc	gag	gcg	1248
Val	Ala	Leu	Thr	Thr	Thr	Ala	Gly	Leu	Met	Ala	Pro	Thr	Val	Glu	Ala	
			405					410						415		
acc	gcg	ggc	ctg	tcc	agc	ctc	gac	ccc	gcg	ttc	atc	gtc	atc	gcc	atc	1296
Thr	Ala	Gly	Leu	Ser	Ser	Leu	Asp	Pro	Ala	Phe	Ile	Val	Ile	Ala	Ile	
			420					425						430		
gcc	gcc	ggc	gcg	acc	gcg	ctc	agc	cac	gtc	aac	gac	tcc	ggc	ttc	tgg	1344
Ala	Ala	Gly	Ala	Thr	Ala	Leu	Ser	His	Val	Asn	Asp	Ser	Gly	Phe	Trp	
		435					440					445				
ctc	gtg	ggg	cgc	ttc	ctg	ggc	atg	gac	gtg	ccc	acg	ctg	cgc	acg		1392
Leu	Val	Gly	Arg	Phe	Leu	Gly	Met	Asp	Val	Pro	Thr	Thr	Leu	Arg	Thr	
	450					455					460					
tgg	acg	gtc	atg	gag	acc	ctc	atc	ggc	ctc	gtc	ggc	ttc	gcg	ctg	gcc	1440
Trp	Thr	Val	Met	Glu	Thr	Leu	Ile	Gly	Leu	Val	Gly	Phe	Ala	Leu	Ala	

465 470 475 480
ttc ctc ggg tac ctg gtc ctg tga
Phe Leu Gly Tyr Leu Val Leu
 485

```
<210> 10103
<211> 487
<212> PRT
<213> Kineococcus radiotolerans SRS30216
```

Met	Glu	Thr	Val	Thr	Pro	Ala	Tyr	Gly	Thr	Ser	Thr	Leu	Leu	Leu	Ile
1				5					10					15	
Ala	Ala	Ala	Ala	Val	Ala	Leu	Leu	Leu	Leu	Leu	Ile	Ile	Arg	Phe	Lys
			20					25					30		
Leu	His	Ala	Phe	Val	Ala	Leu	Val	Leu	Val	Ser	Ala	Val	Thr	Ala	Val
		35					40					45			
Val	Thr	Val	Gly	Pro	Asp	Gly	Ser	Leu	Leu	Asp	Val	Val	Asp	Val	Leu
	50					55					60				
Thr	Ala	Gly	Phe	Gly	Ser	Thr	Leu	Ala	Ser	Val	Ala	Leu	Leu	Val	Gly
65					70					75					80
Phe	Gly	Val	Met	Ile	Gly	Arg	Leu	Leu	Glu	Val	Thr	Gly	Gly	Ala	Gln
			85						90					95	
Val	Leu	Ala	Asp	Thr	Leu	Val	Ala	Arg	Phe	Gly	Glu	Lys	Arg	Ala	Pro
			100					105					110		
Leu	Ala	Leu	Gly	Val	Ala	Ser	Leu	Ile	Phe	Gly	Phe	Pro	Ile	Phe	Phe
		115					120					125			
Asp	Ala	Gly	Leu	Val	Val	Phe	Leu	Pro	Ile	Ile	Phe	Ser	Val	Ala	Arg
	130					135					140				
Arg	Phe	Gly	Gly	Ser	Val	Leu	Thr	Tyr	Ala	Leu	Pro	Ala	Ala	Gly	Ala
145					150					155					160
Phe	Ala	Val	Met	His	Ala	Phe	Val	Pro	Pro	His	Pro	Gly	Pro	Val	Ala
			165						170					175	
Ala	Gly	Glu	Leu	Leu	Gly	Ala	Asp	Ile	Gly	Val	Leu	Ile	Leu	Val	Gly
			180					185					190		
Leu	Val	Leu	Ala	Val	Pro	Thr	Trp	Phe	Thr	Ala	Ser	Tyr	Leu	Phe	Gly
		195					200					205			
Leu	Trp	Ala	Gly	Arg	Arg	Thr	Asp	Val	Pro	Leu	Pro	Ala	Glu	Trp	Ala
	210					215					220				
Glu	Arg	Leu	Ala	Ala	Asn	Thr	Ala	Gly	Gln	Ala	Gly	Pro	Ser	Gly	Thr
225					230					235					240
Ala	Gly	Ala	Ala	Thr	Ala	Pro	Gly	Ala	Thr	Gly	Gly	Thr	Gly	Thr	Pro
			245						250					255	
Gly	Pro	Ala	Ala	Pro	Arg	Phe	Ser	Thr	Val	Leu	Leu	Val	Leu	Leu	Leu
			260					265					270		
Pro	Leu	Val	Leu	Ile	Phe	Leu	Asn	Thr	Gly	Leu	Asn	Thr	Leu	Ala	Thr
		275					280					285			
Ala	Gly	Ala	Val	Asp	Gly	Glu	Ala	Thr	Trp	Val	Gln	Val	Leu	Arg	Leu
	290					295					300				
Val	Gly	Gln	Thr	Pro	Ile	Ala	Leu	Leu	Ile	Ala	Val	Leu	Val	Thr	Met
305					310					315					320
Val	Val	Leu	Ser	Arg	Gly	Arg	Leu	Thr	Arg	Gly	Glu	Val	Glu	Asp	Leu
			325						330				335		
Ala	Asn	Ser	Ser	Leu	Gly	Pro	Val	Cys	Ala	Val	Ile	Leu	Ile	Thr	Gly
			340					345							

PF59083SeqList PF59083.txt

Trp Thr Val Met Glu Thr Leu Ile Gly Leu Val Gly Phe Ala Leu Ala
465 470 475 480
Phe Leu Gly Tyr Leu Val Leu
485

<210> 10104
<211> 1353
<212> DNA
<213> Xanthobacter autotrophicus Py2

<220>
<221> CDS
<222> (1)..(1353)
<223> transl_table=11

<400> 10104
atg ctg ggc atg agc aag gac aca ttt cta ctg gtc gac gcg gcg gtg 48
Met Leu Gly Met Ser Lys Asp Thr Phe Leu Leu Val Asp Ala Ala Val
1 5 10 15
acc atc atc ggc ctc atc gtc ctc atc acg cgc ttc aag gtc cac ccc 96
Thr Ile Ile Gly Leu Ile Val Leu Ile Thr Arg Phe Lys Val His Pro
20 25 30
ttc gtg gcg ttg atc ctg gcc gcc ggc ttc ctg ggg ctc agc tcc ggc 144
Phe Val Ala Leu Ile Leu Ala Ala Gly Phe Leu Gly Leu Ser Ser Gly
35 40 45
atg ccg gtg gac ctc atc atg aag tcg ttc cag gac ggc ttc ggc ggc 192
Met Pro Val Asp Leu Ile Met Lys Ser Phe Gln Asp Gly Phe Gly Gly
50 55 60
gtg ctc ggc ttc gtc ggc atc gtg ctc ggc ctc ggc acc atg ctg ggc 240
Val Leu Gly Phe Val Gly Ile Val Leu Gly Leu Gly Thr Met Leu Gly
65 70 75 80
aag ctg atg gcc gaa tcg ggc ggc gca gac cag atc gcc cag acc ctc 288
Lys Leu Met Ala Glu Ser Gly Gly Ala Asp Gln Ile Ala Gln Thr Leu
85 90 95
atc aat gcc ttc ggc aaa cag cgg gtg cac tgg gcc atc atg ctc gcc 336
Ile Asn Ala Phe Gly Lys Gln Arg Val His Trp Ala Ile Met Leu Ala
100 105 110
gcc ttc ctg gtg ggc att ccc ctg ttc ttc gaa atc ggc ttc gtg ctg 384
Ala Phe Leu Val Gly Ile Pro Leu Phe Phe Glu Ile Gly Phe Val Leu
115 120 125
ctc atc ccg ctt gtc ttc gtc atg gcg agc cgc acc ggc gtg tcg ctg 432
Leu Ile Pro Leu Val Phe Val Met Ala Ser Arg Thr Gly Val Ser Leu
130 135 140
gtg aag gtg ggc att tcg ctt ttg gcg ggt ctc tcg gcg gtg cac ggc 480
Val Lys Val Gly Ile Ser Leu Leu Ala Gly Leu Ser Ala Val His Gly
145 150 155 160
ctg gtg ccg ccc cac ccg ggg ccg ctg ctg gcg gtg ggt gtg ttc ggc 528
Leu Val Pro Pro His Pro Gly Pro Leu Leu Ala Val Gly Val Phe Gly
165 170 175
gcc gat atc ggc aag acc atc ttc tac ggc ctc atc gtc ggc ctg ccc 576
Ala Asp Ile Gly Lys Thr Ile Phe Tyr Gly Leu Ile Val Gly Leu Pro
180 185 190
gcg gcc gcc atc gcc ggc ccc atg ttc ggc tcg ttc att tcg ccg gcg 624
Ala Ala Ala Ile Ala Gly Pro Met Phe Gly Ser Phe Ile Ser Arg Arg
195 200 205
atc ccg ggc cat ccg tct ccg gag ctg gtc gcc cag ttc gtt cag gac 672
Ile Pro Gly His Pro Ser Pro Glu Leu Val Ala Gln Phe Val Gln Asp
210 215 220
gag cgc gcc cac acc ctg ccc ggc ttc ggc gtc acc ctc gcc acc atc 720
Glu Arg Ala His Thr Leu Pro Gly Phe Gly Val Thr Leu Ala Thr Ile
225 230 235 240
ctg ctg ccg gtg gtg ctg atg ctg ctg aag gcg ttc gcc gat gtc gcc 768
Leu Leu Pro Val Val Leu Met Leu Leu Lys Ala Phe Ala Asp Val Ala
245 250 255
ttc gcc gcc ggc cat ccg gtg cgg gcg tgg ctg gac ctc atc ggc cac 816
Phe Ala Ala Gly His Pro Val Arg Ala Trp Leu Asp Leu Ile Gly His
260 265 270
ccc atc acc gcg ctg ctc gcg gcg ctg ctg ctg tcg ctc tac acc ttc 864
Pro Ile Thr Ala Leu Leu Ala Ala Leu Leu Leu Ser Leu Tyr Thr Phe

PF59083SeqList PF59083.txt

275	280	285	
ggc agc gcg cgc ggc ttc tcg cgc gag gtc atc ggc aag cac ctc aac	280	285	912
Gly Ser Ala Arg Gly Phe Ser Arg Glu Val Ile Gly Lys His Leu Asn	290	300	
gac agc ctc ctg ccg gtg gcg ggc atc atc ctg atc gtc ggc gcc ggc	295	315	960
Asp Ser Leu Leu Pro Val Ala Gly Ile Ile Leu Ile Val Gly Ala Gly	310	330	
ggc ggc ttc aag cag atg ctg gtg gcg agc ggc gtg ggc gat gtc att	325	335	1008
Gly Gly Phe Lys Gln Met Leu Val Ala Ser Gly Val Gly Asp Val Ile	340	350	
ggc cat atg gcg gtg cag gcc cat gtg aac ccc atc ctc ctc gcc tgg	345	355	1056
Gly His Met Ala Val Gln Ala His Val Asn Pro Ile Leu Leu Ala Trp	360	365	
ctg gtg gcg gcg gtg atc cgg gtg gcc acg ggc tcc gcc acg gtg gcg	370	380	1104
Leu Val Ala Ala Val Ile Arg Val Ala Thr Gly Ser Ala Thr Val Ala	375	385	
acc atc acc ggg gcc ggc atc gta gcc ccg gtc ctc gcc ctg acg ccg	390	400	1152
Thr Ile Thr Gly Ala Gly Ile Val Ala Pro Val Leu Ala Leu Thr Pro	405	415	
ggc gtc aac cgt gag ctg ctg gtg ctg gcc acc ggc gcc ggc tcg gtg	410	420	1200
Gly Val Asn Arg Glu Leu Val Leu Ala Thr Gly Ala Gly Ser Val	425	430	
gtg ctc tcc cac gtc aac gac gcc ggc ttc tgg ctg gtg aag cag tat	435	440	1248
Val Leu Ser His Val Asn Asp Ala Gly Phe Trp Leu Val Lys Gln Tyr	445		
ttc aac atg acg gtg gag gag acc ttc aag acc tgg acc gcc atg gag			1296
Phe Asn Met Thr Val Glu Glu Thr Phe Lys Thr Trp Thr Ala Met Glu			
acg atc ctg tcg gtg gtg gcc ctg ggc ctg atc atg ctg ctt tcg ctg			1344
Thr Ile Leu Ser Val Val Ala Leu Gly Leu Ile Met Leu Leu Ser Leu			
gtg gtg tag			1353
Val Val			
450			

<210> 10105

<211> 450

<212> PRT

<213> Xanthobacter autotrophicus Py2

<400> 10105

Met Leu Gly Met Ser Lys Asp Thr Phe Leu Leu Val Asp Ala Ala Val	1	5	10	15
Thr Ile Ile Gly Leu Ile Val Leu Ile Thr Arg Phe Lys Val His Pro	20	25	30	35
Phe Val Ala Leu Ile Leu Ala Ala Gly Phe Leu Gly Leu Ser Ser Gly	40	45	50	55
Met Pro Val Asp Leu Ile Met Lys Ser Phe Gln Asp Gly Phe Gly Gly	60	65	70	75
Val Leu Gly Phe Val Gly Ile Val Leu Gly Leu Thr Met Leu Gly	80	85	90	95
Lys Leu Met Ala Glu Ser Gly Gly Ala Asp Gln Ile Ala Gln Thr Leu	100	105	110	115
Ile Asn Ala Phe Gly Lys Gln Arg Val His Trp Ala Ile Met Leu Ala	120	125	130	135
Ala Phe Leu Val Gly Ile Pro Leu Phe Phe Glu Ile Gly Phe Val Leu	140	145	150	155
Leu Ile Pro Leu Val Phe Val Met Ala Ser Arg Thr Gly Val Ser Leu	160	165	170	175
Val Lys Val Gly Ile Ser Leu Leu Ala Gly Leu Ser Ala Val His Gly	180	185	190	195
Leu Val Pro Pro His Pro Gly Pro Leu Leu Ala Val Gly Val Phe Gly	200	205	210	215
Ala Asp Ile Gly Lys Thr Ile Phe Tyr Gly Leu Ile Val Gly Leu Pro	220			
Ala Ala Ala Ile Ala Gly Pro Met Phe Gly Ser Phe Ile Ser Arg Arg				
Ile Pro Gly His Pro Ser Pro Glu Leu Val Ala Gln Phe Val Gln Asp				

PF59083SeqList PF59083.txt

Glu Arg Ala His Thr Leu Pro Gly Phe Gly Val Thr Leu Ala Thr Ile
 225 230 235 240
 Leu Leu Pro Val Val Leu Met Leu Leu Lys Ala Phe Ala Asp Val Ala
 245 250 255
 Phe Ala Ala Gly His Pro Val Arg Ala Trp Leu Asp Leu Ile Gly His
 260 265 270
 Pro Ile Thr Ala Leu Leu Ala Ala Leu Leu Leu Ser Leu Tyr Thr Phe
 275 280 285
 Gly Ser Ala Arg Gly Phe Ser Arg Glu Val Ile Gly Lys His Leu Asn
 290 295 300
 Asp Ser Leu Leu Pro Val Ala Gly Ile Ile Leu Ile Val Gly Ala Gly
 305 310 315 320
 Gly Gly Phe Lys Gln Met Leu Val Ala Ser Gly Val Gly Asp Val Ile
 325 330 335
 Gly His Met Ala Val Gln Ala His Val Asn Pro Ile Leu Leu Ala Trp
 340 345 350
 Leu Val Ala Ala Val Ile Arg Val Ala Thr Gly Ser Ala Thr Val Ala
 355 360 365
 Thr Ile Thr Gly Ala Gly Ile Val Ala Pro Val Leu Ala Leu Thr Pro
 370 375 380
 Gly Val Asn Arg Glu Leu Val Leu Ala Thr Gly Ala Gly Ser Val
 385 390 395 400
 Val Leu Ser His Val Asn Asp Ala Gly Phe Trp Leu Val Lys Gln Tyr
 405 410 415
 Phe Asn Met Thr Val Glu Glu Thr Phe Lys Thr Trp Thr Ala Met Glu
 420 425 430
 Thr Ile Leu Ser Val Val Ala Leu Gly Leu Ile Met Leu Leu Ser Leu
 435 440 445
 Val Val
 450

<210> 10106

<211> 1371

<212> DNA

<213> Bacillus halodurans C-125

<220>

<221> CDS

<222> (1)..(1371)

<223> transl_table=11

<400> 10106

atg gaa gtt tca gga gct caa atg att tta ggt ctt gtc att gcc att	48
Met Glu Val Ser Gly Ala Gln Met Ile Leu Gly Leu Val Ile Ala Ile	
1 5 10 15	
atg gtt tta att ttt cta gtc atc aaa acg aaa gtg cat gtc ttt tta	96
Met Val Leu Ile Phe Leu Val Ile Lys Thr Lys Val His Val Phe Leu	
20 25 30	
gcc ctg atc atc gcg gct tca ata acc ggt cta gtc gga ggg atg gca	144
Ala Leu Ile Ile Ala Ala Ser Ile Thr Gly Leu Val Gly Gly Met Ala	
35 40 45	
ccg cct gat gtt gta agc gcc atc aca gaa gga ttt gga agc acg ctc	192
Pro Pro Asp Val Val Ser Ala Ile Thr Glu Gly Phe Gly Ser Thr Leu	
50 55 60	
ggg tct gtg gcg atc att atc ggt ttc ggt gta atg atg gga cga ata	240
Gly Ser Val Ala Ile Ile Ile Gly Phe Gly Val Met Met Gly Arg Ile	
65 70 75 80	
tta gaa gta tct gga gcg gcc gaa cga cta gct tat acg gtc gtc aaa	288
Leu Glu Val Ser Gly Ala Ala Glu Arg Leu Ala Tyr Thr Val Val Lys	
85 90 95	
gtg tta gga aag cgc aaa gag gag tgg gcg atg gct gtt acg ggc tat	336
Val Leu Gly Lys Arg Lys Glu Glu Trp Ala Met Ala Val Thr Gly Tyr	
100 105 110	
atc gta tcg att cct ata ttt gta gat tct gcc ttt att ata tta agt	384
Ile Val Ser Ile Pro Ile Phe Val Asp Ser Ala Phe Ile Ile Leu Ser	
115 120 125	
aca tta gcg aaa gcg cta tca aag aaa aca ggg aag tcc att gtt acg	432
Thr Leu Ala Lys Ala Leu Ser Lys Lys Thr Gly Lys Ser Ile Val Thr	
130 135 140	

PF59083SeqList PF59083.txt

ctc	gcc	att	gcc	ctt	gct	ggt	gga	gcg	gtc	gtt	atg	cac	cat	gct	gta	480
Leu	Ala	Ile	Ala	Leu	Ala	Gly	Gly	Ala	Val	Val	Met	His	His	Ala	Val	
145					150					155					160	
cca	ccg	aca	cct	ggg	ccg	cta	ggg	ggt	gca	gga	att	ttt	ggt	gtg	gac	528
Pro	Pro	Thr	Pro	Gly	Pro	Leu	Gly	Val	Ala	Gly	Ile	Phe	Gly	Val	Asp	
			165						170					175		
ggt	ggc	tta	atg	atc	tta	tcg	ggg	ttg	atc	ttt	ggg	att	ccg	att	atc	576
Val	Gly	Leu	Met	Ile	Leu	Ser	Gly	Leu	Ile	Phe	Gly	Ile	Pro	Ile	Ile	
			180					185					190			
att	ggt	acc	ggt	tta	tat	gca	aaa	tgg	atc	ggg	aaa	aaa	atc	tat	cag	624
Ile	Val	Thr	Val	Leu	Tyr	Ala	Lys	Trp	Ile	Gly	Lys	Lys	Ile	Tyr	Gln	
			195				200					205				
ctt	ccc	gat	gat	gac	ggc	tta	gga	tgg	att	aga	cca	gag	caa	gag	gtg	672
Leu	Pro	Asp	Asp	Asp	Gly	Leu	Gly	Trp	Ile	Arg	Pro	Glu	Gln	Glu	Val	
	210					215					220					
aac	gtc	gag	gat	tgg	ctt	gaa	gag	aaa	gaa	aac	aaa	gag	cta	cca	tcg	720
Asn	Val	Glu	Asp	Trp	Leu	Glu	Glu	Lys	Glu	Asn	Lys	Glu	Leu	Pro	Ser	
225					230					235					240	
ttg	ctt	cg	tcc	gct	gca	ccg	atc	gtc	gta	ccg	att	ctc	tta	att	ttc	768
Leu	Leu	Arg	Ser	Ala	Ala	Pro	Ile	Val	Val	Pro	Ile	Leu	Leu	Ile	Phe	
				245					250					255		
atg	aat	acg	acg	gta	acg	gcc	atc	gga	tta	gaa	gga	acg	ctc	gta	gag	816
Met	Asn	Thr	Thr	Val	Thr	Ala	Ile	Gly	Leu	Glu	Gly	Thr	Leu	Val	Glu	
				260				265					270			
tac	ggt	caa	ttt	ttc	ggt	tcc	ccc	gtg	atc	gct	gtt	ggg	att	gca	gtc	864
Tyr	Val	Gln	Phe	Phe	Gly	Ser	Pro	Val	Ile	Ala	Val	Gly	Ile	Ala	Val	
			275				280					285				
ctc	ctt	gcc	atc	tat	gga	tta	ttc	aac	cac	gtg	aag	cg	tcg	gaa	gct	912
Leu	Leu	Ala	Ile	Tyr	Gly	Leu	Phe	Asn	His	Val	Lys	Arg	Ser	Glu	Ala	
	290					295					300					
ctt	gat	cga	atg	gag	gaa	ggg	att	cag	aca	gct	ggg	ata	atc	ttg	tta	960
Leu	Asp	Arg	Met	Glu	Glu	Gly	Ile	Gln	Thr	Ala	Gly	Ile	Ile	Leu	Leu	
305					310					315					320	
ggt	aca	gga	gca	ggt	gga	gcc	ctt	ggt	tat	gtg	cta	cg	caa	aca	gga	1008
Val	Thr	Gly	Ala	Gly	Gly	Ala	Leu	Gly	Tyr	Val	Leu	Arg	Gln	Thr	Gly	
				325					330					335		
gct	gga	gat	tat	ata	gcc	gaa	ctt	gta	gtt	gat	aca	gga	att	cct	gcg	1056
Ala	Gly	Asp	Tyr	Ile	Ala	Glu	Leu	Val	Val	Asp	Thr	Gly	Ile	Pro	Ala	
			340					345					350			
att	ttg	ctt	ccg	ttt	gtg	atc	gct	tcg	ctc	gtc	cg	ttg	att	caa	gga	1104
Ile	Leu	Leu	Pro	Phe	Val	Ile	Ala	Ser	Leu	Val	Arg	Leu	Ile	Gln	Gly	
			355				360					365				
agc	ggg	acg	ggt	gcc	atg	ata	acg	gct	gcg	tca	att	tct	gcg	cca	atc	1152
Ser	Gly	Thr	Val	Ala	Met	Ile	Thr	Ala	Ala	Ser	Ile	Ser	Ala	Pro	Ile	
	370					375					380					
tta	aca	ggg	atg	gat	gtg	aac	ctt	gtc	cta	gcc	gcg	caa	gca	gcg	gcc	1200
Leu	Thr	Gly	Met	Asp	Val	Asn	Leu	Val	Leu	Ala	Ala	Gln	Ala	Ala	Ala	
385					390					395					400	
ctc	gga	gcg	atg	gtg	ttt	tcc	tac	ttc	aat	gat	agt	ctg	ttt	tgg	gtc	1248
Leu	Gly	Ala	Met	Val	Phe	Ser	Tyr	Phe	Asn	Asp	Ser	Leu	Phe	Trp	Val	
				405					410					415		
gtg	aac	cg	acg	att	ggg	att	aaa	gac	ccg	aaa	gag	caa	atg	ctc	gtt	1296
Val	Asn	Arg	Thr	Ile	Gly	Ile	Lys	Asp	Pro	Lys	Glu	Gln	Met	Leu	Val	
			420					425					430			
tgg	tct	gtc	cca	aca	acg	ctc	agc	tgg	tta	acg	gca	ctc	gtt	tgc	tta	1344
Trp	Ser	Val	Pro	Thr	Thr	Leu	Ser	Trp	Leu	Thr	Ala	Leu	Val	Cys	Leu	
			435				440					445				
ctt	atc	gcc	aat	ctc	att	ttc	gga	taa								1371
Leu	Ile	Ala	Asn	Leu	Ile	Phe	Gly									
	450					455										

<210> 10107

<211> 456

<212> PRT

<213> Bacillus halodurans C-125

<400> 10107

Met Glu Val Ser Gly Ala Gln Met Ile Leu Gly Leu Val Ile Ala Ile
1 5 10 15

PF59083SeqList PF59083.txt

```

Met Val Leu Ile Phe Leu Val Ile Lys Thr Lys Val His Val Phe Leu
      20      25      30
Ala Leu Ile Ile Ala Ala Ser Ile Thr Gly Leu Val Gly Gly Met Ala
      35      40      45
Pro Pro Asp Val Val Ser Ala Ile Thr Glu Gly Phe Gly Ser Thr Leu
      50      55      60
Gly Ser Val Ala Ile Ile Ile Gly Phe Gly Val Met Met Gly Arg Ile
65      70      75      80
Leu Glu Val Ser Gly Ala Ala Glu Arg Leu Ala Tyr Thr Val Val Lys
      85      90      95
Val Leu Gly Lys Arg Lys Glu Glu Trp Ala Met Ala Val Thr Gly Tyr
      100      105      110
Ile Val Ser Ile Pro Ile Phe Val Asp Ser Ala Phe Ile Ile Leu Ser
      115      120      125
Thr Leu Ala Lys Ala Leu Ser Lys Lys Thr Gly Lys Ser Ile Val Thr
      130      135      140
Leu Ala Ile Ala Leu Ala Gly Gly Ala Val Val Met His His Ala Val
145      150      155      160
Pro Pro Thr Pro Gly Pro Leu Gly Val Ala Gly Ile Phe Gly Val Asp
      165      170      175
Val Gly Leu Met Ile Leu Ser Gly Leu Ile Phe Gly Ile Pro Ile Ile
      180      185      190
Ile Val Thr Val Leu Tyr Ala Lys Trp Ile Gly Lys Lys Ile Tyr Gln
      195      200      205
Leu Pro Asp Asp Asp Gly Leu Gly Trp Ile Arg Pro Glu Gln Glu Val
      210      215      220
Asn Val Glu Asp Trp Leu Glu Glu Lys Glu Asn Lys Glu Leu Pro Ser
225      230      235      240
Leu Leu Arg Ser Ala Ala Pro Ile Val Val Pro Ile Leu Leu Ile Phe
      245      250      255
Met Asn Thr Thr Val Thr Ala Ile Gly Leu Glu Gly Thr Leu Val Glu
      260      265      270
Tyr Val Gln Phe Phe Gly Ser Pro Val Ile Ala Val Gly Ile Ala Val
      275      280      285
Leu Leu Ala Ile Tyr Gly Leu Phe Asn His Val Lys Arg Ser Glu Ala
      290      295      300
Leu Asp Arg Met Glu Glu Gly Ile Gln Thr Ala Gly Ile Ile Leu Leu
305      310      315      320
Val Thr Gly Ala Gly Gly Ala Leu Gly Tyr Val Leu Arg Gln Thr Gly
      325      330      335
Ala Gly Asp Tyr Ile Ala Glu Leu Val Val Asp Thr Gly Ile Pro Ala
      340      345      350
Ile Leu Leu Pro Phe Val Ile Ala Ser Leu Val Arg Leu Ile Gln Gly
      355      360      365
Ser Gly Thr Val Ala Met Ile Thr Ala Ala Ser Ile Ser Ala Pro Ile
      370      375      380
Leu Thr Gly Met Asp Val Asn Leu Val Leu Ala Ala Gln Ala Ala Ala
385      390      395      400
Leu Gly Ala Met Val Phe Ser Tyr Phe Asn Asp Ser Leu Phe Trp Val
      405      410      415
Val Asn Arg Thr Ile Gly Ile Lys Asp Pro Lys Glu Gln Met Leu Val
      420      425      430
Trp Ser Val Pro Thr Thr Leu Ser Trp Leu Thr Ala Leu Val Cys Leu
      435      440      445
Leu Ile Ala Asn Leu Ile Phe Gly
      450      455

```

<210> 10108

<211> 1350

<212> DNA

<213> Pasteurella multocida subsp. multocida str. Pm70

<220>

<221> CDS

<222> (1)..(1350)

<223> transl_table=11

<400> 10108

atg tta att ttg att atg atc atc gca gtc tta gtc tta ttg ctg ctg

PF59083SeqList PF59083.txt

Met	Leu	Ile	Leu	Ile	Met	Ile	Ile	Ala	Val	Leu	Val	Leu	Leu	Leu	Leu	
1				5					10					15		
att	atg	aaa	ttc	cgc	gtg	cat	gcg	ttc	ggt	gca	cta	att	atc	gtc	agt	96
Ile	Met	Lys	Phe	Arg	Val	His	Ala	Phe	Val	Ala	Leu	Ile	Ile	Val	Ser	
			20					25				30				
tta	ctg	acc	gca	ctt	gcg	aca	ggc	ggt	cca	ggt	aat	aaa	att	ctg	cct	144
Leu	Leu	Thr	Ala	Leu	Ala	Thr	Gly	Val	Pro	Val	Asn	Lys	Ile	Leu	Pro	
		35					40				45					
acg	cta	ttg	act	ggc	ttt	ggt	aat	acc	ctt	gct	gcg	ggt	gca	tta	ctc	192
Thr	Leu	Leu	Thr	Gly	Phe	Gly	Asn	Thr	Leu	Ala	Val	Ala	Val	Leu	Leu	
		50				55					60					
ggt	ggt	tta	ggc	gct	atg	att	ggg	cga	tta	ctc	gaa	att	aca	ggc	ggc	240
Val	Gly	Leu	Gly	Ala	Met	Ile	Gly	Arg	Leu	Leu	Glu	Ile	Thr	Gly	Gly	
		65			70			75						80		
gcc	aaa	gtc	ttg	gca	gat	acg	ctc	att	aac	aaa	ttc	ggc	gag	aaa	aaa	288
Ala	Lys	Val	Leu	Ala	Asp	Thr	Leu	Ile	Asn	Lys	Phe	Gly	Glu	Lys	Lys	
			85					90						95		
gcg	cct	ttt	gcc	tta	ggg	gtc	gcg	tcc	tta	ctg	ttt	ggt	ttc	cca	att	336
Ala	Pro	Phe	Ala	Leu	Gly	Val	Ala	Ser	Leu	Leu	Phe	Gly	Phe	Pro	Ile	
			100					105					110			
ttc	ttt	gat	gcg	ggt	tta	gtg	gtg	atg	tta	cca	atc	att	ttc	agt	gta	384
Phe	Phe	Asp	Ala	Gly	Leu	Val	Val	Met	Leu	Pro	Ile	Ile	Phe	Ser	Val	
		115					120					125				
gct	aaa	caa	ttt	ggt	ggc	tca	aca	tta	cgc	tat	gcc	tta	cct	tct	gcg	432
Ala	Lys	Gln	Phe	Gly	Gly	Ser	Thr	Leu	Arg	Tyr	Ala	Leu	Pro	Ser	Ala	
		130				135					140					
ggt	gcc	ttt	gcc	gtc	atg	cat	gct	ttc	ctt	ccg	cct	cat	ccg	ggt	cca	480
Gly	Ala	Phe	Ala	Val	Met	His	Ala	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
		145			150			155						160		
ggt	gca	tcg	ggt	gat	tta	ggt	gct	aat	ggt	tta	ctc	gtg	att	att	att	528
Val	Ala	Ser	Gly	Asp	Leu	Leu	Gly	Ala	Asn	Met	Gly	Leu	Leu	Val	Ile	
				165				170						175		
ggt	ggt	tta	att	tgc	gcg	att	cca	aca	tgg	tat	atc	gct	gct	tat	tta	576
Val	Gly	Leu	Ile	Cys	Ala	Ile	Pro	Thr	Trp	Tyr	Ile	Ala	Ala	Tyr	Leu	
			180					185					190			
ttc	ggt	tta	tat	tcc	ggt	aag	aaa	atc	aac	tta	gca	ctg	cct	aaa	gcc	624
Phe	Gly	Leu	Tyr	Ser	Gly	Lys	Lys	Ile	Asn	Leu	Ala	Leu	Pro	Lys	Ala	
		195					200					205				
ttt	tta	tca	ggt	aat	gct	att	cat	gaa	acg	gct	gct	caa	aat	cca	ccg	672
Phe	Leu	Ser	Gly	Asn	Ala	Ile	His	Glu	Thr	Ala	Ala	Gln	Asn	Pro	Pro	
		210				215					220					
agt	ttc	aaa	aaa	gtg	cta	ttt	att	ctt	ctg	tta	cct	atc	tgt	tta	att	720
Ser	Phe	Lys	Lys	Val	Leu	Phe	Ile	Leu	Leu	Leu	Pro	Ile	Cys	Leu	Ile	
		225			230			235						240		
cta	ttt	gac	aca	ggt	tta	aat	aca	tta	agt	ggt	gcc	aaa	gtg	att	gat	768
Leu	Phe	Asp	Thr	Gly	Leu	Asn	Thr	Leu	Ser	Val	Ala	Lys	Val	Ile	Asp	
			245					250					255			
ggc	tca	caa	gtg	tgg	gtc	gaa	agc	tta	cgc	tta	tta	ggc	aaa	acc	cct	816
Gly	Ser	Gln	Val	Trp	Val	Glu	Ser	Leu	Arg	Leu	Leu	Gly	Lys	Thr	Pro	
		260					265						270			
atc	gca	ctc	ctt	att	act	ttg	att	ggt	gcc	atc	att	tta	tta	aaa	gaa	864
Ile	Ala	Leu	Leu	Ile	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Lys	Glu	
		275					280					285				
caa	cgt	agc	tat	gaa	caa	att	gaa	aaa	att	tgt	gat	aac	gct	tta	ggc	912
Gln	Arg	Ser	Tyr	Glu	Gln	Ile	Glu	Lys	Ile	Cys	Asp	Asn	Ala	Leu	Gly	
		290				295					300					
cca	att	tgt	gcc	att	gtc	ttg	ggt	acc	ggg	gct	ggg	ggg	atg	ttt	ggc	960
Pro	Ile	Cys	Ala	Ile	Val	Leu	Val	Thr	Gly	Ala	Gly	Gly	Met	Phe	Gly	
		305			310					315					320	
ggt	gta	tta	cgc	gcg	agc	ggc	att	ggt	aac	gaa	tta	tcc	gca	atg	ctg	1008
Gly	Val	Leu	Arg	Ala	Ser	Gly	Ile	Gly	Asn	Glu	Leu	Ser	Ala	Met	Leu	
			325					330					335			
tct	gat	aca	ggt	tta	cct	ggt	att	ggt	gct	gca	ttt	att	att	gca	ctt	1056
Ser	Asp	Thr	Gly	Leu	Pro	Val	Ile	Val	Ala	Ala	Phe	Ile	Ile	Ala	Leu	
			340					345					350			
gcc	tta	cgt	ggt	gcc	caa	ggt	tca	gcc	act	ggt	gcc	tta	acc	acc	gcc	1104
Ala	Leu	Arg	Val	Ala	Gln	Gly	Ser	Ala	Thr	Val	Ala	Leu	Thr	Thr	Ala	
		355				360						365				
tct	gcg	ctc	att	gca	cca	act	ggt	gct	gca	aca	act	gga	ctc	agt	caa	1152

PF59083SeqList PF59083.txt

Ser	Ala	Leu	Ile	Ala	Pro	Thr	Val	Ala	Ala	Thr	Thr	Gly	Leu	Ser	Gln	
370						375					380					
ctc	gat	tta	tgc	ttt	att	gtg	att	gcc	att	gcc	tct	ggg	gca	aca	gct	1200
Leu	Asp	Leu	Cys	Phe	Ile	Val	Ile	Ala	Ile	Ala	Ser	Gly	Ala	Thr	Ala	
385					390					395					400	
tta	tca	cac	gtc	aat	gac	tca	ggg	ttc	tgg	ctt	gtg	agc	cgt	ttc	tta	1248
Leu	Ser	His	Val	Asn	Asp	Ser	Gly	Phe	Trp	Leu	Val	Ser	Arg	Phe	Leu	
				405				410						415		
gaa	atg	gat	gaa	aaa	acc	aca	tta	aaa	acc	tgg	acc	gtg	atg	gaa	acc	1296
Glu	Met	Asp	Glu	Lys	Thr	Thr	Leu	Lys	Thr	Trp	Thr	Val	Met	Glu	Thr	
			420					425					430			
tta	att	ggg	ctt	ggt	gtt	ttc	gct	ctg	gct	gtt	att	ggg	agt	att	ctc	1344
Leu	Ile	Gly	Leu	Val	Gly	Phe	Ala	Leu	Ala	Val	Ile	Gly	Ser	Ile	Leu	
		435					440					445				
ttt	taa															1350
Phe																

<210> 10109

<211> 449

<212> PRT

<213> Pasteurella multocida subsp. multocida str. Pm70

<400> 10109

Met	Leu	Ile	Leu	Ile	Met	Ile	Ile	Ala	Val	Leu	Val	Leu	Leu	Leu	Leu	
1				5					10					15		
Ile	Met	Lys	Phe	Arg	Val	His	Ala	Phe	Val	Ala	Leu	Ile	Ile	Val	Ser	
			20					25					30			
Leu	Leu	Thr	Ala	Leu	Ala	Thr	Gly	Val	Pro	Val	Asn	Lys	Ile	Leu	Pro	
		35					40					45				
Thr	Leu	Leu	Thr	Gly	Phe	Gly	Asn	Thr	Leu	Ala	Ala	Val	Ala	Leu	Leu	
	50					55				60						
Val	Gly	Leu	Gly	Ala	Met	Ile	Gly	Arg	Leu	Leu	Glu	Ile	Thr	Gly	Gly	
65					70				75					80		
Ala	Lys	Val	Leu	Ala	Asp	Thr	Leu	Ile	Asn	Lys	Phe	Gly	Glu	Lys	Lys	
				85					90					95		
Ala	Pro	Phe	Ala	Leu	Gly	Val	Ala	Ser	Leu	Leu	Phe	Gly	Phe	Pro	Ile	
		100					105						110			
Phe	Phe	Asp	Ala	Gly	Leu	Val	Val	Met	Leu	Pro	Ile	Ile	Phe	Ser	Val	
		115					120					125				
Ala	Lys	Gln	Phe	Gly	Gly	Ser	Thr	Leu	Arg	Tyr	Ala	Leu	Pro	Ser	Ala	
	130					135					140					
Gly	Ala	Phe	Ala	Val	Met	His	Ala	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
145					150				155					160		
Val	Ala	Ser	Gly	Asp	Leu	Leu	Gly	Ala	Asn	Met	Gly	Leu	Leu	Val	Ile	
				165					170					175		
Val	Gly	Leu	Ile	Cys	Ala	Ile	Pro	Thr	Trp	Tyr	Ile	Ala	Ala	Tyr	Leu	
		180					185						190			
Phe	Gly	Leu	Tyr	Ser	Gly	Lys	Lys	Ile	Asn	Leu	Ala	Leu	Pro	Lys	Ala	
		195					200					205				
Phe	Leu	Ser	Gly	Asn	Ala	Ile	His	Glu	Thr	Ala	Ala	Gln	Asn	Pro	Pro	
	210					215					220					
Ser	Phe	Lys	Lys	Val	Leu	Phe	Ile	Leu	Leu	Leu	Pro	Ile	Cys	Leu	Ile	
225					230				235					240		
Leu	Phe	Asp	Thr	Gly	Leu	Asn	Thr	Leu	Ser	Val	Ala	Lys	Val	Ile	Asp	
			245						250					255		
Gly	Ser	Gln	Val	Trp	Val	Glu	Ser	Leu	Arg	Leu	Leu	Gly	Lys	Thr	Pro	
		260					265						270			
Ile	Ala	Leu	Ile	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Lys	Glu		
		275				280						285				
Gln	Arg	Ser	Tyr	Glu	Gln	Ile	Glu	Lys	Ile	Cys	Asp	Asn	Ala	Leu	Gly	
	290					295					300					
Pro	Ile	Cys	Ala	Ile	Val	Leu	Val	Thr	Gly	Ala	Gly	Gly	Met	Phe	Gly	
305					310					315				320		
Gly	Val	Leu	Arg	Ala	Ser	Gly	Ile	Gly	Asn	Glu	Leu	Ser	Ala	Met	Leu	
				325					330					335		
Ser	Asp	Thr	Gly	Leu	Pro	Val	Ile	Val	Ala	Ala	Phe	Ile	Ile	Ala	Leu	
			340					345					350			
Ala	Leu	Arg	Val	Ala	Gln	Gly	Ser	Ala	Thr	Val	Ala	Leu	Thr	Thr	Ala	

PF59083SeqList PF59083.txt

tac	agc	gcg	aaa	acc	ttc	agc	gaa	gaa	gag	atg	ccg	agc	ttt	ggc	gtc	672
Tyr	Ser	Ala	Lys	Thr	Phe	Ser	Glu	Glu	Glu	Met	Pro	Ser	Phe	Gly	Val	
	210					215					220					
agc	gtc	tg	acc	tct	ctg	gtg	ccg	gta	gta	ctg	atg	gcg	atg	cgt	gcg	720
Ser	Val	Trp	Thr	Ser	Leu	Val	Pro	Val	Val	Leu	Met	Ala	Met	Arg	Ala	
225					230					235					240	
att	gcc	gaa	atg	atc	ctg	ccg	aaa	gg	cac	gct	ttc	ctg	ccg	gta	gcg	768
Ile	Ala	Glu	Met	Ile	Leu	Pro	Lys	Gly	His	Ala	Phe	Leu	Pro	Val	Ala	
				245					250					255		
gag	ttc	ctc	gg	gac	ccg	gta	atg	gct	acg	ctg	att	gcc	gtg	ctg	att	816
Glu	Phe	Leu	Gly	Asp	Pro	Val	Met	Ala	Thr	Leu	Ile	Ala	Val	Leu	Ile	
			260					265					270			
gcg	atg	ttc	acc	ttt	gg	ctg	aac	cgt	gg	cgt	tca	atg	gat	cag	att	864
Ala	Met	Phe	Thr	Phe	Gly	Leu	Asn	Arg	Gly	Arg	Ser	Met	Asp	Gln	Ile	
			275				280					285				
aac	gac	acg	ctg	g	tct	tcc	atc	aaa	atc	att	gcg	atg	atg	ctg	ttg	912
Asn	Asp	Thr	Leu	Val	Ser	Ser	Ile	Lys	Ile	Ile	Ala	Met	Met	Leu	Leu	
	290					295					300					
atc	atc	gg	gg	ggc	gg	gcg	ttc	aag	cag	gtg	ctg	gta	gac	agc	ggc	960
Ile	Ile	Gly	Gly	Gly	Gly	Ala	Phe	Lys	Gln	Val	Leu	Val	Asp	Ser	Gly	
305				310						315					320	
gtg	gac	aaa	tac	att	gct	tcc	atg	atg	cac	gaa	acc	aac	att	tct	ccg	1008
Val	Asp	Lys	Tyr	Ile	Ala	Ser	Met	Met	His	Glu	Thr	Asn	Ile	Ser	Pro	
				325					330					335		
ctg	ctg	atg	gcc	tg	tcg	att	gct	gcc	gta	ctg	cgt	atc	gcg	ctg	gg	1056
Leu	Leu	Met	Ala	Trp	Ser	Ile	Ala	Ala	Val	Leu	Arg	Ile	Ala	Leu	Gly	
			340					345					350			
tcc	gca	acc	g	gcg	gca	atc	act	gcg	gg	gg	atc	gcg	gca	ccg	ctg	1104
Ser	Ala	Thr	Val	Ala	Ala	Ile	Thr	Ala	Gly	Gly	Ile	Ala	Ala	Pro	Leu	
			355				360					365				
att	gca	acg	acg	gg	g	agc	ccg	gag	ctg	atg	g	att	gcg	gtg	gg	1152
Ile	Ala	Thr	Thr	Gly	Val	Ser	Pro	Glu	Leu	Met	Val	Ile	Ala	Val	Gly	
	370					375					380					
tcc	gg	agt	gtg	att	ttc	tct	cat	gtg	aac	gat	ccg	ggc	ttc	tg	ctg	1200
Ser	Gly	Ser	Val	Ile	Phe	Ser	His	Val	Asn	Asp	Pro	Gly	Phe	Trp	Leu	
385					390				395						400	
ttc	aaa	gag	tac	ttt	aac	ctg	act	atc	ggc	gag	acc	atc	aaa	tcc	tg	1248
Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Thr	Ile	Gly	Glu	Thr	Ile	Lys	Ser	Trp	
				405					410					415		
tcg	atg	ctg	gaa	acc	att	atc	tcg	gtg	tgc	gg	ctg	gta	ggc	tgt	ctg	1296
Ser	Met	Leu	Glu	Thr	Ile	Ile	Ser	Val	Cys	Gly	Leu	Val	Gly	Cys	Leu	
			420					425					430			
ctg	ctg	aat	atg	gtg	att	tga										1317
Leu	Leu	Asn	Met	Val	Ile											
		435														

<210> 10111

<211> 438

<212> PRT

<213> Escherichia coli 0157:H7 EDL933

<220>

<221> misc_feature

<222> (208)..(208)

<223> The Xaa at location 208 stands for Leu, or Phe.

<400> 10111

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

PF59083SeqList PF59083.txt

Ile Gln Trp Ala Val Val Leu Thr Gly Phe Thr Val Gly Phe Ala Leu
 100 105 110
 Phe Tyr Glu Val Gly Phe Val Leu Met Leu Pro Leu Val Phe Thr Ile
 115 120 125
 Ala Ala Ser Ala Asn Ile Pro Leu Leu Tyr Val Gly Val Pro Met Ala
 130 135 140
 Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Gly Pro
 145 150 155 160
 Thr Ala Ile Ala Thr Ile Phe Asn Ala Asp Met Gly Lys Thr Leu Leu
 165 170 175
 Tyr Gly Thr Ile Leu Ala Ile Pro Thr Val Ile Leu Ala Gly Pro Val
 180 185 190
 Tyr Ala Arg Val Leu Lys Gly Ile Asp Lys Pro Ile Pro Glu Gly Xaa
 195 200 205
 Tyr Ser Ala Lys Thr Phe Ser Glu Glu Glu Met Pro Ser Phe Gly Val
 210 215 220
 Ser Val Trp Thr Ser Leu Val Pro Val Val Leu Met Ala Met Arg Ala
 225 230 235 240
 Ile Ala Glu Met Ile Leu Pro Lys Gly His Ala Phe Leu Pro Val Ala
 245 250 255
 Glu Phe Leu Gly Asp Pro Val Met Ala Thr Leu Ile Ala Val Leu Ile
 260 265 270
 Ala Met Phe Thr Phe Gly Leu Asn Arg Gly Arg Ser Met Asp Gln Ile
 275 280 285
 Asn Asp Thr Leu Val Ser Ser Ile Lys Ile Ile Ala Met Met Leu Leu
 290 295 300
 Ile Ile Gly Gly Gly Gly Ala Phe Lys Gln Val Leu Val Asp Ser Gly
 305 310 315 320
 Val Asp Lys Tyr Ile Ala Ser Met Met His Glu Thr Asn Ile Ser Pro
 325 330 335
 Leu Leu Met Ala Trp Ser Ile Ala Ala Val Leu Arg Ile Ala Leu Gly
 340 345 350
 Ser Ala Thr Val Ala Ala Ile Thr Ala Gly Gly Ile Ala Ala Pro Leu
 355 360 365
 Ile Ala Thr Thr Gly Val Ser Pro Glu Leu Met Val Ile Ala Val Gly
 370 375 380
 Ser Gly Ser Val Ile Phe Ser His Val Asn Asp Pro Gly Phe Trp Leu
 385 390 395 400
 Phe Lys Glu Tyr Phe Asn Leu Thr Ile Gly Glu Thr Ile Lys Ser Trp
 405 410 415
 Ser Met Leu Glu Thr Ile Ile Ser Val Cys Gly Leu Val Gly Cys Leu
 420 425 430
 Leu Leu Asn Met Val Ile
 435

<210> 10112

<211> 1317

<212> DNA

<213> Clostridium acetobutylicum ATCC 824

<220>

<221> CDS

<222> (1)..(1317)

<223> transl_table=11

<400> 10112

atg cca tta tta att gtt gtt att ggc gtc gca tta cta tta cta ctt	48
Met Pro Leu Leu Ile Val Val Ile Gly Val Ala Leu Leu Leu Leu	
1 5 10 15	
atg att aaa ttc aaa gta aac gga ttc ata tcc cta att ctt gta gct	96
Met Ile Lys Phe Lys Val Asn Gly Phe Ile Ser Leu Ile Leu Val Ala	
20 25 30	
ttg gtt gtt ggt atc gcc gaa ggt atg aat cct gca aaa gct gtt tct	144
Leu Val Val Gly Ile Ala Glu Gly Met Asn Pro Ala Lys Ala Val Ser	
35 40 45	
tca att caa aac ggt gtt gga agc acc tta agc agt ttg gca cta att	192
Ser Ile Gln Asn Gly Val Gly Ser Thr Leu Ser Ser Leu Ala Leu Ile	
50 55 60	
tta ggt ttt ggt gct atg ttt gga aaa tta ata gct gat tct ggt gct	240

PF59083SeqList PF59083.txt

Leu 65	Gly	Phe	Gly	Ala	Met 70	Phe	Gly	Lys	Leu	Ile 75	Ala	Asp	Ser	Gly	Ala 80	
gct	caa	agg	att	tct	aga	agt	tta	att	aat	aaa	ttt	ggt	gta	aaa	aaa	288
Ala	Gln	Arg	Ile	Ser 85	Arg	Ser	Leu	Ile	Asn 90	Lys	Phe	Gly	Val	Lys 95	Lys	
att	caa	tgg	gct	ggt	gta	tta	acg	ggt	ttc	ata	ggt	ggc	att	gct	atg	336
Ile	Gln	Trp	Ala	Val 100	Val	Leu	Thr	Gly 105	Phe	Ile	Val	Gly	Ile	Ala	Met	
ttc	tat	gag	gta	ggt	ttt	ggt	cta	ctt	ata	cct	ctt	ggt	ttt	act	att	384
Phe	Tyr		Glu	Val 115	Gly	Phe	Val	Leu 120	Ile	Pro	Leu	Val 125	Phe	Thr	Ile	
gct	gaa	ttc	aca	gaa	ctt	cct	ctt	tta	tac	ata	ggc	ggt	cct	atg	gct	432
Ala	Glu	Phe	Thr	Glu	Leu	Pro 135	Leu	Leu	Tyr	Ile	Gly 140	Val	Pro	Met	Ala	
gca	gct	tta	tct	gtc	act	cac	gga	ttt	tta	cct	cct	cac	cct	gga	cct	480
Ala 145	Ala	Leu	Ser	Val 150	Thr	His	Gly	Phe	Leu	Pro 155	Pro	His	Pro	Gly	Pro 160	
ggt	gca	ata	gct	aca	ata	tat	ggt	gca	agc	att	agc	atg	act	ctt	gta	528
Val	Ala	Ile	Ala	Thr 165	Ile	Tyr	Gly	Ala	Ser 170	Ile	Ser	Met	Thr	Leu	Val 175	
tat	gga	att	gta	ata	gct	ata	cct	aca	gta	ata	ggt	gca	gga	cct	ggt	576
Tyr	Gly	Ile	Val 180	Ile	Ala	Ile	Pro	Thr 185	Val	Ile	Val	Ala	Gly 190	Pro	Val	
ttg	act	aag	ttt	tta	aaa	cgt	ttt	gat	cat	aaa	tct	tca	aaa	aac	ctt	624
Leu	Thr	Lys 195	Phe	Leu	Lys	Arg	Phe	Asp 200	His	Lys	Ser	Ser 205	Lys	Asn	Leu	
ttt	aaa	act	aag	gtc	ttt	gat	gaa	gat	gaa	atg	cca	agt	ttc	tca	tta	672
Phe	Lys 210	Thr	Lys	Val	Phe	Asp 215	Glu	Asp	Glu	Met	Pro 220	Ser	Phe	Ser	Leu	
agc	gta	tta	act	gct	att	ggt	cct	cct	att	ctt	atg	gcc	ttt	tca	gct	720
Ser 225	Val	Leu	Thr	Ala 230	Ile	Val	Pro	Pro	Ile	Leu 235	Met	Ala	Phe	Ser	Ala 240	
ggt	tgt	gaa	atc	aca	cta	cca	aaa	aca	tct	cct	ata	aga	cat	ttt	gca	768
Val	Cys	Glu	Ile	Thr 245	Leu	Pro	Lys	Thr	Ser 250	Pro	Ile	Arg	His	Phe	Ala 255	
gaa	ttc	ggt	gga	agt	cct	atg	atg	gca	atg	ttt	ata	tca	atc	att	gta	816
Glu	Phe	Val 260	Gly	Ser	Pro	Met	Met	Ala 265	Met	Phe	Ile	Ser	Ile	Ile	Val	
gct	atc	ttt	act	ctt	ggt	ata	atg	cgc	gga	aag	aaa	atg	gaa	gaa	ata	864
Ala	Ile	Phe 275	Thr	Leu	Gly	Ile	Met	Arg 280	Gly	Lys	Lys	Met	Glu	Glu	Ile	
atg	aga	act	tta	gct	gaa	gcc	gca	agt	tcc	att	gca	atg	atc	ctt	tta	912
Met	Arg 290	Thr	Leu	Ala	Glu	Ala 295	Ala	Ser	Ser	Ile	Ala 300	Met	Ile	Leu	Leu	
ata	gta	gct	gga	ggt	ggt	ttc	aag	caa	gta	cta	ata	gac	agt	ggt		960
Ile 305	Val	Ala	Gly	Gly 310	Gly	Ala	Phe	Lys	Gln	Val 315	Leu	Ile	Asp	Ser	Gly 320	
ggt	gga	aaa	tat	atc	gct	tct	att	atg	ggt	gga	agt	aat	ata	tct	cct	1008
Val	Gly	Lys	Tyr 325	Ile	Ala	Ser	Ile	Met	Val 330	Gly	Ser	Asn	Ile	Ser	Pro 335	
cta	atc	ttg	gct	tgg	gcg	att	gca	gca	att	tta	aga	tta	tct	ctt	ggt	1056
Leu	Ile	Leu	Ala	Trp 340	Ala	Ile	Ala	Ala 345	Ile	Leu	Arg	Leu	Ser	Leu	Gly	
tct	gcc	act	ggt	tct	gct	atg	act	act	gcc	ggt	ata	gta	ctt	cct	ctt	1104
Ser	Ala	Thr 355	Val	Ser	Ala	Met	Thr 360	Thr	Ala	Gly	Ile	Val 365	Leu	Pro	Leu	
att	cct	tca	acc	cat	gca	aac	cca	gca	tta	atg	ggt	tta	gca	act	ggc	1152
Ile	Pro 370	Ser	Thr	His	Ala	Asn 375	Pro	Ala	Leu	Met	Val 380	Leu	Ala	Thr	Gly	
gca	ggt	agt	ctt	att	ttc	Ser	His	Val	Asn	gat	cca	ggt	ttc	tgg	atg	1200
Ala 385	Gly	Ser	Leu	Ile	Phe 390	Ser	His	Val	Asn	Asp 395	Pro	Gly	Phe	Trp	Met	
ttc	aaa	gaa	tat	ttt	gga	ctt	agc	ata	gga	gaa	aca	atg	gct	tca	tgg	1248
Phe	Lys	Glu	Tyr 405	Phe	Gly	Leu	Ser	Ile	Gly 410	Glu	Thr	Met	Ala	Ser	Trp	
tct	act	tta	gaa	act	ata	att	tca	att	atg	ggg	tta	att	ggt	ggt	tta	1296
Ser	Thr	Leu	Glu	Thr 420	Ile	Ile	Ser	Ile	Met	Gly	Leu	Ile	Gly	Val	Leu	
gct	tta	aat	atg	ggt	gga	tag										1317

Ala Leu Asn Met Val Gly
435

<210> 10113

<211> 438

<212> PRT

<213> Clostridium acetobutylicum ATCC 824

<400> 10113

```

Met Pro Leu Leu Ile Val Val Ile Gly Val Ala Leu Leu Leu Leu Leu
1      5      10      15
Met Ile Lys Phe Lys Val Asn Gly Phe Ile Ser Leu Ile Leu Val Ala
      20      25      30
Leu Val Val Gly Ile Ala Glu Gly Met Asn Pro Ala Lys Ala Val Ser
      35      40      45
Ser Ile Gln Asn Gly Val Gly Ser Thr Leu Ser Ser Leu Ala Leu Ile
      50      55      60
Leu Gly Phe Gly Ala Met Phe Gly Lys Leu Ile Ala Asp Ser Gly Ala
65      70      75      80
Ala Gln Arg Ile Ser Arg Ser Leu Ile Asn Lys Phe Gly Val Lys Lys
      85      90      95
Ile Gln Trp Ala Val Val Leu Thr Gly Phe Ile Val Gly Ile Ala Met
      100      105      110
Phe Tyr Glu Val Gly Phe Val Leu Leu Ile Pro Leu Val Phe Thr Ile
      115      120      125
Ala Glu Phe Thr Glu Leu Pro Leu Leu Tyr Ile Gly Val Pro Met Ala
130      135      140
Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Gly Pro
145      150      155      160
Val Ala Ile Ala Thr Ile Tyr Gly Ala Ser Ile Ser Met Thr Leu Val
      165      170      175
Tyr Gly Ile Val Ile Ala Ile Pro Thr Val Ile Val Ala Gly Pro Val
      180      185      190
Leu Thr Lys Phe Leu Lys Arg Phe Asp His Lys Ser Ser Lys Asn Leu
      195      200      205
Phe Lys Thr Lys Val Phe Asp Glu Asp Glu Met Pro Ser Phe Ser Leu
210      215      220
Ser Val Leu Thr Ala Ile Val Pro Pro Ile Leu Met Ala Phe Ser Ala
225      230      235      240
Val Cys Glu Ile Thr Leu Pro Lys Thr Ser Pro Ile Arg His Phe Ala
      245      250      255
Glu Phe Val Gly Ser Pro Met Met Ala Met Phe Ile Ser Ile Ile Val
      260      265      270
Ala Ile Phe Thr Leu Gly Ile Met Arg Gly Lys Lys Met Glu Glu Ile
      275      280      285
Met Arg Thr Leu Ala Glu Ala Ala Ser Ser Ile Ala Met Ile Leu Leu
290      295      300
Ile Val Ala Gly Gly Gly Ala Phe Lys Gln Val Leu Ile Asp Ser Gly
305      310      315      320
Val Gly Lys Tyr Ile Ala Ser Ile Met Val Gly Ser Asn Ile Ser Pro
      325      330      335
Leu Ile Leu Ala Trp Ala Ile Ala Ala Ile Leu Arg Leu Ser Leu Gly
      340      345      350
Ser Ala Thr Val Ser Ala Met Thr Thr Ala Gly Ile Val Leu Pro Leu
      355      360      365
Ile Pro Ser Thr His Ala Asn Pro Ala Leu Met Val Leu Ala Thr Gly
370      375      380
Ala Gly Ser Leu Ile Phe Ser His Val Asn Asp Pro Gly Phe Trp Met
385      390      395      400
Phe Lys Glu Tyr Phe Gly Leu Ser Ile Gly Glu Thr Met Ala Ser Trp
      405      410      415
Ser Thr Leu Glu Thr Ile Ile Ser Ile Met Gly Leu Ile Gly Val Leu
420      425      430
Ala Leu Asn Met Val Gly
435

```

<210> 10114

<211> 1338

<212> DNA

<213> salmonella enterica subsp. enterica serovar Typhi str. CT18

<220>

<221> CDS

<222> (1)..(1338)

<223> transl_table=11

<400> 10114

atg	cac	gct	caa	atc	tgg	gta	gtg	agc	acg	ctg	ctg	atc	agc	atc	gtg	48
Met	His	Ala	Gln	Ile	Trp	Val	Val	Ser	Thr	Leu	Leu	Ile	Ser	Ile	Val	
1				5				10					15			
tta	atc	gta	ttg	acc	atc	gtg	aag	ttt	aaa	ttc	cac	ccc	ttc	ctg	gcg	96
Leu	Ile	Val	Leu	Thr	Ile	Val	Lys	Phe	Lys	Phe	His	Pro	Phe	Leu	Ala	
		20					25			30						
tta	ctg	ctc	gcc	agt	ttc	ttt	gtc	ggc	gcg	atg	atg	ggc	ata	ggg	ccg	144
Leu	Leu	Ala	Ser	Phe	Phe	Val	Gly	Ala	Met	Met	Gly	Ile	Gly	Pro		
		35				40				45						
ctg	gag	atg	gtc	acg	gcg	ata	gaa	aac	gga	ata	ggc	ggg	acg	ctc	ggt	192
Leu	Glu	Met	Val	Thr	Ala	Ile	Glu	Asn	Gly	Ile	Gly	Gly	Thr	Leu	Gly	
	50				55				60							
ttt	ctg	gcc	gcc	ggt	atc	ggt	ctt	ggc	acc	atc	ctc	ggc	aaa	atg	atg	240
Phe	Leu	Ala	Ala	Val	Ile	Gly	Leu	Gly	Thr	Ile	Leu	Gly	Lys	Met	Met	
	65			70				75						80		
gag	ggt	tcc	ggc	gcg	gcg	gaa	cgc	atc	ggg	ctt	acg	ctc	cag	cgc	tgc	288
Glu	Val	Ser	Gly	Ala	Ala	Glu	Arg	Ile	Gly	Leu	Thr	Leu	Gln	Arg	Cys	
			85					90					95			
cgc	tgg	ctc	tct	gct	gac	gtg	atc	atg	gta	ctg	gtg	ggg	ctg	att	tgc	336
Arg	Trp	Leu	Ser	Ala	Asp	Val	Ile	Met	Val	Leu	Val	Gly	Leu	Ile	Cys	
			100					105					110			
gga	atc	acg	ttg	ttc	gtg	gaa	gtg	ggc	gtc	gtg	ttg	ctc	atc	cca	ctg	384
Gly	Ile	Thr	Leu	Phe	Val	Glu	Val	Gly	Val	Val	Leu	Leu	Ile	Pro	Leu	
		115				120						125				
gcg	ttt	tct	atc	gct	aaa	aag	acc	cat	acc	tcg	ctg	ctg	aag	ctg	gcc	432
Ala	Phe	Ser	Ile	Ala	Lys	Lys	Thr	His	Thr	Ser	Leu	Leu	Lys	Leu	Ala	
	130				135						140					
att	ccg	ctg	tgt	acc	gcg	ctg	atg	gcc	gtc	cat	tgc	gtg	gta	ccg	ccg	480
Ile	Pro	Leu	Cys	Thr	Ala	Leu	Met	Ala	Val	His	Cys	Val	Val	Pro	Pro	
	145			150				155						160		
cat	ccg	gct	gcg	ctg	ttt	gtc	gca	aat	aaa	ctg	ggg	gcg	gat	atc	ggc	528
His	Pro	Ala	Ala	Leu	Phe	Val	Ala	Asn	Lys	Leu	Gly	Ala	Asp	Ile	Gly	
			165					170					175			
tcg	gtg	att	gtc	tac	ggt	ctg	ctg	gtc	gga	ctg	atg	gcc	tca	ttg	gtc	576
Ser	Val	Ile	Val	Tyr	Gly	Leu	Leu	Val	Gly	Leu	Met	Ala	Ser	Leu	Val	
		180				185							190			
ggc	ggc	ccg	ctg	ttc	tta	aag	ttt	ctg	ggg	aat	cgt	ctg	ccg	ttc	aag	624
Gly	Gly	Pro	Leu	Phe	Leu	Lys	Phe	Leu	Gly	Asn	Arg	Leu	Pro	Phe	Lys	
		195				200						205				
ccc	gta	ccg	aca	gag	ttt	gcg	gat	ctt	gaa	gtg	cgt	gcc	gaa	aac	acc	672
Pro	Val	Pro	Thr	Glu	Phe	Ala	Asp	Leu	Glu	Val	Arg	Ala	Glu	Asn	Thr	
	210					215					220					
ctg	ccg	tcg	ctg	ggc	gca	acg	ctg	ttt	acc	gtt	ctg	ctg	ccg	att	ggc	720
Leu	Pro	Ser	Leu	Gly	Ala	Thr	Leu	Phe	Thr	Val	Leu	Leu	Pro	Ile	Gly	
	225			230				235						240		
ctg	atg	ctg	gtg	aaa	acc	gtc	gct	gaa	ctg	aat	atg	gcg	aaa	gac	ggc	768
Leu	Met	Leu	Val	Lys	Thr	Val	Ala	Glu	Leu	Asn	Met	Ala	Lys	Asp	Gly	
			245					250					255			
acg	ttg	tat	acg	ctg	ctg	gag	ttt	atc	ggg	aat	ccg	atc	acc	gcg	atg	816
Thr	Leu	Tyr	Thr	Leu	Leu	Glu	Phe	Ile	Gly	Asn	Pro	Ile	Thr	Ala	Met	
		260					265						270			
ttt	atc	gct	gtc	ttt	gtg	gcg	tat	tac	ata	ctc	ggg	ctg	cgc	cag	cat	864
Phe	Ile	Ala	Val	Phe	Val	Ala	Tyr	Tyr	Ile	Leu	Gly	Leu	Arg	Gln	His	
		275				280						285				
atg	ggg	atg	agc	gcg	cta	ctt	acc	cac	acc	gaa	aac	ggc	ttt	ggc	gcc	912
Met	Gly	Met	Ser	Ala	Leu	Leu	Thr	His	Thr	Glu	Asn	Gly	Phe	Gly	Ala	
	290					295					300					
att	gcg	aac	atc	ctg	ctg	att	atc	ggc	gcg	ggc	ggc	gcg	ttc	aac	gcc	960
Ile	Ala	Asn	Ile	Leu	Leu	Ile	Ile	Gly	Ala	Gly	Gly	Ala	Phe	Asn	Ala	
	305			310				315						320		
att	ctc	aaa	agt	agc	gga	ctg	gcg	gac	acg	ctg	gcg	gtg	atc	ctc	tca	1008

PF59083SeqList PF59083.txt

Ile	Leu	Lys	Ser	Ser	Gly	Leu	Ala	Asp	Thr	Leu	Ala	Val	Ile	Leu	Ser	
				325					330					335		
aat	atg	cat	atg	cac	ccg	att	ctg	ctg	gca	tgg	ctg	gta	gcg	ctg	att	1056
Asn	Met	His	Met	His	Pro	Ile	Leu	Leu	Ala	Trp	Leu	Val	Ala	Leu	Ile	
			340					345					350			
ctg	cac	gcg	gct	gtc	ggc	tct	gcg	acg	gtg	gcg	atg	atg	ggc	gcc	acc	1104
Leu	His	Ala	Ala	Val	Gly	Ser	Ala	Thr	Val	Ala	Met	Met	Gly	Ala	Thr	
		355					360					365				
gcg	att	gtt	gcg	ccc	atg	ctg	ccg	ctc	tat	cct	gac	gtt	agc	ccg	gag	1152
Ala	Ile	Val	Ala	Pro	Met	Leu	Pro	Leu	Tyr	Pro	Asp	Val	Ser	Pro	Glu	
	370					375					380					
atc	atc	gct	att	gcc	atc	ggg	tcc	ggc	acc	att	ggc	tgc	acg	atc	gtg	1200
Ile	Ile	Ala	Ile	Ala	Ile	Gly	Ser	Gly	Thr	Ile	Gly	Cys	Thr	Ile	Val	
385					390				395						400	
acc	gat	tcc	ctg	ttc	tgg	ctg	gtc	aag	cag	tat	tgc	ggc	gct	acg	ctg	1248
Thr	Asp	Ser	Leu	Phe	Trp	Leu	Val	Lys	Gln	Tyr	Cys	Gly	Ala	Thr	Leu	
				405				410						415		
aat	gaa	acg	ttt	aaa	tac	tat	acg	acg	gcc	acg	ttt	atc	gca	tct	gtc	1296
Asn	Glu	Thr	Phe	Lys	Tyr	Tyr	Thr	Thr	Ala	Thr	Phe	Ile	Ala	Ser	Val	
			420					425					430			
gtt	gca	ctg	gct	ggc	aca	ttc	ctg	ctt	tcc	ttt	atc	atc	tga			1338
Val	Ala	Leu	Ala	Gly	Thr	Phe	Leu	Leu	Ser	Phe	Ile	Ile				
		435					440					445				

<210> 10115

<211> 445

<212> PRT

<213> Salmonella enterica subsp. enterica serovar Typhi str. CT18

<400> 10115

Met	His	Ala	Gln	Ile	Trp	Val	Val	Ser	Thr	Leu	Leu	Ile	Ser	Ile	Val	
1				5					10					15		
Leu	Ile	Val	Leu	Thr	Ile	Val	Lys	Phe	Lys	Phe	His	Pro	Phe	Leu	Ala	
		20					25						30			
Leu	Leu	Leu	Ala	Ser	Phe	Phe	Val	Gly	Ala	Met	Met	Gly	Ile	Gly	Pro	
		35					40					45				
Leu	Glu	Met	Val	Thr	Ala	Ile	Glu	Asn	Gly	Ile	Gly	Gly	Thr	Leu	Gly	
	50					55			60							
Phe	Leu	Ala	Ala	Val	Ile	Gly	Leu	Gly	Thr	Ile	Leu	Gly	Lys	Met	Met	
65					70				75						80	
Glu	Val	Ser	Gly	Ala	Ala	Glu	Arg	Ile	Gly	Leu	Thr	Leu	Gln	Arg	Cys	
			85				90						95			
Arg	Trp	Leu	Ser	Ala	Asp	Val	Ile	Met	Val	Leu	Val	Gly	Leu	Ile	Cys	
		100					105						110			
Gly	Ile	Thr	Leu	Phe	Val	Glu	Val	Gly	Val	Val	Leu	Leu	Ile	Pro	Leu	
		115				120						125				
Ala	Phe	Ser	Ile	Ala	Lys	Lys	Thr	His	Thr	Ser	Leu	Leu	Lys	Leu	Ala	
	130				135						140					
Ile	Pro	Leu	Cys	Thr	Ala	Leu	Met	Ala	Val	His	Cys	Val	Val	Pro	Pro	
145					150				155					160		
His	Pro	Ala	Ala	Leu	Phe	Val	Ala	Asn	Lys	Leu	Gly	Ala	Asp	Ile	Gly	
			165					170					175			
Ser	Val	Ile	Val	Tyr	Gly	Leu	Leu	Val	Gly	Leu	Met	Ala	Ser	Leu	Val	
		180					185						190			
Gly	Gly	Pro	Leu	Phe	Leu	Lys	Phe	Leu	Gly	Asn	Arg	Leu	Pro	Phe	Lys	
		195					200					205				
Pro	Val	Pro	Thr	Glu	Phe	Ala	Asp	Leu	Glu	Val	Arg	Ala	Glu	Asn	Thr	
	210				215						220					
Leu	Pro	Ser	Leu	Gly	Ala	Thr	Leu	Phe	Thr	Val	Leu	Leu	Pro	Ile	Gly	
225					230					235					240	
Leu	Met	Leu	Val	Lys	Thr	Val	Ala	Glu	Leu	Asn	Met	Ala	Lys	Asp	Gly	
			245					250					255			
Thr	Leu	Tyr	Thr	Leu	Leu	Glu	Phe	Ile	Gly	Asn	Pro	Ile	Thr	Ala	Met	
		260					265						270			
Phe	Ile	Ala	Val	Phe	Val	Ala	Tyr	Tyr	Ile	Leu	Gly	Leu	Arg	Gln	His	
		275					280					285				
Met	Gly	Met	Ser	Ala	Leu	Leu	Thr	His	Thr	Glu	Asn	Gly	Phe	Gly	Ala	
	290				295						300					
Ile	Ala	Asn	Ile	Leu	Leu	Ile	Ile	Gly	Ala	Gly	Gly	Ala	Phe	Asn	Ala	

PF59083SeqList PF59083.txt

```

305          310          315          320
Ile Leu Lys Ser Ser Gly Leu Ala Asp Thr Leu Ala Val Ile Leu Ser
          325          330          335
Asn Met His Met His Pro Ile Leu Leu Ala Trp Leu Val Ala Leu Ile
          340          345          350
Leu His Ala Val Gly Ser Ala Thr Val Ala Met Met Gly Ala Thr
          355          360          365
Ala Ile Val Ala Pro Met Leu Pro Leu Tyr Pro Asp Val Ser Pro Glu
          370          375          380
Ile Ile Ala Ile Ala Ile Gly Ser Gly Thr Ile Gly Cys Thr Ile Val
385          390          395          400
Thr Asp Ser Leu Phe Trp Leu Val Lys Gln Tyr Cys Gly Ala Thr Leu
          405          410          415
Asn Glu Thr Phe Lys Tyr Tyr Thr Thr Ala Thr Phe Ile Ala Ser Val
          420          425          430
Val Ala Leu Ala Gly Thr Phe Leu Leu Ser Phe Ile Ile
          435          440          445

```

<210> 10116
 <211> 1497
 <212> DNA
 <213> Salmonella typhimurium LT2

<220>
 <221> CDS
 <222> (1)..(1497)
 <223> transl_table=11

```

<400> 10116
atg aca agt tta ccg acc cca att atc ggt ctg atc gtt gcc gtt ttc      48
Met Thr Ser Leu Pro Thr Pro Ile Ile Gly Leu Ile Val Ala Val Phe
  1          5          10          15
gtg ctg gta tgg ctg gtg tta cgc acc cgt gtt cat gcg ctg atc gcg      96
Val Leu Val Trp Leu Val Leu Arg Thr Arg Val His Ala Leu Ile Ala
          20          25          30
atg ctg gcg gcg gcc tgt att gcc ggt ctg ttg ggg gga atg ggc att      144
Met Leu Ala Ala Ala Cys Ile Ala Gly Leu Leu Gly Gly Met Gly Ile
          35          40          45
gat aaa acg ctc tct gtc atc acc agc gga ttc ggt acg acg ctg ggc      192
Asp Lys Thr Leu Ser Val Ile Thr Ser Gly Phe Thr Thr Thr Leu Gly
          50          55          60
agc att ggc ctg gtg att ggt ctc ggc gta atg atg ggg cgc ttg ctg      240
Ser Ile Gly Leu Val Ile Gly Leu Gly Val Met Met Gly Arg Leu Leu
          65          70          75          80
gag gtt tcc ggc gcg gcg gag cgt atc gcc tgg agc ttt atc aaa tgg      288
Glu Val Ser Gly Ala Ala Glu Arg Ile Ala Trp Ser Phe Ile Lys Trp
          85          90          95
ctg ggg aaa cgc cgt gaa gag tgg gcg ctg gcg atc acg ggt tat att      336
Leu Gly Lys Arg Glu Glu Trp Ala Leu Ala Ile Thr Gly Tyr Ile
          100          105          110
gtc agc atc ccc att ttc gtc gat tcc gct ttt gtc att ctt tat ccg      384
Val Ser Ile Pro Ile Phe Val Asp Ser Ala Phe Val Ile Leu Tyr Pro
          115          120          125
gtg gcg aaa gcg ctg gcg aaa agc ggt aag cgt tcg cta ctg acg ctg      432
Val Ala Lys Ala Leu Ala Lys Ser Gly Lys Arg Ser Leu Leu Thr Leu
          130          135          140
ggc gtc gcg ctg gcg ggc ggg ctg gtg gtc act cac cat acg gta cct      480
Gly Val Ala Leu Ala Gly Gly Leu Val Val Thr His His Thr Val Pro
          145          150          155          160
ccg acg ccc ggt ccg ctg ggg gta gcc ggg att ttt aac gtc gac atc      528
Pro Thr Pro Gly Pro Leu Gly Val Ala Gly Ile Phe Asn Val Asp Ile
          165          170          175
ggc gca atg tta ttg acc ggg atg gcg ctg gcg gtg ccc tgt gtg atc      576
Gly Ala Met Leu Leu Thr Gly Met Ala Leu Ala Val Pro Cys Val Ile
          180          185          190
ggc att gtg ttc tat gcg cag tgg ctg gat aaa cgc tac cct gat ttc      624
Gly Ile Val Phe Tyr Ala Gln Trp Leu Asp Lys Arg Tyr Pro Asp Phe
          195          200          205
gtg ccg cgc acg ctg aac gcc gat gaa gtc aat gcc gcg ctg gag cag      672

```

PF59083SeqList PF59083.txt

Val	Pro	Arg	Thr	Leu	Asn	Ala	Asp	Glu	Val	Asn	Ala	Ala	Leu	Glu	Gln	
210	210					215				220						
tac	aat	aaa	gag	aaa	gag	caa	aag	gaa	ctg	ccg	agc	ctg	acg	ctt	tct	720
Tyr	Asn	Lys	Glu	Lys	Glu	Gln	Lys	Glu	Leu	Pro	Ser	Leu	Thr	Leu	Ser	
225					230					235					240	
ctg	ctg	cct	att	gtg	gtg	ccg	atc	gtg	ctg	atc	ttc	ctg	aag	gct	atc	768
Leu	Leu	Pro	Ile	Val	Val	Pro	Ile	Val	Leu	Ile	Phe	Leu	Lys	Ala	Ile	
			245						250					255		
tgt	tcc	acc	ctc	gcc	act	gta	gaa	gga	tgg	tcc	ggc	ctg	gcg	acg	cat	816
Cys	Ser	Thr	Leu	Ala	Thr	Val	Glu	Gly	Trp	Ser	Gly	Leu	Ala	Thr	His	
			260					265						270		
ccg	gtg	gta	cag	gca	atc	aac	ttt	gtg	gga	agt	ccg	gtg	atc	gcg	ttg	864
Pro	Val	Val	Gln	Ala	Ile	Asn	Phe	Val	Gly	Ser	Pro	Val	Ile	Ala	Leu	
			275				280							285		
gcc	atc	agc	gtt	ctg	ctg	gcg	gtg	tat	acg	ctg	gtg	ccg	cg	atg	gat	912
Ala	Ile	Ser	Val	Leu	Leu	Ala	Val	Tyr	Thr	Leu	Val	Pro	Arg	Met	Asp	
			290			295					300					
aaa	cat	acc	acc	gca	gag	cgt	ctg	gaa	gag	ggc	ttg	caa	agc	gcc	ggg	960
Lys	His	Thr	Thr	Ala	Glu	Arg	Leu	Glu	Glu	Gly	Leu	Gln	Ser	Ala	Gly	
305					310					315					320	
att	atc	tta	ctg	gtc	acg	ggc	gct	ggc	ggc	gcg	ttg	ggc	gcg	atc	ctg	1008
Ile	Ile	Leu	Leu	Val	Thr	Gly	Ala	Gly	Gly	Ala	Leu	Gly	Ala	Ile	Leu	
			325					330						335		
cg	gac	agc	ggc	gcg	ggg	caa	cag	ctg	gcg	gag	cag	gtt	gcc	aac	ctg	1056
Arg	Asp	Ser	Gly	Ala	Gly	Gln	Gln	Ala	Glu	Gln	Val	Ala	Asn	Leu		
			340					345						350		
ccg	atc	tcg	ccg	atc	ctg	atc	ccg	ttt	atc	gtg	gcg	acg	ttg	gta	cg	1104
Pro	Ile	Ser	Pro	Ile	Leu	Ile	Pro	Phe	Ile	Val	Ala	Thr	Leu	Val	Arg	
			355				360							365		
ctg	att	cag	gga	tcg	ggg	acg	gtg	gcg	atg	atc	act	gcc	gcc	tcg	att	1152
Leu	Ile	Gln	Gly	Ser	Gly	Thr	Val	Ala	Met	Ile	Thr	Ala	Ala	Ser	Ile	
			370			375					380					
tcc	gcg	ccg	atc	ctg	gcg	cag	atc	ccc	ggc	atc	aat	atg	ttg	ctt	gcc	1200
Ser	Ala	Pro	Ile	Leu	Ala	Gln	Ile	Pro	Gly	Ile	Asn	Met	Leu	Leu	Ala	
385					390					395					400	
gct	cag	gcc	gca	acg	atg	ggg	tcg	ctg	ttc	ttc	ggc	tac	ttc	aac	gat	1248
Ala	Gln	Ala	Ala	Thr	Met	Gly	Ser	Leu	Phe	Phe	Gly	Tyr	Phe	Asn	Asp	
			405					410						415		
agc	ctg	ttc	tgg	gtg	gtt	aac	cg	atg	atg	ggc	gtc	tct	gat	gtc	aaa	1296
Ser	Leu	Phe	Trp	Val	Val	Asn	Arg	Met	Met	Gly	Val	Ser	Asp	Val	Lys	
			420					425						430		
cag	cag	atg	gtg	gtt	tgg	tct	gta	ccg	acg	acc	att	gcc	tgg	gcg	att	1344
Gln	Gln	Met	Val	Val	Trp	Ser	Val	Pro	Thr	Thr	Ile	Ala	Trp	Ala	Ile	
			435				440							445		
ggc	ggc	acc	ggc	gtg	gtg	ctg	att	aac	ctg	ctg	ttc	ggc	tcc	ggc	ggc	1392
Gly	Gly	Thr	Gly	Val	Val	Leu	Ile	Asn	Leu	Leu	Phe	Gly	Ser	Gly	Gly	
			450			455					460					
agt	tgg	ctc	gat	ccg	tta	ctg	ccg	att	gtt	gtt	ctg	gcg	gca	att	atg	1440
Ser	Trp	Leu	Asp	Pro	Leu	Leu	Pro	Ile	Val	Val	Leu	Ala	Ala	Ile	Met	
465					470					475					480	
ctg	tgg	gtg	cgt	tgg	cag	gcg	cag	ggg	atc	aaa	gac	aag	ctg	gta	gtt	1488
Leu	Trp	Val	Arg	Trp	Gln	Ala	Gln	Gly	Ile	Lys	Asp	Lys	Leu	Val	Val	
			485					490						495		
aag	gat	taa														1497
Lys	Asp															

<210> 10117
 <211> 498
 <212> PRT
 <213> Salmonella typhimurium LT2

<400> 10117
 Met Thr Ser Leu Pro Thr Pro Ile Ile Gly Leu Ile Val Ala Val Phe
 1 5 10 15
 Val Leu Val Trp Leu Val Leu Arg Thr Arg Val His Ala Leu Ile Ala
 20 25 30
 Met Leu Ala Ala Ala Cys Ile Ala Gly Leu Leu Gly Gly Met Gly Ile
 35 40 45

PF59083SeqList PF59083.txt

Asp Lys Thr Leu Ser Val Ile Thr Ser Gly Phe Gly Thr Thr Leu Gly
50 55 60
Ser Ile Gly Leu Val Ile Gly Leu Gly Val Met Met Gly Arg Leu Leu
65 70 75 80
Glu Val Ser Gly Ala Glu Arg Ile Ala Trp Ser Phe Ile Lys Trp
85 90 95
Leu Gly Lys Arg Arg Glu Glu Trp Ala Leu Ala Ile Thr Gly Tyr Ile
100 105 110
Val Ser Ile Pro Ile Phe Val Asp Ser Ala Phe Val Ile Leu Tyr Pro
115 120 125
Val Ala Lys Ala Leu Ala Lys Ser Gly Lys Arg Ser Leu Leu Thr Leu
130 135 140
Gly Val Ala Leu Ala Gly Gly Leu Val Val Thr His His Thr Val Pro
145 150 155 160
Pro Thr Pro Gly Pro Leu Gly Val Ala Gly Ile Phe Asn Val Asp Ile
165 170 175
Gly Ala Met Leu Leu Thr Gly Met Ala Leu Ala Val Pro Cys Val Ile
180 185 190
Gly Ile Val Phe Tyr Ala Gln Trp Leu Asp Lys Arg Tyr Pro Asp Phe
195 200 205
Val Pro Arg Thr Leu Asn Ala Asp Glu Val Asn Ala Leu Glu Gln
210 215 220
Tyr Asn Lys Glu Lys Glu Gln Lys Glu Leu Pro Ser Leu Thr Leu Ser
225 230 235 240
Leu Leu Pro Ile Val Pro Ile Val Leu Ile Phe Leu Lys Ala Ile
245 250 255
Cys Ser Thr Leu Ala Thr Val Glu Gly Trp Ser Gly Leu Ala Thr His
260 265 270
Pro Val Val Gln Ala Ile Asn Phe Val Gly Ser Pro Val Ile Ala Leu
275 280 285
Ala Ile Ser Val Leu Leu Ala Val Tyr Thr Leu Val Pro Arg Met Asp
290 295 300
Lys His Thr Thr Ala Glu Arg Leu Glu Glu Gly Leu Gln Ser Ala Gly
305 310 315 320
Ile Ile Leu Leu Val Thr Gly Ala Gly Gly Ala Leu Gly Ala Ile Leu
325 330 335
Arg Asp Ser Gly Ala Gly Gln Gln Leu Ala Glu Gln Val Ala Asn Leu
340 345 350
Pro Ile Ser Pro Ile Leu Ile Pro Phe Ile Val Ala Thr Leu Val Arg
355 360 365
Leu Ile Gln Gly Ser Gly Thr Val Ala Met Ile Thr Ala Ala Ser Ile
370 375 380
Ser Ala Pro Ile Leu Ala Gln Ile Pro Gly Ile Asn Met Leu Leu Ala
385 390 395 400
Ala Gln Ala Ala Thr Met Gly Ser Leu Phe Phe Gly Tyr Phe Asn Asp
405 410 415
Ser Leu Phe Trp Val Val Asn Arg Met Met Gly Val Ser Asp Val Lys
420 425 430
Gln Gln Met Val Val Trp Ser Val Pro Thr Thr Ile Ala Trp Ala Ile
435 440 445
Gly Gly Thr Gly Val Val Leu Ile Asn Leu Leu Phe Gly Ser Gly Gly
450 455 460
Ser Trp Leu Asp Pro Leu Leu Pro Ile Val Val Leu Ala Ala Ile Met
465 470 475 480
Leu Trp Val Arg Trp Gln Ala Gln Gly Ile Lys Asp Lys Leu Val Val
485 490 495
Lys Asp

<210> 10118
<211> 1317
<212> DNA
<213> Salmonella typhimurium LT2

<220>
<221> CDS
<222> (1)..(1317)
<223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 10118
atg cca tta gtc atc gtt gct atc ggt gtt atc ttg tta ctt ctt ctg      48
Met Pro Leu Val Ile Val Ala Ile Gly Val Ile Leu Leu Leu Leu Leu
1      5      10      15
atg atc cgc ttc aaa atg aac gga ttt atc gcc ctt gtc ctg gta gcg      96
Met Ile Arg Phe Lys Met Asn Gly Phe Ile Ala Leu Val Leu Val Ala
20      25      30
ctc gct gtc ggg ttg atg cag gga atg cct ctg gat aaa gtc atc ggc      144
Leu Ala Val Gly Leu Met Gln Gly Met Pro Leu Asp Lys Val Ile Gly
35      40      45
tcc atc aaa gcc ggt gtc ggt ggt acg ctt ggc agt ctg gcc ctg att      192
Ser Ile Lys Ala Gly Val Gly Gly Thr Leu Gly Ser Leu Ala Leu Ile
50      55      60
atg ggg ttc ggc gcc atg ctg ggc aaa atg ctt gcc gac tgc ggc ggc      240
Met Gly Phe Gly Ala Met Leu Gly Lys Met Leu Ala Asp Cys Gly Gly
65      70      75      80
gct caa cgt atc gcc act acc ctg atc gcg aaa ttt ggt aaa aag cat      288
Ala Gln Arg Ile Ala Thr Thr Leu Ile Ala Lys Phe Gly Lys Lys His
85      90      95
att cag tgg gcc gta gtg tta acc ggc ttt acc gtc gcc ttc gct ctg      336
Ile Gln Trp Ala Val Val Leu Thr Gly Phe Thr Val Gly Phe Ala Leu
100      105      110
ttc tat gaa gtg ggc ttc gtt ctg atg ctg ccg ctg gta ttc acc att      384
Phe Tyr Glu Val Gly Phe Val Leu Met Leu Pro Leu Val Phe Thr Ile
115      120      125
gcc gca gcg gcg aat atc ccg cta ctg tac gtc ggc gtg ccg atg gcc      432
Ala Ala Ala Ala Asn Ile Pro Leu Leu Tyr Val Gly Val Pro Met Ala
130      135      140
gcg gcg ctc tcc gtc aca cac ggc ttc ctg ccg ccg cac ccg ggt cca      480
Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Gly Pro
145      150      155      160
acc gca atc gcc acg att ttc cat gcc gat atg ggt aag acg ctg ctg      528
Thr Ala Ile Ala Thr Ile Phe His Ala Asp Met Gly Lys Thr Leu Leu
165      170      175
ttt ggt acg att ctg gcg atc ccg acc gtg atc ctt gcc gga ccg gtt      576
Phe Gly Thr Ile Leu Ala Ile Pro Thr Val Ile Leu Ala Gly Pro Val
180      185      190
tac gcc cgt ttc ctg aaa ggc atc gat aag ccg atc cca gaa ggc ctg      624
Tyr Ala Arg Phe Leu Lys Gly Ile Asp Lys Pro Ile Pro Glu Gly Leu
195      200      205
tac agc gcg aaa act ttt acg gaa gaa gag atg ccg ggc ttt ggc gtc      672
Tyr Ser Ala Lys Thr Phe Thr Glu Glu Glu Met Pro Gly Phe Gly Val
210      215      220
agc gtc tgg acg tcg ctg gtt ccg gtt att ctg atg gcg atg cgt gcg      720
Ser Val Trp Thr Ser Leu Val Pro Val Ile Leu Met Ala Met Arg Ala
225      230      235      240
att gcc gag atg att ctg cca aaa ggc cac gct ttc ctg ccc gtt gcc      768
Ile Ala Glu Met Ile Leu Pro Lys Gly His Ala Phe Leu Pro Val Ala
245      250      255
gag ttc ctg ggc gac ccg gta atg gct acg tta att gcc gta ctg att      816
Glu Phe Leu Gly Asp Pro Val Met Ala Thr Leu Ile Ala Val Leu Ile
260      265      270
gcg atg ttc acc ttt ggc ctg aac cgc ggg cgt tcc atg gat cag att      864
Ala Met Phe Thr Phe Gly Leu Asn Arg Gly Arg Ser Met Asp Gln Ile
275      280      285
aac gat acg ctg gtc tct tcc atc aaa att atc gcc atg atg ctg ctg      912
Asn Asp Thr Leu Val Ser Ser Ile Lys Ile Ile Ala Met Met Leu Leu
290      295      300
atc atc ggc ggc ggc ggc gca ttc aag cag gtg ctg gtc gat agc ggc      960
Ile Ile Gly Gly Gly Gly Ala Phe Lys Gln Val Leu Val Asp Ser Gly
305      310      315      320
gtg gat aaa tac atc gct tca atg atg cat gaa acc aat gtc tct ccg      1008
Val Asp Lys Tyr Ile Ala Ser Met Met His Glu Thr Asn Val Ser Pro
325      330      335
ctg ttg atg gcg tgg tct atc gcg gcg gtt ctg cgt atc gcg ctg ggc      1056
Leu Leu Met Ala Trp Ser Ile Ala Ala Val Leu Arg Ile Ala Leu Gly
340      345      350
tct gcg act gtc gcg gcg att acc gca ggc ggc att gcg gcg ccg ctg      1104
Ser Ala Thr Val Ala Ala Ile Thr Ala Gly Gly Ile Ala Ala Pro Leu

```

PF59083SeqList PF59083.txt

atc	gcc	act	acc	ggc	gtt	agc	cct	gaa	ctg	atg	gtt	atc	gcg	gtc	ggt	1152
Ile	Ala	Thr	Thr	Gly	Val	Ser	Pro	Glu	Leu	Met	Val	Ile	Ala	Val	Gly	
	370					375					380					
tcc	ggg	agc	gtg	att	ttc	tct	cac	gtc	aac	gac	ccg	ggc	ttc	tgg	ctg	1200
Ser	Gly	Ser	Val	Ile	Phe	Ser	His	Val	Asn	Asp	Pro	Gly	Phe	Trp	Leu	
	385				390					395					400	
ttc	aaa	gag	tat	ttc	aat	ttg	act	atc	ggc	gag	acc	att	aaa	tcc	tgg	1248
Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Thr	Ile	Gly	Glu	Thr	Ile	Lys	Ser	Trp	
				405					410					415		
tcg	atg	ctg	gaa	acg	atc	atc	tcc	gtc	tgc	ggc	ctg	atc	ggc	tgt	ctg	1296
Ser	Met	Leu	Glu	Thr	Ile	Ile	Ser	Val	Cys	Gly	Leu	Ile	Gly	Cys	Leu	
			420					425					430			
ctg	ttg	ggt	atg	gtg	gtt	taa										1317
Leu	Leu	Gly	Met	Val	Val											
		435														

<210> 10119

<211> 438

<212> PRT

<213> Salmonella typhimurium LT2

<400> 10119

Met	Pro	Leu	Val	Ile	Val	Ala	Ile	Gly	Val	Ile	Leu	Leu	Leu	Leu	Leu	
1				5					10					15		
Met	Ile	Arg	Phe	Lys	Met	Asn	Gly	Phe	Ile	Ala	Leu	Val	Leu	Val	Ala	
			20					25					30			
Leu	Ala	Val	Gly	Leu	Met	Gln	Gly	Met	Pro	Leu	Asp	Lys	Val	Ile	Gly	
		35					40					45				
Ser	Ile	Lys	Ala	Gly	Val	Gly	Gly	Thr	Leu	Gly	Ser	Leu	Ala	Leu	Ile	
	50					55					60					
Met	Gly	Phe	Gly	Ala	Met	Leu	Gly	Lys	Met	Leu	Ala	Asp	Cys	Gly	Gly	
65					70					75					80	
Ala	Gln	Arg	Ile	Ala	Thr	Thr	Leu	Ile	Ala	Lys	Phe	Gly	Lys	Lys	His	
			85						90					95		
Ile	Gln	Trp	Ala	Val	Val	Leu	Thr	Gly	Phe	Thr	Val	Gly	Phe	Ala	Leu	
			100					105					110			
Phe	Tyr	Glu	Val	Gly	Phe	Val	Leu	Met	Leu	Pro	Leu	Val	Phe	Thr	Ile	
		115					120					125				
Ala	Ala	Ala	Ala	Asn	Ile	Pro	Leu	Leu	Tyr	Val	Gly	Val	Pro	Met	Ala	
		130				135					140					
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
145					150					155					160	
Thr	Ala	Ile	Ala	Thr	Ile	Phe	His	Ala	Asp	Met	Gly	Lys	Thr	Leu	Leu	
			165						170					175		
Phe	Gly	Thr	Ile	Leu	Ala	Ile	Pro	Thr	Val	Ile	Leu	Ala	Gly	Pro	Val	
			180					185					190			
Tyr	Ala	Arg	Phe	Leu	Lys	Gly	Ile	Asp	Lys	Pro	Ile	Pro	Glu	Gly	Leu	
		195					200					205				
Tyr	Ser	Ala	Lys	Thr	Phe	Thr	Glu	Glu	Glu	Met	Pro	Gly	Phe	Gly	Val	
	210					215					220					
Ser	Val	Trp	Thr	Ser	Leu	Val	Pro	Val	Ile	Leu	Met	Ala	Met	Arg	Ala	
225					230					235					240	
Ile	Ala	Glu	Met	Ile	Leu	Pro	Lys	Gly	His	Ala	Phe	Leu	Pro	Val	Ala	
			245						250					255		
Glu	Phe	Leu	Gly	Asp	Pro	Val	Met	Ala	Thr	Leu	Ile	Ala	Val	Leu	Ile	
			260					265					270			
Ala	Met	Phe	Thr	Phe	Gly	Leu	Asn	Arg	Gly	Arg	Ser	Met	Asp	Gln	Ile	
		275					280					285				
Asn	Asp	Thr	Leu	Val	Ser	Ser	Ile	Lys	Ile	Ile	Ala	Met	Met	Leu	Leu	
	290					295					300					
Ile	Ile	Gly	Gly	Gly	Gly	Ala	Phe	Lys	Gln	Val	Leu	Val	Asp	Ser	Gly	
305					310					315					320	
Val	Asp	Lys	Tyr	Ile	Ala	Ser	Met	Met	His	Glu	Thr	Asn	Val	Ser	Pro	
			325						330					335		
Leu	Leu	Met	Ala	Trp	Ser	Ile	Ala	Ala	Val	Leu	Arg	Ile	Ala	Leu	Gly	
			340					345					350			
Ser	Ala	Thr	Val	Ala	Ala	Ile	Thr	Ala	Gly	Gly	Ile	Ala	Ala	Pro	Leu	
		355					360					365				

PF59083SeqList PF59083.txt

Ile Ala Thr Thr Gly Val Ser Pro Glu Leu Met Val Ile Ala Val Gly
 370 375 380
 Ser Gly Ser Val Ile Phe Ser His Val Asn Asp Pro Gly Phe Trp Leu
 385 390 395 400
 Phe Lys Glu Tyr Phe Asn Leu Thr Ile Gly Glu Thr Ile Lys Ser Trp
 405 410 415
 Ser Met Leu Glu Thr Ile Ile Ser Val Cys Gly Leu Ile Gly Cys Leu
 420 425 430
 Leu Leu Gly Met Val Val
 435

<210> 10120
 <211> 1341
 <212> DNA
 <213> Salmonella typhimurium LT2

<220>
 <221> CDS
 <222> (1)..(1341)
 <223> transl_table=11

<400> 10120
 gtg agt aca tta aca ctg gtt tta acc gcc gtc ggt tcc gtc tta ctg 48
 Met Ser Thr Leu Thr Leu Val Leu Thr Ala Val Gly Ser Val Leu Leu
 1 5 10 15
 ctg ctg ttt ttg gtg atg aag gcg cgt atg cac gcc ttc gtc gcg tta 96
 Leu Leu Phe Leu Val Met Lys Ala Arg Met His Ala Phe Val Ala Leu
 20 25 30
 atg gtc gtc tcg atg ggc gcg ggg ctt ttt tca ggg atg ccg ctt gat 144
 Met Val Ser Met Gly Ala Gly Leu Phe Ser Gly Met Pro Leu Asp
 35 40 45
 aaa atc gcc gcg acc atg gaa aaa ggg atg ggc ggc acg ctg gga ttc 192
 Lys Ile Ala Ala Thr Met Glu Lys Gly Met Gly Gly Thr Leu Gly Phe
 50 55 60
 ctg gcg att gtg gtc gcg ctg ggg gcg atg ttc ggc aag att ctg cac 240
 Leu Ala Ile Val Val Ala Leu Gly Ala Met Phe Gly Lys Ile Leu His
 65 70 75 80
 gag acc ggc gcg gtc gat cag att gcc gtc aag atg ctg aaa tct ttc 288
 Glu Thr Gly Ala Val Asp Gln Ile Ala Val Lys Met Leu Lys Ser Phe
 85 90 95
 ggt cat agc cgc gcg cat tat gcc att ggc ctg gcc ggt ctg att tgc 336
 Gly His Ser Arg Ala His Tyr Ala Ile Gly Leu Ala Gly Leu Ile Cys
 100 105 110
 gcg cta ccg ctg ttc ttt gaa gtg gcg att gtg ctg ctg ata agc gtg 384
 Ala Leu Pro Leu Phe Phe Glu Val Ala Ile Val Leu Ile Ser Val
 115 120 125
 gcg ttc tca atg gcg cgc cac acc gga acg aac ctg gtg aag ctg gtc 432
 Ala Phe Ser Met Ala Arg His Thr Gly Thr Asn Leu Val Lys Leu Val
 130 135 140
 att ccg ctg ttt gcg ggc gtg gcg gct gcc gca ggc ttc ctg ctg ccg 480
 Ile Pro Leu Phe Ala Gly Val Ala Ala Ala Ala Ala Phe Leu Leu Pro
 145 150 155 160
 gga cct gcg ccg atg ctg ctg gca tcc caa atg cac gct gac ttt ggc 528
 Gly Pro Ala Pro Met Leu Leu Ala Ser Gln Met His Ala Asp Phe Gly
 165 170 175
 tgg atg atc ctg att ggc ctg tgc gca gcc att ccg ggc atg att atc 576
 Trp Met Ile Leu Ile Gly Leu Cys Ala Ala Ile Pro Gly Met Ile Ile
 180 185 190
 gcc ggg ccg ctg tgg ggc aat ttc atc agc cgt tac gtt gaa ctg cat 624
 Ala Gly Pro Leu Trp Gly Asn Phe Ile Ser Arg Tyr Val Glu Leu His
 195 200 205
 gta ccg gaa gac att acc gag ccg cat ctg ggc gaa ggc aaa atg cct 672
 Val Pro Glu Asp Ile Thr Glu Pro His Leu Gly Glu Gly Lys Met Pro
 210 215 220
 tct ttc ggc ttc agc ctg ctg atc ctg ctg ccg ttg gtg ctg gta 720
 Ser Phe Gly Phe Ser Leu Ser Leu Ile Leu Leu Pro Leu Val Leu Val
 225 230 235 240
 ggg ctg aaa acg atc gcc gcg cgt ttt gtg ccg gaa ggt tcc acc gct 768
 Gly Leu Lys Thr Ile Ala Ala Arg Phe Val Pro Glu Gly Ser Thr Ala

PF59083SeqList PF59083.txt

245																250																255																816
tac Tyr	gaa Glu	tgg Trp	ttt Phe 260	gag Glu	ttt Phe	atc Ile	ggt Gly	cac His 265	ccc Pro	ttc Phe	act Thr	gcg Ala	att Ile 270	ctg Leu	gtc Val																																	
275																280																285																864
gct Ala	tgt Cys	ctg Leu	gta Val	gcg Ala	att Ile	tat Tyr	ggc Gly	ctg Leu	gcg Ala	atg Met	cgt Arg	cag Gln	ggg Gly	atg Met	ccg Pro																																	
290																295																300																912
aaa Lys	gac Asp	aaa Lys	gtg Val	atg Met	gaa Glu	atc Ile	tgt Cys	ggc Gly	cac His	gcg Ala	ctg Leu	caa Gln	ccg Pro	gcg Ala	ggc Gly																																	
305																310																315																960
att Ile	atc Ile	ctg Leu	ctg Leu	gtg Val	att Ile	ggc Gly	gca Ala	ggc Gly	ggg Gly	gtg Val	ttc Phe	aaa Lys	cag Gln	gta Val	ctg Leu 320																																	
325																330																335																1008
gtt Val	gac Asp	tcc Ser	ggc Gly	gtc Val	ggc Gly	ccg Pro	gcg Ala	ctg Leu	ggc Gly	gaa Glu	gcg Ala	tta Leu	acc Thr	ggt Gly	atg Met																																	
340																345																350																1056
gga Gly	ctg Leu	ccg Pro	att Ile	gcc Ala	att Ile	acc Thr	tgc Cys	ttt Phe	gtg Val	ctg Leu	gcg Ala	gcg Ala	gca Ala	gtg Val	cgc Arg																																	
355																360																365																1104
atc Ile	att Ile	cag Gln	ggt Gly	tcc Ser	gcg Ala	acc Thr	gtg Val	gcg Ala	tgt Cys	tta Leu	acc Thr	gcg Ala	gtc Val	ggt Gly	ctg Leu																																	
370																375																380																1152
gtg Val	atg Met	ccg Pro	gtc Val	ata Ile	gag Glu	caa Gln	ctg Leu	aat Asn	ttc Phe	tcc Ser	ggc Gly	gcg Ala	cag Gln	atg Met	gct Ala																																	
385																390																395																1200
gcg Ala	ctc Leu	tct Ser	atc Ile	tgt Cys	atc Ile	gcc Ala	ggc Gly	ggt Gly	tca Ser	att Ile	gtg Val	gtt Val	tct Ser	cat His	gtt Val 400																																	
405																410																415																1248
aac Asn	gac Asp	gct Ala	ggc Gly	ttc Phe	tgg Trp	ctg Leu	ttc Phe	ggt Gly	aaa Lys	ttt Phe	acc Thr	ggc Gly	gcg Ala	acc Thr	gaa Glu																																	
420																425																430																1296
gcg Ala	cag Gln	acg Thr	tta Leu	aaa Lys	acc Thr	tgg Trp	acg Thr	atg Met	atg Met	gaa Glu	act Thr	atc Ile	ctc Leu	ggt Gly	acg Thr																																	
435																440																445																1341
gtc Val	ggc Gly	gcg Ala	att Ile	gtc Val	ggg Gly	atg Met	att Ile	gct Ala	ttc Phe	caa Gln	ctg Leu	ctg Leu	agc Ser	tga																																		

$\langle 210 \rangle$ 10121

<211> 446

<212> PRT

<213> salmonella typhimurium LT2

$\langle 400 \rangle$ 10121

Met	Ser	Thr	Leu	Thr	Leu	Val	Leu	Thr	Ala	Val	Gly	Ser	Val	Leu	Leu
1				5					10					15	
Leu	Leu	Phe	Leu	Val	Met	Lys	Ala	Arg	Met	His	Ala	Phe	Val	Ala	Leu
			20					25					30		
Met	Val	Val	Ser	Met	Gly	Ala	Gly	Leu	Phe	Ser	Gly	Met	Pro	Leu	Asp
		35					40					45			
Lys	Ile	Ala	Ala	Thr	Met	Glu	Lys	Gly	Met	Gly	Gly	Thr	Leu	Gly	Phe
	50					55					60				
Leu	Ala	Ile	Val	Val	Ala	Leu	Gly	Ala	Met	Phe	Gly	Lys	Ile	Leu	His
65					70					75					80
Glu	Thr	Gly	Ala	Val	Asp	Gln	Ile	Ala	Val	Lys	Met	Leu	Lys	Ser	Phe
				85					90					95	
Gly	His	Ser	Arg	Ala	His	Tyr	Ala	Ile	Gly	Leu	Ala	Gly	Leu	Ile	Cys
			100					105					110		
Ala	Leu	Pro	Leu	Phe	Phe	Glu	Val	Ala	Ile	Val	Leu	Leu	Ile	Ser	Val
		115					120					125			
Ala	Phe	Ser	Met	Ala	Arg	His	Thr	Gly	Thr	Asn	Leu	Val	Lys	Leu	Val
	130					135					140				
Ile	Pro	Leu	Phe	Ala	Gly	Val	Ala	Ala	Ala	Ala	Phe	Leu	Leu	Pro	
145					150					155					160
Gly	Pro	Ala	Pro	Met	Leu	Leu	Ala	Ser	Gln	Met	His	Ala	Asp	Phe	Gly
				165					170					175	
Trp	Met	Ile	Leu	Ile	Gly	Leu	Cys	Ala	Ala	Ile	Pro	Gly	Met	Ile	Ile
			180					185					190		
Ala	Gly	Pro	Leu	Trp	Gly	Asn	Phe	Ile	Ser	Arg	Tyr	Val	Glu	Leu	His

Seite 10705

PF59083SeqList PF59083.txt

Val	Pro	Glu	Asp	Ile	Thr	Glu	Pro	His	Leu	Gly	Glu	Gly	Lys	Met	Pro
210	210	210	210	210	210	210	210	210	210	210	210	210	210	210	210
Ser	Phe	Gly	Phe	Ser	Leu	Ser	Leu	Ile	Leu	Leu	Pro	Leu	Val	Leu	Val
225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225
Gly	Leu	Lys	Thr	Ile	Ala	Ala	Arg	Phe	Val	Pro	Glu	Gly	Ser	Thr	Ala
230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230
Tyr	Glu	Trp	Phe	Glu	Phe	Ile	Gly	His	Pro	Phe	Thr	Ala	Ile	Leu	Val
245	245	245	245	245	245	245	245	245	245	245	245	245	245	245	245
Ala	Cys	Leu	Val	Ala	Ile	Tyr	Gly	Leu	Ala	Met	Arg	Gln	Gly	Met	Pro
250	250	250	250	250	250	250	250	250	250	250	250	250	250	250	250
Lys	Asp	Lys	Val	Met	Glu	Ile	Cys	Gly	His	Ala	Leu	Gln	Pro	Ala	Gly
260	260	260	260	260	260	260	260	260	260	260	260	260	260	260	260
Ile	Ile	Leu	Leu	Val	Ile	Gly	Ala	Gly	Gly	Val	Phe	Lys	Gln	Val	Leu
270	270	270	270	270	270	270	270	270	270	270	270	270	270	270	270
Val	Asp	Ser	Gly	Val	Gly	Pro	Ala	Leu	Gly	Glu	Ala	Leu	Thr	Gly	Met
280	280	280	280	280	280	280	280	280	280	280	280	280	280	280	280
Gly	Leu	Pro	Ile	Ala	Ile	Thr	Cys	Phe	Val	Leu	Ala	Ala	Ala	Val	Arg
290	290	290	290	290	290	290	290	290	290	290	290	290	290	290	290
Ile	Ile	Gln	Gly	Ser	Ala	Thr	Val	Ala	Cys	Leu	Thr	Ala	Val	Gly	Leu
300	300	300	300	300	300	300	300	300	300	300	300	300	300	300	300
Val	Met	Pro	Val	Ile	Glu	Gln	Leu	Asn	Phe	Ser	Gly	Ala	Gln	Met	Ala
310	310	310	310	310	310	310	310	310	310	310	310	310	310	310	310
Ala	Leu	Ser	Ile	Cys	Ile	Ala	Gly	Gly	Ser	Ile	Val	Val	Ser	His	Val
320	320	320	320	320	320	320	320	320	320	320	320	320	320	320	320
Asn	Asp	Ala	Gly	Phe	Trp	Leu	Phe	Gly	Lys	Phe	Thr	Gly	Ala	Thr	Glu
330	330	330	330	330	330	330	330	330	330	330	330	330	330	330	330
Ala	Gln	Thr	Leu	Lys	Thr	Trp	Thr	Met	Met	Glu	Thr	Ile	Leu	Gly	Thr
340	340	340	340	340	340	340	340	340	340	340	340	340	340	340	340
Val	Gly	Ala	Ile	Val	Gly	Met	Ile	Ala	Phe	Gln	Leu	Leu	Ser		
350	350	350	350	350	350	350	350	350	350	350	350	350	350		

<210> 10122
 <211> 1338
 <212> DNA
 <213> Salmonella typhimurium LT2

<220>
 <221> CDS
 <222> (1)..(1338)
 <223> transl_table=11

<400> 10122	
atg cac gct caa atc tgg gta gtg agc acg ctg ctg atc agc atc gtg	48
Met His Ala Gln Ile Trp Val Val Ser Thr Leu Leu Ile Ser Ile Val	
1 5 10 15	
tta atc gta ttg acc atc gtg aag ttt aaa ttc cac ccc ttc ctg gcg	96
Leu Ile Val Leu Thr Ile Val Lys Phe Lys Phe His Pro Phe Leu Ala	
20 25 30	
tta ctg ctc gcc agt ttc ttt gtc gcc gcg atg atg ggc atg ggg ccg	144
Leu Leu Leu Ala Ser Phe Phe Val Gly Ala Met Met Gly Met Gly Pro	
35 40 45	
ctg gag atg gtc acg gcg ata gaa aac gga ata ggc ggt acg ctc ggt	192
Leu Glu Met Val Thr Ala Ile Glu Asn Gly Ile Gly Thr Leu Gly	
50 55 60	
ttt ctg gcc gcc gtt atc ggt ctt ggc acc atc ctc ggc aaa atg atg	240
Phe Leu Ala Ala Val Ile Gly Leu Gly Thr Ile Leu Gly Lys Met Met	
65 70 75 80	
gag gtt tcc ggc gcg gaa cgc atc ggg ctt acg ctc cag cgc tgc	288
Glu Val Ser Gly Ala Ala Glu Arg Ile Gly Leu Thr Leu Gln Arg Cys	
85 90 95	
cgc tgg ctc tct gct gac gtg atc atg gta ctg gtg ggg ctg att tgc	336
Arg Trp Leu Ser Ala Asp Val Ile Met Val Leu Val Gly Leu Ile Cys	
100 105 110	
ggt atc acg ttg ttc gtg gaa gtg ggc gtc gtg ttg ctc atc cca ctg	384
Gly Ile Thr Leu Phe Val Glu Val Gly Val Val Leu Leu Ile Pro Leu	
115 120 125	
gcg ttt tct atc gct aaa aag acc cat acc tcg ctg ctg aag ctg gcc	432
Ala Phe Ser Ile Ala Lys Lys Thr His Thr Ser Leu Lys Leu Ala	

PF59083SeqList PF59083.txt

```

130      135      140
att ccg ctg tgt acc gcg ctg atg gcc gtc cat tgc gtg gta ccg ccg      480
Ile Pro Leu Cys Thr Ala Leu Met Ala Val His Cys Val Val Pro Pro
145      150      155      160
cat ccg gct gcg ctg ttt gtc gca aat aaa ctg ggg gcg gat atc ggc      528
His Pro Ala Ala Leu Phe Val Ala Asn Lys Leu Gly Ala Asp Ile Gly
165      170      175
tcg gtg att gtc tac ggt cta ctg gtc ggg ctg atg gca tca ttg gtc      576
Ser Val Ile Val Tyr Gly Leu Leu Val Gly Leu Met Ala Ser Leu Val
180      185      190
ggc ggt ccg ctg ttc tta aag ttt ctg ggt aat cgt ctg ccg ttc aag      624
Gly Gly Pro Leu Phe Leu Lys Phe Leu Gly Asn Arg Leu Pro Phe Lys
195      200      205      210
ccc gta ccg aca gag ttt gcg gat ctt gaa gtg cgc gcc gaa aac acc      672
Pro Val Pro Thr Glu Phe Ala Asp Leu Glu Val Arg Ala Glu Asn Thr
215      220      225      230
ctg ccg tcg ctg ggc gca acg ctg ttt acc gtt ctg ctg ccg att ggc      720
Leu Pro Ser Leu Gly Ala Thr Leu Phe Thr Val Leu Leu Pro Ile Gly
235      240      245      250
ctg atg ctg gtg aaa acc gtc gct gaa ctg aat atg gcg aaa gac ggc      768
Leu Met Leu Val Lys Thr Val Ala Glu Leu Asn Met Ala Lys Asp Gly
255      260      265      270
acg ttg tat acg ctg ctg gag ttt atc ggt aat ccg atc acc gca atg      816
Thr Leu Tyr Thr Leu Leu Glu Phe Ile Gly Asn Pro Ile Thr Ala Met
275      280      285      290
ttt atc gct gtc ttt gtg gcg tat tac ata ctc ggt ctg cgc cag cat      864
Phe Ile Ala Val Phe Val Ala Tyr Tyr Ile Leu Gly Leu Arg Gln His
295      300      305      310
atg ggt atg ggc aca cta ctt acc cac acc gaa aac ggc ttt ggc gcc      912
Met Gly Met Gly Thr Leu Thr His Thr Glu Asn Gly Phe Gly Ala
315      320      325      330
att gcg aac atc ctg ctg att atc ggc gcg ggc ggc gcg ttc aac gcc      960
Ile Ala Asn Ile Leu Leu Ile Ile Gly Ala Gly Gly Ala Phe Asn Ala
335      340      345      350
att ctg aaa agt agc ggc ctg gcg gac acg ctg gcg gtg atc ctc tca      1008
Ile Leu Lys Ser Ser Gly Leu Ala Asp Thr Leu Ala Val Ile Leu Ser
355      360      365      370
aat atg cat atg cac ccg att ctg ctg gca tgg ctg gta gcg ctg att      1056
Asn Met His Met His Pro Ile Leu Leu Ala Trp Leu Val Ala Leu Ile
375      380      385      390
ctg cac gcg gcg gtc gga tct gcg acg gtg gcg atg atg ggc gcc acc      1104
Leu His Ala Ala Val Gly Ser Ala Thr Val Ala Met Met Gly Ala Thr
395      400      405      410
gcg att gtt gcg ccc atg ctg ccg ctc tat cct gac gtc agc ccg gag      1152
Ala Ile Val Ala Pro Met Leu Pro Leu Tyr Pro Asp Val Ser Pro Glu
415      420      425      430
atc att gcg att gcc att ggt tcc ggc gcc att ggc tgc acg atc gtg      1200
Ile Ile Ala Ile Ala Ile Gly Ser Gly Ala Ile Gly Cys Thr Ile Val
435      440      445
acc gat tcc ctg ttc tgg ctg gtc aag cag tat tgc ggc gct acg ctg      1248
Thr Asp Ser Leu Phe Trp Leu Val Lys Gln Tyr Cys Gly Ala Thr Leu
445      450      455      460
aat gaa acg ttt aaa tac tat acg acg gcc acg ttt atc gca tct gtc      1296
Asn Glu Thr Phe Lys Tyr Tyr Thr Thr Ala Thr Phe Ile Ala Ser Val
465      470      475      480
gtt gca ctg gct ggc aca ttc ctg ctt tcc ttt atc atc tga      1338
Val Ala Leu Ala Gly Thr Phe Leu Leu Ser Phe Ile Ile
485      490      495      500

```

<210> 10123
 <211> 445
 <212> PRT
 <213> Salmonella typhimurium LT2

<400> 10123
 Met His Ala Gln Ile Trp Val Val Ser Thr Leu Leu Ile Ser Ile Val
 1 5 10 15
 Leu Ile Val Leu Thr Ile Val Lys Phe Lys Phe His Pro Phe Leu Ala
 20 25 30

PF59083SeqList PF59083.txt

Leu Leu Leu Ala Ser Phe Phe Val Gly Ala Met Met Gly Met Gly Pro
35 40 45
Leu Glu Met Val Thr Ala Ile Glu Asn Gly Ile Gly Gly Thr Leu Gly
50 55 60
Phe Leu Ala Ala Val Ile Gly Leu Gly Thr Ile Leu Gly Lys Met Met
65 70 75 80
Glu Val Ser Gly Ala Ala Glu Arg Ile Gly Leu Thr Leu Gln Arg Cys
85 90 95
Arg Trp Leu Ser Ala Asp Val Ile Met Val Leu Val Gly Leu Ile Cys
100 105 110
Gly Ile Thr Leu Phe Val Glu Val Gly Val Val Leu Leu Ile Pro Leu
115 120 125
Ala Phe Ser Ile Ala Lys Lys Thr His Thr Ser Leu Leu Lys Leu Ala
130 135 140
Ile Pro Leu Cys Thr Ala Leu Met Ala Val His Cys Val Val Pro Pro
145 150 155 160
His Pro Ala Ala Leu Phe Val Ala Asn Lys Leu Gly Ala Asp Ile Gly
165 170 175
Ser Val Ile Val Tyr Gly Leu Leu Val Gly Leu Met Ala Ser Leu Val
180 185 190
Gly Gly Pro Leu Phe Leu Lys Phe Leu Gly Asn Arg Leu Pro Phe Lys
195 200 205
Pro Val Pro Thr Glu Phe Ala Asp Leu Glu Val Arg Ala Glu Asn Thr
210 215 220
Leu Pro Ser Leu Gly Ala Thr Leu Phe Thr Val Leu Leu Pro Ile Gly
225 230 235 240
Leu Met Leu Val Lys Thr Val Ala Glu Leu Asn Met Ala Lys Asp Gly
245 250 255
Thr Leu Tyr Thr Leu Leu Glu Phe Ile Gly Asn Pro Ile Thr Ala Met
260 265 270
Phe Ile Ala Val Phe Val Ala Tyr Tyr Ile Leu Gly Leu Arg Gln His
275 280 285
Met Gly Met Gly Thr Leu Leu Thr His Thr Glu Asn Gly Phe Gly Ala
290 295 300
Ile Ala Asn Ile Leu Leu Ile Ile Gly Ala Gly Gly Ala Phe Asn Ala
305 310 315 320
Ile Leu Lys Ser Ser Gly Leu Ala Asp Thr Leu Ala Val Ile Leu Ser
325 330 335
Asn Met His Met His Pro Ile Leu Leu Ala Trp Leu Val Ala Leu Ile
340 345 350
Leu His Ala Ala Val Gly Ser Ala Thr Val Ala Met Met Gly Ala Thr
355 360 365
Ala Ile Val Ala Pro Met Leu Pro Leu Tyr Pro Asp Val Ser Pro Glu
370 375 380
Ile Ile Ala Ile Ala Ile Gly Ser Gly Ala Ile Gly Cys Thr Ile Val
385 390 395 400
Thr Asp Ser Leu Phe Trp Leu Val Lys Gln Tyr Cys Gly Ala Thr Leu
405 410 415
Asn Glu Thr Phe Lys Tyr Tyr Thr Thr Ala Thr Phe Ile Ala Ser Val
420 425 430
Val Ala Leu Ala Gly Thr Phe Leu Leu Ser Phe Ile Ile
435 440 445

<210> 10124

<211> 1320

<212> DNA

<213> Salmonella typhimurium LT2

<220>

<221> CDS

<222> (1)..(1320)

<223> transl_table=11

<400> 10124

atg cca tta ata att att gcg gca ggc gtt gcg ctg ctg ttg gtt tta
Met Pro Leu Ile Ile Ile Ala Ala Gly Val Ala Leu Leu Leu Val Leu
1 5 10 15
atg att ggc ttt aaa gtt aac ggc ttt atc gcc ctt gtt ctg gtt gcc
Met Ile Gly Phe Lys Val Asn Gly Phe Ile Ala Leu Val Leu Val Ala
16 21 26 31 36 41 46 51 56 61 66 71 76 81 86 91 96

48

96

PF59083SeqList PF59083.txt

	20	25	30													
gcc	gtg	gtg	gga	ttt	gcc	gaa	ggg	atg	ggc	gcg	caa	gac	gtc	ctg	cac	144
Ala	Val	Val	Gly	Phe	Ala	Glu	Gly	Met	Gly	Ala	Gln	Asp	Val	Leu	His	
		35					40					45				
tcc	ata	caa	aac	gga	att	ggc	ggt	act	ctg	ggc	gga	ctc	gcc	atg	atc	192
Ser	Ile	Gln	Asn	Gly	Ile	Gly	Gly	Thr	Leu	Gly	Gly	Leu	Ala	Met	Ile	
		50				55					60					
ctc	ggt	ttt	ggc	gcg	atg	ctg	gga	aga	tta	att	tcc	gat	acc	ggc	gcc	240
Leu	Gly	Phe	Gly	Ala	Met	Leu	Gly	Arg	Leu	Ile	Ser	Asp	Thr	Gly	Ala	
		65			70					75					80	
gcg	cag	cgc	att	gcg	acg	acg	ctc	att	aat	acg	ttc	ggc	aaa	aaa	cgc	288
Ala	Gln	Arg	Ile	Ala	Thr	Thr	Leu	Ile	Asn	Thr	Phe	Gly	Lys	Lys	Arg	
			85						90					95		
gtg	caa	tgg	gcg	ctg	gtg	atc	acc	ggg	ctt	atc	gtc	ggc	ctg	gca	atg	336
Val	Gln	Trp	Ala	Leu	Val	Ile	Thr	Gly	Leu	Ile	Val	Gly	Leu	Ala	Met	
			100					105					110			
ttt	ttt	gaa	gtc	gga	ttc	gta	ctg	ctg	ttg	ccg	ctc	gtt	ttt	acg	att	384
Phe	Phe	Glu	Val	Gly	Phe	Val	Leu	Leu	Leu	Pro	Leu	Val	Phe	Thr	Ile	
		115				120						125				
gtg	gcc	tca	tcg	gga	ctg	ccc	ttg	ctg	tat	gtc	ggg	gtt	cca	atg	gtc	432
Val	Ala	Ser	Ser	Gly	Leu	Pro	Leu	Leu	Tyr	Val	Gly	Val	Pro	Met	Val	
		130				135					140					
gcc	gcc	tta	tcc	ggt	acg	cac	tgc	ttc	ctg	ccg	ccg	cat	ccc	ggc	cct	480
Ala	Ala	Leu	Ser	Val	Thr	His	Cys	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
				145	150					155				160		
act	gct	att	gcg	aca	att	ttt	gag	gca	aat	ctc	ggt	acg	acc	ctg	ctg	528
Thr	Ala	Ile	Ala	Thr	Ile	Phe	Glu	Ala	Asn	Leu	Gly	Thr	Thr	Leu	Leu	
			165					170						175		
tat	ggg	tta	atc	att	acc	ata	ccg	acc	gtg	att	gtt	gcc	ggc	cct	ctg	576
Tyr	Gly	Leu	Ile	Thr	Ile	Pro	Thr	Val	Ile	Val	Val	Ala	Gly	Pro	Leu	
			180				185						190			
ttt	tca	aaa	ttg	ctg	gcg	cgc	ttt	gag	aaa	gcg	ccg	cct	gaa	gga	tta	624
Phe	Ser	Lys	Leu	Leu	Ala	Arg	Phe	Glu	Lys	Ala	Pro	Pro	Glu	Gly	Leu	
		195				200						205				
ttt	aat	cct	cac	cta	ttc	agt	gaa	gag	gag	atg	ccg	tca	ttc	tg	aac	672
Phe	Asn	Pro	His	Leu	Phe	Ser	Glu	Glu	Glu	Met	Pro	Ser	Phe	Trp	Asn	
		210				215					220					
agt	att	ttt	gcc	gcc	gtg	atc	ccg	gtc	att	ctg	atg	gcc	atc	gca	gcg	720
Ser	Ile	Phe	Ala	Ala	Val	Ile	Pro	Val	Ile	Leu	Met	Ala	Ile	Ala	Ala	
					225	230				235				240		
gta	tgt	gaa	atc	acg	ctg	cca	aaa	acg	aat	gcc	gtg	cg	ggt	ttc	ttc	768
Val	Cys	Glu	Ile	Thr	Leu	Pro	Lys	Thr	Asn	Ala	Val	Arg	Val	Phe	Phe	
			245					250						255		
gaa	ttt	atc	ggt	aat	cca	gca	gtg	gcg	ttg	ttt	att	gcc	att	atc	atc	816
Glu	Phe	Ile	Gly	Asn	Pro	Ala	Val	Ala	Leu	Phe	Ile	Ala	Ile	Ile	Ile	
			260				265						270			
gcc	att	ttt	acg	ctg	ggc	cga	cg	aac	gga	cgt	acg	ggt	gag	cag	gtg	864
Ala	Ile	Phe	Thr	Leu	Gly	Arg	Arg	Asn	Gly	Arg	Thr	Val	Glu	Gln	Val	
		275				280					285					
atg	gat	atc	gtc	ggc	gag	tcc	att	ggc	gct	att	gcg	atg	att	ggt	ttt	912
Met	Asp	Ile	Val	Gly	Glu	Ser	Ile	Gly	Ala	Ile	Ala	Met	Ile	Val	Phe	
		290			295						300					
atc	atc	gcg	ggc	ggc	ggc	gcg	ttt	aag	caa	gtg	ctg	gtg	gat	agc	ggc	960
Ile	Ile	Ala	Gly	Gly	Gly	Ala	Phe	Lys	Gln	Val	Leu	Val	Asp	Ser	Gly	
					305	310				315					320	
gtg	ggt	caa	tat	atc	tcg	caa	tta	atg	acc	ggc	acc	tcg	cta	tct	ccg	1008
Val	Gly	Gln	Tyr	Ile	Ser	Gln	Leu	Met	Thr	Gly	Thr	Ser	Leu	Ser	Pro	
			325					330						335		
tta	tta	atg	tgc	tg	acg	gta	gcc	gcc	gtg	ctg	cgt	att	gcg	cta	ggt	1056
Leu	Leu	Met	Cys	Trp	Thr	Val	Ala	Ala	Val	Leu	Arg	Ile	Ala	Leu	Gly	
			340				345						350			
tcc	gcg	acc	gtg	gct	gcg	ata	acc	aca	gcg	ggc	gtc	gta	ttg	ccg	att	1104
Ser	Ala	Thr	Val	Ala	Ala	Ile	Thr	Thr	Ala	Gly	Val	Val	Leu	Pro	Ile	
		355				360						365				
att	aac	gta	acc	cac	gcc	gat	ccg	gcg	tta	atg	gta	ctg	gcg	aca	ggc	1152
Ile	Asn	Val	Thr	His	Ala	Asp	Pro	Ala	Leu	Met	Val	Leu	Ala	Thr	Gly	
		370			375						380					
gcg	gga	agc	ggt	att	gca	tca	cat	ggt	aac	gat	ccc	ggt	ttt	tg	ctg	1200
Ala	Gly	Ser	Val	Ile	Ala	Ser	His	Val	Asn	Asp	Pro	Gly	Phe	Trp	Leu	

PF59083SeqList PF59083.txt

385	ttt	aaa	ggg	tat	ttt	aat	ctt	agc	gtc	ggg	gaa	acc	cta	cgc	acc	tgg	1248
	Phe	Lys	Gly	Tyr	Phe	Asn	Leu	Ser	Val	Gly	Glu	Thr	Leu	Arg	Thr	Trp	
				405						410					415		
	acc	gtt	atg	gaa	aca	ttg	att	tct	gtc	atg	ggg	ttg	ctg	ggc	gta	ctg	1296
	Thr	Val	Met	Glu	Thr	Leu	Ile	Ser	Val	Met	Gly	Leu	Leu	Gly	Val	Leu	
				420					425					430			
	gcg	ctg	aat	gcg	gtt	ctg	cat	taa									1320
	Ala	Leu	Asn	Ala	Val	Leu	His										
			435														

<210> 10125
 <211> 439
 <212> PRT
 <213> Salmonella typhimurium LT2

<400> 10125
 Met Pro Leu Ile Ile Ile Ala Ala Gly Val Ala Leu Leu Leu Val Leu
 1 5 10 15
 Met Ile Gly Phe Lys Val Asn Gly Phe Ile Ala Leu Val Leu Val Ala
 20 25 30
 Ala Val Val Gly Phe Ala Glu Gly Met Gly Ala Gln Asp Val Leu His
 35 40 45
 Ser Ile Gln Asn Gly Ile Gly Gly Thr Leu Gly Gly Leu Ala Met Ile
 50 55 60
 Leu Gly Phe Gly Ala Met Leu Gly Arg Leu Ile Ser Asp Thr Gly Ala
 65 70 75 80
 Ala Gln Arg Ile Ala Thr Thr Leu Ile Asn Thr Phe Gly Lys Lys Arg
 85 90 95
 Val Gln Trp Ala Leu Val Ile Thr Gly Leu Ile Val Gly Leu Ala Met
 100 105 110
 Phe Phe Glu Val Gly Phe Val Leu Leu Leu Pro Leu Val Phe Thr Ile
 115 120 125
 Val Ala Ser Ser Gly Leu Pro Leu Leu Tyr Val Gly Val Pro Met Val
 130 135 140
 Ala Ala Leu Ser Val Thr His Cys Phe Leu Pro Pro His Pro Gly Pro
 145 150 155 160
 Thr Ala Ile Ala Thr Ile Phe Glu Ala Asn Leu Gly Thr Thr Leu Leu
 165 170 175
 Tyr Gly Leu Ile Thr Ile Pro Thr Val Ile Val Ala Gly Pro Leu
 180 185 190
 Phe Ser Lys Leu Leu Ala Arg Phe Glu Lys Ala Pro Pro Glu Gly Leu
 195 200 205
 Phe Asn Pro His Leu Phe Ser Glu Glu Glu Met Pro Ser Phe Trp Asn
 210 215 220
 Ser Ile Phe Ala Ala Val Ile Pro Val Ile Leu Met Ala Ile Ala Ala
 225 230 235 240
 Val Cys Glu Ile Thr Leu Pro Lys Thr Asn Ala Val Arg Val Phe Phe
 245 250 255
 Glu Phe Ile Gly Asn Pro Ala Val Ala Leu Phe Ile Ala Ile Ile Ile
 260 265 270
 Ala Ile Phe Thr Leu Gly Arg Arg Asn Gly Arg Thr Val Glu Gln Val
 275 280 285
 Met Asp Ile Val Gly Glu Ser Ile Gly Ala Ile Ala Met Ile Val Phe
 290 295 300
 Ile Ile Ala Gly Gly Gly Ala Phe Lys Gln Val Leu Val Asp Ser Gly
 305 310 315 320
 Val Gly Gln Tyr Ile Ser Gln Leu Met Thr Gly Thr Ser Leu Ser Pro
 325 330 335
 Leu Leu Met Cys Trp Thr Val Ala Ala Val Leu Arg Ile Ala Leu Gly
 340 345 350
 Ser Ala Thr Val Ala Ala Ile Thr Thr Ala Gly Val Val Leu Pro Ile
 355 360 365
 Ile Asn Val Thr His Ala Asp Pro Ala Leu Met Val Leu Ala Thr Gly
 370 375 380
 Ala Gly Ser Val Ile Ala Ser His Val Asn Asp Pro Gly Phe Trp Leu
 385 390 395 400
 Phe Lys Gly Tyr Phe Asn Leu Ser Val Gly Glu Thr Leu Arg Thr Trp
 405 410 415

PF59083SeqList PF59083.txt

Thr Val Met Glu Thr Leu Ile Ser Val Met Gly Leu Leu Gly Val Leu
 420 425 430
 Ala Leu Asn Ala Val Leu His
 435

<210> 10126
 <211> 1392
 <212> DNA
 <213> Corynebacterium glutamicum ATCC 13032

<220>
 <221> CDS
 <222> (1)..(1392)
 <223> transl_table=11

<400> 10126
 atg gac acc tgg gaa caa acc ctt gga aca ggg cca ctg cta ggc att 48
 Met Asp Thr Trp Glu Gln Thr Leu Gly Thr Gly Pro Leu Leu Gly Ile
 1 5 10 15
 gca gcc ggc gcc att gcc ctc atc ttg gtt ctc gtc atc gtt ttt aaa 96
 Ala Ala Gly Ala Ile Ala Leu Ile Leu Val Leu Val Ile Val Phe Lys
 20 25 30
 ctc cat gct ttt ctc acc cta ata ctg gtt tca att gtt acc gca ctt 144
 Leu His Ala Phe Leu Thr Leu Ile Leu Val Ser Ile Val Thr Ala Leu
 35 40 45
 gct gcc ggc att ccc gtc acc gca gta gtg gac act ctc ctt gac ggt 192
 Ala Ala Gly Ile Pro Val Thr Ala Val Val Asp Thr Leu Leu Asp Gly
 50 55 60
 ttt ggt aaa aca ctc gcc tcg gtc gcc cta ttg gta ggc ctg ggt gcc 240
 Phe Gly Lys Thr Leu Ala Ser Val Ala Leu Val Gly Leu Gly Ala
 65 70 75 80
 atg ctt ggt cga ttg gtt gaa aca tcc ggt ggc gca aaa tct cta gcc 288
 Met Leu Gly Arg Leu Val Glu Thr Ser Gly Gly Ala Lys Ser Leu Ala
 85 90 95
 gac act atg gtg cga atc ttc ggt gaa aaa cga gca gct ttc gca ctc 336
 Asp Thr Met Val Arg Ile Phe Gly Glu Lys Arg Ala Ala Phe Ala Leu
 100 105 110
 ggt gtc gca tcg ctg atc atg gga ttc cct atc ttc ttc gat gct ggc 384
 Gly Val Ala Ser Leu Ile Met Gly Phe Pro Ile Phe Phe Asp Ala Gly
 115 120 125
 ctc gtg gtc atg ctc cca gtg atc ttc gca gta gct cga cgc ctc aac 432
 Leu Val Val Met Leu Pro Val Ile Phe Ala Val Ala Arg Arg Leu Asn
 130 135 140
 ggc tcc gtc ctt act ttt ggt atc cct gca gct ggc gcc ttc tct gtc 480
 Gly Ser Val Leu Thr Phe Gly Ile Pro Ala Ala Gly Ala Phe Ser Val
 145 150 155 160
 atg cac gtg ttc gtc cca cct cac cca ggc cca att gca gcc tct gaa 528
 Met His Val Phe Val Pro Pro His Pro Gly Pro Ile Ala Ala Ser Glu
 165 170 175
 ttc ttc ggc gca caa gtt gga tac gta cta atc gct ggc atc atc gtt 576
 Phe Phe Gly Ala Gln Val Gly Tyr Val Leu Ile Ala Gly Ile Ile Val
 180 185 190
 gca cta ccc acc tgg tat tta acc ggt tac ctg cta ggt aag ttc tta 624
 Ala Leu Pro Thr Trp Tyr Leu Thr Gly Tyr Leu Leu Gly Lys Phe Leu
 195 200 205
 ggc cga aag ttc ccc ctt ccc gta ccc gat cta ctc agt ggt gga gca 672
 Gly Arg Lys Phe Pro Leu Pro Val Pro Asp Leu Leu Ser Gly Gly Ala
 210 215 220
 cag gaa gat gat cag cct cag aac cca gct aac gca gtg tcg atc att 720
 Gln Glu Asp Asp Gln Pro Gln Asn Pro Ala Asn Ala Val Ser Ile Ile
 225 230 235 240
 gtc att ttg ctc att cct atg ctc ctt att ttt ggc aat acc gga aca 768
 Val Ile Leu Leu Ile Pro Met Leu Leu Ile Phe Gly Asn Thr Gly Thr
 245 250 255
 tca atg gca gtt tcc gcc ggc ctc cta gat gca gaa tcc acc atg gtg 816
 Ser Met Ala Val Ser Ala Gly Leu Leu Asp Ala Glu Ser Thr Met Val
 260 265 270
 aaa att cta gga ttc ctc ggc gaa aca cca gtg gca ctg ctc att acc 864
 Lys Ile Leu Gly Phe Leu Gly Glu Thr Pro Val Ala Leu Leu Ile Thr

PF59083SeqList PF59083.txt

275	280	285	
ttg atc att gcc ctg ttc ttc cta ggc aac cga cgt ggc att aat ggt	912		
Leu Ile Ile Ala Leu Phe Phe Leu Gly Asn Arg Arg Gly Ile Asn Gly			
290	295	300	
tct gct cta gag aaa acc atc gaa ggc gca ctc ggc cca atc tgt tca	960		
Ser Ala Leu Glu Lys Thr 310 Ile Glu Gly Ala Leu 315			
305	310	315	
gtc gta tta atc act ggc gcc ggt ggc atg ttc ggt gga gtg cta cgc	1008		
Val Val Leu Ile Thr Gly Ala Gly Gly Met Phe Gly Gly Val Leu Arg			
325	330	335	
acg tct gga att gga gga gcg ctt gca gac tcc atg gca gat cta gga	1056		
Thr Ser Gly Ile Gly Gly Ala Leu Ala Asp Ser Met Ala Asp Leu Gly			
340	345	350	
ctt cca gtt atc gca ggt tgt ttc atc gtg gca gcc gtc ctt cgt gtc	1104		
Leu Pro Val Ile Ala Gly Cys Phe Ile Val Ala Val Leu Arg Val			
355	360	365	
gcg cag ggt tct gcc acc gtt gcg cta acc acc gcc gca gca ctc atg	1152		
Ala Gln Gly Ser Ala Thr Val Ala Leu Thr Thr Ala Ala Ala Leu Met			
370	375	380	
gca cct gct gtt gcc gct gct gac ttt aac gaa ttc cag ctt gct gcc	1200		
Ala Pro Ala Val Ala 390 Ala Asp Phe Asn Glu Phe Gln Leu Ala Ala			
385	390	400	
atc gtt att tcc act gcc gct ggt tct gtt att gcc agc cac gtc aac	1248		
Ile Val Ile Ser Thr Ala Ala Gly Ser Val Ile Ala Ser His Val Asn			
405	410	415	
gac tcc gga ttc tgg ctc gtt ggt cga ctc atg aac gcc gac gta ccc	1296		
Asp Ser Gly Phe Trp Leu Val Gly Arg Leu Met Asn Ala Asp Val Pro			
420	425	430	
acc acg cta aaa act tgg acc gta aac caa acc tgc att gcg att gtg	1344		
Thr Thr 435 Leu Lys Thr Trp Thr 440 Val Asn Gln Thr Cys 445			
435	440	445	
gga ttt gtg atg gcc tat gca atg ttc gga ttg gca tcg ctt gca	1389		
Gly Phe Val Met Ala Tyr Ala Met Phe Gly Leu Ala Ser Leu Ala			
450	455	460	
tag			1392

<210> 10127

<211> 463

<212> PRT

<213> Corynebacterium glutamicum ATCC 13032

<400> 10127

Met Asp Thr Trp Glu Gln Thr Leu Gly Thr Gly Pro Leu Leu Gly Ile	
1 5 10 15	
Ala Ala Gly Ala Ile Ala Leu Ile Leu Val Leu Val Ile Val Phe Lys	
20 25 30	
Leu His Ala Phe Leu Thr Leu Ile Leu Val Ser Ile Val Thr Ala Leu	
35 40 45	
Ala Ala Gly Ile Pro Val Thr Ala Val Val Asp Thr Leu Leu Asp Gly	
50 55 60	
Phe Gly Lys Thr Leu Ala Ser Val Ala Leu Leu Val Gly Leu Gly Ala	
65 70 75 80	
Met Leu Gly Arg Leu Val Glu Thr Ser Gly Gly Ala Lys Ser Leu Ala	
85 90 95	
Asp Thr Met Val Arg Ile Phe Gly Glu Lys Arg Ala Ala Phe Ala Leu	
100 105 110	
Gly Val Ala Ser Leu Ile Met Gly Phe Pro Ile Phe Phe Asp Ala Gly	
115 120 125	
Leu Val Val Met Leu Pro Val Ile Phe Ala Val Ala Arg Arg Leu Asn	
130 135 140	
Gly Ser Val Leu Thr Phe Gly Ile Pro Ala Ala Gly Ala Phe Ser Val	
145 150 155 160	
Met His Val Phe Val Pro Pro His Pro Gly Pro Ile Ala Ala Ser Glu	
165 170 175	
Phe Phe Gly Ala Gln Val Gly Tyr Val Leu Ile Ala Gly Ile Ile Val	
180 185 190	
Ala Leu Pro Thr Trp Tyr Leu Thr Gly Tyr Leu Leu Gly Lys Phe Leu	

PF59083SeqList PF59083.txt

aaa gct att tct aag gaa act	aaa aaa tca att gta tct ttg ggg cta	432
Lys Ala Ile Ser Lys Glu Thr	Lys Lys Ser Ile Val Ser Leu Gly Leu	
130	140	
gct ctt gca tca gga ctg gta atc act cac tct ctt gtt cca cct act		480
Ala Leu Ala Ser Gly Leu Val Ile Thr His Ser	Leu Val Pro Pro Thr	
145	155	160
cct ggt cca gtt ggt gtt gct gga atc ttt ggt gtc agt gtt tca agt		528
Pro Gly Pro Val Gly Val Ala Gly Ile Phe Gly Val Ser Val Ser Ser		
165	170	175
att att tta tat gga att ata att tca atc cca atg gtt tta gct tgc		576
Ile Ile Leu Tyr Gly Ile Ile Ile Ser Ile Pro Met Val Leu Ala Cys		
180	185	190
tta gta ttt gca aaa tat gca gga aat aaa att tgg caa ata cct act		624
Leu Val Phe Ala Lys Tyr Ala Gly Asn Lys Ile Trp Gln Ile Pro Thr		
195	200	205
agt aat gga aaa tgg aca aga gat aaa aat tat gta gat gat tta aaa		672
Ser Asn Gly Lys Trp Thr Arg Asp Lys Asn Tyr Val Asp Asp Leu Lys		
210	215	220
act tca agt gtt tat gat gaa tct aac tta cct tct gca ttt tta tct		720
Thr Ser Ser Val Tyr Asp Glu Ser Asn Leu Pro Ser Ala Phe Leu Ser		
225	230	235
ttt tct cca atc gta gtt cct att att tta att tta tta gga act gtt		768
Phe Ser Pro Ile Val Val Pro Ile Ile Leu Ile Leu Leu Gly Thr Val		
245	250	255
aca gat aca atg aaa ctt gag gga aag att ata tca ttt att caa ttc		816
Thr Asp Thr Met Lys Leu Glu Gly Lys Ile Ile Ser Phe Ile Gln Phe		
260	265	270
ata gga act cct gta ata gca gta gga att ggc ttg ctt att aca att		864
Ile Gly Thr Pro Val Ile Ala Val Gly Ile Gly Leu Leu Ile Thr Ile		
275	280	285
tat ggt tta aca aga agt tta gat aaa caa aaa gtt tta gaa gaa gtt		912
Tyr Gly Leu Thr Arg Ser Leu Asp Lys Gln Lys Val Leu Glu Glu Val		
290	295	300
gaa att gga ata aaa tca gct gga aca att att tta att act ggt gct		960
Glu Ile Gly Ile Lys Ser Ala Gly Thr Ile Ile Leu Ile Thr Gly Ala		
305	310	315
ggt gga gct ttt gga atg tta atc aga gat agt ggt gta gga gat gtt		1008
Gly Gly Ala Phe Gly Met Leu Ile Arg Asp Ser Gly Val Gly Asp Val		
325	330	335
atc gct aaa tca tta gtt gat aca gca tta cca cct att tta tta cct		1056
Ile Ala Lys Ser Leu Val Asp Thr Ala Leu Pro Pro Ile Leu Leu Pro		
340	345	350
ttt ata att gca act tta att cgt ttt att caa gga agt ggt act gtt		1104
Phe Ile Ile Ala Thr Leu Ile Arg Phe Ile Gln Gly Ser Gly Thr Val		
355	360	365
gct atg att aca gca gct tct att act gct cca atc att aca aaa tta		1152
Ala Met Ile Thr Ala Ala Ser Ile Thr Ala Pro Ile Ile Thr Lys Leu		
370	375	380
aat gtt aat cct gtt ctc gct gct ctt gca gcc tgt gta ggt tct ctt		1200
Asn Val Asn Pro Val Leu Ala Ala Leu Ala Cys Val Gly Ser Leu		
385	390	400
ttc ttc tca tat ttc aat gat agt ttc ttc tgg gtt atc aat cgt tca		1248
Phe Phe Ser Tyr Phe Asn Asp Ser Phe Phe Trp Val Ile Asn Arg Ser		
405	410	415
ata gga att aca gaa gga aaa gaa caa tta aga ctt tat tct gtt gca		1296
Ile Gly Ile Thr Glu Gly Lys Glu Gln Leu Arg Leu Tyr Ser Val Ala		
420	425	430
agt aca att gct tgg gca gta gga att att att tta tta ata ctt aat		1344
Ser Thr Ile Ala Trp Ala Val Gly Ile Ile Ile Leu Leu Ile Leu Asn		
435	440	445
ata ttt att aaa taa		1359
Ile Phe Ile Lys		
450		

<210> 10129

<211> 452

<212> PRT

<213> *Fusobacterium nucleatum* subsp. *nucleatum* ATCC 25586

PF59083SeqList PF59083.txt

```

<400> 10129
Met Glu Gln Gln Ile Leu Ile Gly Leu Leu Val Gly Ile Ile Cys Leu
1      5      10      15
Ile Phe Met Ile Val Lys Thr Lys Ile His Thr Phe Leu Ala Leu Ile
20      25      30
Val Ala Thr Ile Ile Val Gly Ile Val Gly Gly Ile Glu Tyr Pro Gln
35      40      45
Ile Ile Gly Ser Ile Thr Lys Gly Phe Gly Gly Thr Leu Gly Ser Ile
50      55      60
Gly Ile Ile Ile Gly Phe Gly Val Met Met Gly Gln Leu Phe Glu Val
65      70      75      80
Ser Gly Ala Ala Lys Lys Met Ala Leu Cys Phe Leu Lys Ile Phe Gly
85      90      95
Lys Gly Lys Glu Glu Leu Ala Met Ala Ile Thr Gly Phe Leu Val Ser
100     105     110
Ile Pro Ile Phe Cys Asp Ser Gly Phe Val Ile Leu Thr Pro Leu Ile
115     120     125
Lys Ala Ile Ser Lys Glu Thr Lys Lys Ser Ile Val Ser Leu Gly Leu
130     135     140
Ala Leu Ala Ser Gly Leu Val Ile Thr His Ser Leu Val Pro Pro Thr
145     150     155     160
Pro Gly Pro Val Gly Val Ala Gly Ile Phe Gly Val Ser Val Ser Ser
165     170     175
Ile Ile Leu Tyr Gly Ile Ile Ile Ser Ile Pro Met Val Leu Ala Cys
180     185     190
Leu Val Phe Ala Lys Tyr Ala Gly Asn Lys Ile Trp Gln Ile Pro Thr
195     200     205
Ser Asn Gly Lys Trp Thr Arg Asp Lys Asn Tyr Val Asp Asp Leu Lys
210     215     220
Thr Ser Ser Val Tyr Asp Glu Ser Asn Leu Pro Ser Ala Phe Leu Ser
225     230     235     240
Phe Ser Pro Ile Val Val Pro Ile Ile Leu Ile Leu Leu Gly Thr Val
245     250     255
Thr Asp Thr Met Lys Leu Glu Gly Lys Ile Ile Ser Phe Ile Gln Phe
260     265     270
Ile Gly Thr Pro Val Ile Ala Val Gly Ile Gly Leu Leu Ile Thr Ile
275     280     285
Tyr Gly Leu Thr Arg Ser Leu Asp Lys Gln Lys Val Leu Glu Glu Val
290     295     300
Glu Ile Gly Ile Lys Ser Ala Gly Thr Ile Ile Leu Ile Thr Gly Ala
305     310     315     320
Gly Gly Ala Phe Gly Met Leu Ile Arg Asp Ser Gly Val Gly Asp Val
325     330     335
Ile Ala Lys Ser Leu Val Asp Thr Ala Leu Pro Pro Ile Leu Leu Pro
340     345     350
Phe Ile Ile Ala Thr Leu Ile Arg Phe Ile Gln Gly Ser Gly Thr Val
355     360     365
Ala Met Ile Thr Ala Ala Ser Ile Thr Ala Pro Ile Ile Thr Lys Leu
370     375     380
Asn Val Asn Pro Val Leu Ala Ala Leu Ala Ala Cys Val Gly Ser Leu
385     390     395     400
Phe Phe Ser Tyr Phe Asn Asp Ser Phe Phe Trp Val Ile Asn Arg Ser
405     410     415
Ile Gly Ile Thr Glu Gly Lys Glu Gln Leu Arg Leu Tyr Ser Val Ala
420     425     430
Ser Thr Ile Ala Trp Ala Val Gly Ile Ile Ile Leu Leu Ile Leu Asn
435     440     445
Ile Phe Ile Lys
450

```

<210> 10130

<211> 1479

<212> DNA

<213> Streptomyces coelicolor A3(2)

<220>

<221> CDS

<222> (1)..(1479)

<223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 10130
atg tcc tac tcg tcc ctc cgt ctt gcc gcc gcc gag gcc cca ccc cac      48
Met Ser Tyr Ser Ser Leu Arg Leu Ala Ala Ala Glu Ala Pro Pro His
1      5      10      15
acc ggc ggt ctg ctc acc ctg atc gac ggc acc gcc ggt ctg ctg acc      96
Thr Gly Gly Leu Leu Thr Leu Ile Asp Gly Thr Ala Gly Leu Leu Thr
20      25      30
gtc gcc gcc atc ggc atc gcg ctg ctg ctc ttc ctc atc atc aag gtg      144
Val Ala Ala Ile Gly Ile Ala Leu Leu Phe Leu Ile Ile Lys Val
35      40      45
cgg ctt cag ccc ttc gtc gcg ctg ctc gcc gtc tcc ata gcc gtc ggc      192
Arg Leu Gln Pro Phe Val Ala Leu Leu Ala Val Ser Ile Ala Val Gly
50      55      60
ctg ctc gcc ggc ctg tcg gtc acc gaa ctc ttc ggc acc gtg cag aag      240
Leu Leu Ala Gly Leu Ser Val Thr Glu Leu Phe Gly Thr Val Gln Lys
65      70      75      80
tcg gac gcc gtc tcg acc atc gag tcc ggc atg ggc ggc atc ctc ggc      288
Ser Asp Ala Val Ser Thr Ile Glu Ser Gly Met Gly Gly Ile Leu Gly
85      90      95
cac gtc gcc atc atc atc ggc ctg ggc acc atg ctc ggc gcg atc ctc      336
His Val Ala Ile Ile Ile Gly Leu Gly Thr Met Leu Gly Ala Ile Leu
100      105      110
gaa gtc agc ggc ggc gcc cag gtg ctg gcc tcc cgc ctg ctc ggc ctc      384
Glu Val Ser Gly Gly Ala Gln Val Leu Ala Ser Arg Leu Leu Gly Leu
115      120      125
ttc ggg gag aag cgg gcc ccg ctc gcc atg ggc ctc acc ggt ctg atc      432
Phe Gly Glu Lys Arg Ala Pro Leu Ala Met Gly Leu Thr Gly Leu Ile
130      135      140
ttc ggc atc ccg gtc ttc phe gac gtg ggc atc ttc gtc ctc gcg ccc      480
Phe Gly Ile Pro Val Phe Phe Asp Val Gly Ile Phe Val Leu Ala Pro
145      150      155      160
atc gtc tac gcc gcc gcc aag cgc tcc ggc aag tcg atc ctg ctc tac      528
Ile Val Tyr Ala Ala Ala Lys Arg Ser Gly Lys Ser Ile Leu Leu Tyr
165      170      175
tgc ctg ccg ctg ctg gcc ggc ctg tcc atg acc cac gcc ttc ctg ccg      576
Cys Leu Pro Leu Leu Ala Gly Leu Ser Met Thr His Ala Phe Leu Pro
180      185      190
ccg cac ccc ggc ccg gtg gcc gcc gcc gga ctg ctg aac gtc aag ctc      624
Pro His Pro Gly Pro Val Ala Ala Ala Gly Leu Leu Asn Val Lys Leu
195      200      205
ggc tgg atc atc ctc atg ggc atc gtc tgc ggc atc ccc gcc gtc ctc      672
Gly Trp Ile Ile Leu Met Gly Ile Val Cys Gly Ile Pro Ala Val Leu
210      215      220
gcc gcc tgg gtg ttc tcc gcc Ala Trp Ile Gly Arg Arg Ile ttc gtg ccc      720
Ala Ala Trp Val Phe Ser Ala Trp Ile Gly Arg Arg Ile Phe Val Pro
225      230      235      240
gtg ccg cag gac atg gtc gag gcg tcc gag gag gcc aag cag gcc gtc      768
Val Pro Gln Asp Met Val Glu Ala Ser Glu Glu Ala Lys Gln Ala Val
245      250      255
atc gag gag cag cgc aag gcc ggc gtc gcg ccg aac gag agc ccc gtc      816
Ile Glu Glu Gln Arg Lys Ala Gly Val Ala Pro Asn Glu Ser Pro Val
260      265      270
gcg ctc ggc acc gtc ctc ggc atc atc ggc acc ccg ttg gtc ctg atc      864
Ala Leu Gly Thr Val Leu Gly Ile Ile Gly Thr Pro Leu Val Leu Ile
275      280      285
ctc gcc gcg acc ttc tcc tcc atc gcc ctg gac ccg tcc acc ctc cgc      912
Leu Ala Ala Thr Phe Ser Ser Ile Ala Leu Asp Pro Ser Thr Leu Arg
290      295      300
tcg gtg atc gag ttc ttc ggc aac ccg ttc gtc gcg ctg acc atc gcc      960
Ser Val Ile Glu Phe Phe Gly Asn Pro Phe Val Ala Leu Thr Ile Ala
305      310      315      320
ctg ctc ctc gcc tac tac ctg ctc ggc atc cgg cgc ggc tgg tcc cgc      1008
Leu Leu Leu Ala Tyr Tyr Leu Leu Gly Ile Arg Arg Gly Trp Ser Arg
325      330      335
aag tcc ctg gag acc gtc tcg acg gcc tcg ctg aag ccg gtc ggc aac      1056
Lys Ser Leu Glu Thr Val Ser Thr Ala Ser Leu Lys Pro Val Gly Asn
340      345      350
atc ctg ctg gtg gtc ggc gcg ggc ggc ggc ggc ggc gtc ctc aag      1104
350

```

PF59083SeqList PF59083.txt

Ile	Leu	Leu	Val	Val	Gly	Ala	Gly	Gly	Val	Phe	Gly	Ala	Val	Leu	Lys	
		355					360				365					
gcc	agc	ggc	gtc	gcc	cag	gca	ctc	tcc	gac	acc	ttc	aac	gac	gtc	ggc	1152
Ala	Ser	Gly	Val	Ala	Gln	Ala	Leu	Ser	Asp	Thr	Phe	Asn	Asp	Val	Gly	
	370					375					380					
ctg	ccg	gtg	atc	gtc	ctc	gcc	tac	ctg	atc	tcc	gtg	gtg	ctg	cgg	gtc	1200
Leu	Pro	Val	Ile	Val	Leu	Ala	Tyr	Leu	Ile	Ser	Val	Val	Leu	Arg	Val	
	385				390					395					400	
gcg	cag	ggc	tcg	gcg	acg	gtg	gcc	atc	gtg	acg	acg	gcg	ggc	atc	gtg	1248
Ala	Gln	Gly	Ser	Ala	Thr	Val	Ala	Ile	Val	Thr	Thr	Ala	Gly	Ile	Val	
				405					410					415		
gcg	ccg	ctg	ctg	gcc	gag	ggc	gac	cac	tcg	cag	gcg	ttc	gtc	gcg	ctg	1296
Ala	Pro	Leu	Leu	Ala	Glu	Gly	Asp	His	Ser	Gln	Ala	Phe	Val	Ala	Leu	
			420				425						430			
gtc	atc	atg	gcc	atc	tcg	gcg	ggc	tcc	atc	ttc	gcc	tcg	cac	gtc	aac	1344
Val	Ile	Met	Ala	Ile	Ser	Ala	Gly	Ser	Ile	Phe	Ala	Ser	His	Val	Asn	
		435					440					445				
gac	ggc	ggc	ttc	tgg	atg	gtc	gcc	aag	tac	ttc	ggc	atc	agc	gag	cgg	1392
Asp	Gly	Gly	Phe	Trp	Met	Val	Ala	Lys	Tyr	Phe	Gly	Ile	Ser	Glu	Arg	
	450					455					460					
gac	acg	ctc	aag	acg	tgg	acc	gtg	ctg	gag	agc	gtc	ctg	tcc	gtc	gcc	1440
Asp	Thr	Leu	Lys	Thr	Trp	Thr	Val	Leu	Glu	Ser	Val	Leu	Ser	Val	Ala	
	465				470					475					480	
ggg	ttc	gtg	gtg	gcc	gcg	gtg	gtg	agc	ctg	ttc	gtg	tag				1479
Gly	Phe	Val	Val	Ala	Ala	Val	Val	Ser	Leu	Phe	Val					
				485					490							

<210> 10131

<211> 492

<212> PRT

<213> Streptomyces coelicolor A3(2)

<400> 10131

Met	Ser	Tyr	Ser	Ser	Leu	Arg	Leu	Ala	Ala	Ala	Glu	Ala	Pro	Pro	His	
1				5					10					15		
Thr	Gly	Gly	Leu	Leu	Thr	Leu	Ile	Asp	Gly	Thr	Ala	Gly	Leu	Leu	Thr	
			20					25					30			
Val	Ala	Ala	Ile	Gly	Ile	Ala	Leu	Leu	Leu	Phe	Leu	Ile	Ile	Lys	Val	
		35				40						45				
Arg	Leu	Gln	Pro	Phe	Val	Ala	Leu	Leu	Ala	Val	Ser	Ile	Ala	Val	Gly	
	50					55					60					
Leu	Leu	Ala	Gly	Leu	Ser	Val	Thr	Glu	Leu	Phe	Gly	Thr	Val	Gln	Lys	
	65				70					75					80	
Ser	Asp	Ala	Val	Ser	Thr	Ile	Glu	Ser	Gly	Met	Gly	Gly	Ile	Leu	Gly	
				85					90					95		
His	Val	Ala	Ile	Ile	Ile	Gly	Leu	Gly	Thr	Met	Leu	Gly	Ala	Ile	Leu	
			100					105					110			
Glu	Val	Ser	Gly	Gly	Ala	Gln	Val	Leu	Ala	Ser	Arg	Leu	Leu	Gly	Leu	
		115				120						125				
Phe	Gly	Glu	Lys	Arg	Ala	Pro	Leu	Ala	Met	Gly	Leu	Thr	Gly	Leu	Ile	
	130					135					140					
Phe	Gly	Ile	Pro	Val	Phe	Phe	Asp	Val	Gly	Ile	Phe	Val	Leu	Ala	Pro	
	145				150					155				160		
Ile	Val	Tyr	Ala	Ala	Lys	Arg	Ser	Gly	Lys	Ser	Ile	Leu	Leu	Tyr		
			165					170					175			
Cys	Leu	Pro	Leu	Leu	Ala	Gly	Leu	Ser	Met	Thr	His	Ala	Phe	Leu	Pro	
			180					185					190			
Pro	His	Pro	Gly	Pro	Val	Ala	Ala	Ala	Gly	Leu	Leu	Asn	Val	Lys	Leu	
		195				200						205				
Gly	Trp	Ile	Ile	Leu	Met	Gly	Ile	Val	Cys	Gly	Ile	Pro	Ala	Val	Leu	
	210					215					220					
Ala	Ala	Trp	Val	Phe	Ser	Ala	Trp	Ile	Gly	Arg	Arg	Ile	Phe	Val	Pro	
	225				230					235					240	
Val	Pro	Gln	Asp	Met	Val	Glu	Ala	Ser	Glu	Glu	Ala	Lys	Gln	Ala	Val	
				245					250					255		
Ile	Glu	Glu	Gln	Arg	Lys	Ala	Gly	Val	Ala	Pro	Asn	Glu	Ser	Pro	Val	
			260					265					270			
Ala	Leu	Gly	Thr	Val	Leu	Gly	Ile	Ile	Gly	Thr	Pro	Leu	Val	Leu	Ile	
		275					280						285			

PF59083SeqList PF59083.txt

Leu Ala Ala Thr Phe Ser Ser Ile Ala Leu Asp Pro Ser Thr Leu Arg
 290 295 300
 Ser Val Ile Glu Phe Phe Gly Asn Pro Phe Val Ala Leu Thr Ile Ala
 305 310 315 320
 Leu Leu Leu Ala Tyr Tyr Leu Leu Gly Ile Arg Arg Gly Trp Ser Arg
 325 330 335
 Lys Ser Leu Glu Thr Val Ser Thr Ala Ser Leu Lys Pro Val Gly Asn
 340 345 350
 Ile Leu Leu Val Val Gly Ala Gly Gly Val Phe Gly Ala Val Leu Lys
 355 360 365
 Ala Ser Gly Val Ala Gln Ala Leu Ser Asp Thr Phe Asn Asp Val Gly
 370 375 380
 Leu Pro Val Ile Val Leu Ala Tyr Leu Ile Ser Val Val Leu Arg Val
 385 390 400
 Ala Gln Gly Ser Ala Thr Val Ala Ile Val Thr Thr Ala Gly Ile Val
 405 410 415
 Ala Pro Leu Leu Ala Glu Gly Asp His Ser Gln Ala Phe Val Ala Leu
 420 425 430
 Val Ile Met Ala Ile Ser Ala Gly Ser Ile Phe Ala Ser His Val Asn
 435 440 445
 Asp Gly Gly Phe Trp Met Val Ala Lys Tyr Phe Gly Ile Ser Glu Arg
 450 455 460
 Asp Thr Leu Lys Thr Trp Thr Val Leu Glu Ser Val Leu Ser Val Ala
 465 470 475 480
 Gly Phe Val Val Ala Val Val Ser Leu Phe Val
 485 490

<210> 10132
 <211> 1347
 <212> DNA
 <213> Oceanobacillus iheyensis HTE831

<220>
 <221> CDS
 <222> (1)..(1347)
 <223> transl_table=11

<400> 10132
 atg cca tta att att gta gca tta gct gta gta tta cta ttg cta ctc 48
 Met Pro Leu Ile Ile Val Ala Leu Ala Val Val Leu Leu Leu 15
 1 5 10 15
 ata atg aaa tgg aat tta aat aca ttt att tca ttg att att gta tca 96
 Ile Met Lys Trp Asn Leu Asn Thr Phe Ile Ser Leu Ile Ile Val Ser 20 25 30
 ttc cta act gcc ttg gct tta ggg atg cca tta gga gaa att gtt aca 144
 Phe Leu Thr Ala Leu Ala Leu Gly Met Pro Leu Gly Glu Ile Val Thr 35 40 45
 tcg att gaa ggt gga ctt ggc ggt aca tta ggt gac att gcc ctc atc 192
 Ser Ile Glu Gly Gly Leu Gly Gly Thr Leu Gly Asp Ile Ala Leu Ile 50 55 60
 ttt ggt ttt ggt gca ata tta ggg aaa cta gtt gca gat gct ggt ggg 240
 Phe Gly Phe Gly Ala Ile Leu Gly Lys Leu Val Ala Asp Ala Gly Gly 65 70 75 80
 gca cag cga att gct ctg aca ttg att cac aaa ttt gga gaa aaa cga 288
 Ala Gln Arg Ile Ala Leu Thr Leu Ile His Lys Phe Gly Glu Lys Arg 85 90 95
 atc caa tgg gcg gta gta att gca tca ttc att att ggt gta gcg tta 336
 Ile Gln Trp Ala Val Val Ile Ala Ser Phe Ile Ile Gly Val Ala Leu 100 105 110
 ttc ttc gaa gta ggg tta gtt cta cta ata ccg att ata tac caa att 384
 Phe Phe Glu Val Gly Leu Val Leu Leu Ile Pro Ile Ile Tyr Gln Ile 115 120 125
 gca aaa gaa att aaa ata cct tta tta tat tta ggt tta cca atg acg 432
 Ala Lys Glu Ile Lys Ile Pro Leu Leu Tyr Leu Gly Leu Pro Met Thr 130 135 140
 gca gcg tta tcc gta acg cat ggt ttt tta cca cca cat ccg ggt cca 480
 Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Gly Pro 145 150 155 160
 aca gta att gct cag caa tac gga gca aat att gga atg gta ctt att 528
 165 170

PF59083SeqList PF59083.txt

Thr	Val	Ile	Ala	Gln	Gln	Tyr	Gly	Ala	Asn	Ile	Gly	Met	Val	Leu	Ile	
				165					170					175		
tat	ggg	att	att	att	gcg	gtt	cca	acg	gtt	att	tta	gct	ggg	cca	cta	576
Tyr	Gly	Ile	Ile	Ile	Ala	Val	Pro	Thr	Val	Ile	Leu	Ala	Gly	Pro	Leu	
			180					185					190			
ttt	act	aaa	ggt	gct	aag	aaa	att	gtt	cca	gat	gca	ttt	tca	aaa	gtt	624
Phe	Thr	Lys	Val	Ala	Lys	Lys	Ile	Val	Pro	Asp	Ala	Phe	Ser	Lys	Val	
		195					200					205				
ggt	aat	ctt	gga	tca	ctt	ggt	ggg	gca	aaa	tca	ttt	cca	gaa	gag	gaa	672
Gly	Asn	Leu	Gly	Ser	Leu	Gly	Gly	Ala	Lys	Ser	Phe	Pro	Glu	Glu	Glu	
	210					215					220					
aca	ccg	agc	ttt	gca	gtt	agt	gca	tta	acc	gca	cta	ttc	cct	gta	att	720
Thr	Pro	Ser	Phe	Ala	Val	Ser	Ala	Leu	Thr	Ala	Leu	Phe	Pro	Val	Ile	
225				230			235								240	
tta	atg	gca	att	aca	gta	gtt	gat	tta	ctg	caa	gat	atc	ggg	gat		768
Leu	Met	Ala	Ile	Thr	Val	Val	Asp	Leu	Leu	Gln	Asp	Ile	Gly	Asp		
			245				250						255			
gtg	tcg	gat	aat	att	ctt	ttt	gaa	att	atg	cg	atg	att	gga	caa	cca	816
Val	Ser	Asp	Asn	Ile	Leu	Phe	Glu	Ile	Met	Arg	Met	Ile	Gly	Gln	Pro	
			260				265						270			
aca	aca	gca	tta	ttg	att	tct	tta	ttt	gca	atc	tat	aca	atg	ggg		864
Thr	Thr	Ala	Leu	Leu	Ile	Ser	Leu	Leu	Ala	Ile	Tyr	Thr	Met	Gly		
		275					280				285					
att	gct	cgt	aaa	ata	ccg	atg	aaa	caa	ttg	atg	aca	tct	gca	gaa	gaa	912
Ile	Ala	Arg	Lys	Ile	Pro	Met	Lys	Gln	Leu	Met	Thr	Ser	Ala	Glu	Glu	
	290					295					300					
tct	gtt	cg	gct	ata	ggg	atg	atg	tta	ctt	att	att	ggg	ggg	ggc	gga	960
Ser	Val	Arg	Ala	Ile	Gly	Met	Met	Leu	Leu	Ile	Ile	Gly	Gly	Gly	Gly	
305				310						315					320	
gcc	tta	aaa	caa	gtc	tta	att	gat	ggc	ggg	gtc	ggg	gac	tct	gtt	gct	1008
Ala	Leu	Lys	Gln	Val	Leu	Ile	Asp	Gly	Gly	Val	Gly	Asp	Ser	Val	Ala	
			325					330						335		
gct	tta	ttt	gat	gga	acg	agt	atg	tcc	cca	ata	ttt	ctt	gct	tg	ttg	1056
Ala	Leu	Phe	Asp	Gly	Thr	Ser	Met	Ser	Pro	Ile	Phe	Leu	Ala	Trp	Leu	
			340				345						350			
att	gct	gca	atc	tta	aga	att	gca	ctt	ggg	tct	gca	act	gta	gca	gca	1104
Ile	Ala	Ala	Ile	Leu	Arg	Ile	Ala	Leu	Gly	Ser	Ala	Thr	Val	Ala	Ala	
		355					360				365					
tta	aca	act	gta	ggg	atg	gta	atc	cca	tta	atg	gaa	ggg	aca	gat	gta	1152
Leu	Thr	Thr	Val	Gly	Met	Val	Ile	Pro	Leu	Met	Glu	Gly	Thr	Asp	Val	
	370					375					380					
aac	ctt	gcc	tta	atg	gtg	tta	gca	act	ggg	gca	ggg	agc	ttg	att	gcg	1200
Asn	Leu	Ala	Leu	Met	Val	Leu	Ala	Thr	Gly	Ala	Gly	Ser	Leu	Ile	Ala	
385				390						395					400	
tcc	cac	gta	aat	gat	aca	gga	ttc	tgg	atc	ttt	aaa	gaa	tac	ttt	aat	1248
Ser	His	Val	Asn	Asp	Thr	Gly	Phe	Trp	Ile	Phe	Lys	Glu	Tyr	Phe	Asn	
			405					410						415		
tta	tcc	atg	aaa	gaa	acc	ttc	gca	aca	tgg	acg	tta	ctt	gaa	aca	gta	1296
Leu	Ser	Met	Lys	Glu	Thr	Phe	Ala	Thr	Trp	Thr	Leu	Leu	Glu	Thr	Val	
			420				425						430			
att	tca	gtc	gca	ggg	cta	gtg	ttt	aca	cta	gcg	tta	agt	tta	att	gta	1344
Ile	Ser	Val	Ala	Gly	Leu	Val	Phe	Thr	Leu	Ala	Leu	Ser	Leu	Ile	Val	
		435					440					445				
taa																1347

<210> 10133
 <211> 448
 <212> PRT
 <213> Oceanobacillus iheyensis HTE831

<400> 10133
 Met Pro Leu Ile Ile Val Ala Leu Ala Val Val Leu Leu Leu Leu Leu
 1 5 10 15
 Ile Met Lys Trp Asn Leu Asn Thr Phe Ile Ser Leu Ile Ile Val Ser
 20 25 30
 Phe Leu Thr Ala Leu Ala Leu Gly Met Pro Leu Gly Glu Ile Val Thr
 35 40 45

PF59083SeqList PF59083.txt

Ser Ile Glu Gly Gly Leu Gly Gly Thr Leu Gly Asp Ile Ala Leu Ile
50 55 60
Phe Gly Phe Gly Ala Ile Leu Gly Lys Leu Val Ala Asp Ala Gly Gly
65 70 75 80
Ala Gln Arg Ile Ala Leu Thr Leu Ile His Lys Phe Gly Glu Lys Arg
85 90 95
Ile Gln Trp Ala Val Val Ile Ala Ser Phe Ile Ile Gly Val Ala Leu
100 105 110
Phe Phe Glu Val Gly Leu Val Leu Ile Pro Ile Ile Tyr Gln Ile
115 120 125
Ala Lys Glu Ile Lys Ile Pro Leu Leu Tyr Leu Gly Leu Pro Met Thr
130 135 140
Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Gly Pro
145 150 155 160
Thr Val Ile Ala Gln Tyr Gly Ala Asn Ile Gly Met Val Leu Ile
165 170 175
Tyr Gly Ile Ile Ile Ala Val Pro Thr Val Ile Leu Ala Gly Pro Leu
180 185 190
Phe Thr Lys Val Ala Lys Lys Ile Val Pro Asp Ala Phe Ser Lys Val
195 200 205
Gly Asn Leu Gly Ser Leu Gly Ala Lys Ser Phe Pro Glu Glu Glu
210 215 220
Thr Pro Ser Phe Ala Val Ser Ala Leu Thr Ala Leu Phe Pro Val Ile
225 230 235 240
Leu Met Ala Ile Thr Val Val Asp Leu Leu Gln Asp Ile Gly Asp
245 250 255
Val Ser Asp Asn Ile Leu Phe Glu Ile Met Arg Met Ile Gly Gln Pro
260 265 270
Thr Thr Ala Leu Leu Ile Ser Leu Leu Leu Ala Ile Tyr Thr Met Gly
275 280 285
Ile Ala Arg Lys Ile Pro Met Lys Gln Leu Met Thr Ser Ala Glu Glu
290 295 300
Ser Val Arg Ala Ile Gly Met Met Leu Leu Ile Ile Gly Gly Gly Gly
305 310 315 320
Ala Leu Lys Gln Val Leu Ile Asp Gly Gly Val Gly Asp Ser Val Ala
325 330 335
Ala Leu Phe Asp Gly Thr Ser Met Ser Pro Ile Phe Leu Ala Trp Leu
340 345 350
Ile Ala Ala Ile Leu Arg Ile Ala Leu Gly Ser Ala Thr Val Ala Ala
355 360 365
Leu Thr Thr Val Gly Met Val Ile Pro Leu Met Glu Gly Thr Asp Val
370 375 380
Asn Leu Ala Leu Met Val Leu Ala Thr Gly Ala Gly Ser Leu Ile Ala
385 390 400
Ser His Val Asn Asp Thr Gly Phe Trp Ile Phe Lys Glu Tyr Phe Asn
405 410 415
Leu Ser Met Lys Glu Thr Phe Ala Thr Trp Thr Leu Leu Glu Thr Val
420 425 430
Ile Ser Val Ala Gly Leu Val Phe Thr Leu Ala Leu Ser Leu Ile Val
435 440 445

<210> 10134

<211> 1317

<212> DNA

<213> Shigella flexneri 2a str. 301

<220>

<221> CDS

<222> (1)..(1317)

<223> transl_table=11

<400> 10134

atg cca tta gtc att gtt gct atc ggt gta atc ttg ttg ttg ctc ctg 48
Met Pro Leu Val Ile Val Ala Ile Gly Val Ile Leu Leu Leu Leu Leu
1 5 10 15

atg atc cgc ttc aaa atg aac ggc ttc atc gct ctc gtc ctc gtg gcg 96
Met Ile Arg Phe Lys Met Asn Gly Phe Ile Ala Leu Val Leu Val Ala
20 25 30

ctt gct gtt gga tta atg caa gga atg ccg ctg gat aaa gtt att ggc 144
Seite 10720

PF59083SeqList PF59083.txt

Leu	Ala	Val	Gly	Leu	Met	Gln	Gly	Met	Pro	Leu	Asp	Lys	Val	Ile	Gly	
tcc	atc	aaa	gcc	ggt	gtc	ggc	ggg	acg	ctc	ggt	agc	ctt	gcc	ctg	atc	192
Ser	Ile	Lys	Ala	Gly	Val	Gly	Gly	Thr	Leu	Gly	Ser	Leu	Ala	Leu	Ile	
atg	ggt	ttt	ggc	gca	atg	ctg	ggc	aaa	atg	ctg	gca	gac	tgc	ggt	ggc	240
Met	Gly	Phe	Gly	Ala	Met	Leu	Gly	Lys	Met	Leu	Ala	Asp	Cys	Gly	Gly	
gca	caa	cgt	atc	gcc	acc	acg	ctg	att	gcc	aaa	ttt	ggt	aaa	aag	cac	288
Ala	Gln	Arg	Ile	Ala	Thr	Thr	Leu	Ile	Ala	Lys	Phe	Gly	Lys	Lys	His	
atc	cag	tgg	gcg	gtg	gtg	tta	acc	ggt	ttt	acc	ggt	ggt	ttt	gcc	ctg	336
Ile	Gln	Trp	Ala	Val	Val	Leu	Thr	Gly	Phe	Thr	Val	Gly	Phe	Ala	Leu	
ttc	tat	gaa	gtg	ggc	ttc	gtg	ctg	atg	ctg	ccg	ctg	gtg	ttt	acc	atc	384
Phe	Tyr	Glu	Val	Gly	Phe	Val	Leu	Met	Leu	Pro	Leu	Val	Phe	Thr	Ile	
gcg	gct	tcc	gcg	aat	att	cca	ttg	ctg	tat	gtt	ggt	gta	cca	atg	gcg	432
Ala	Ala	Ser	Ala	Asn	Ile	Pro	Leu	Leu	Tyr	Val	Gly	Val	Pro	Met	Ala	
gct	gca	ctg	tct	gtg	acc	cac	ggc	ttc	ctg	cca	ccg	cat	ccg	ggc	ccg	480
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
act	gcg	att	gcc	acc	att	ttc	aat	gcc	gat	atg	ggt	aaa	acc	ctg	ctg	528
Thr	Ala	Ile	Ala	Thr	Ile	Phe	Asn	Ala	Asp	Met	Gly	Lys	Thr	Leu	Leu	
tac	ggt	act	att	ctg	gca	atc	ccg	acc	gtg	att	ctc	gcc	ggt	ccg	gtt	576
Tyr	Gly	Thr	Ile	Leu	Ala	Ile	Pro	Thr	Val	Ile	Leu	Ala	Gly	Pro	Val	
tac	gct	cg	gtg	ttg	aaa	ggt	atc	gat	aag	cca	atc	ccg	gaa	ggt	ctc	624
Tyr	Ala	Arg	Val	Leu	Lys	Gly	Ile	Asp	Lys	Pro	Ile	Pro	Glu	Gly	Leu	
tac	agc	gcg	aaa	acc	ttc	agc	gaa	gaa	gag	atg	ccg	agc	ttt	ggc	gtc	672
Tyr	Ser	Ala	Lys	Thr	Phe	Ser	Glu	Glu	Glu	Met	Pro	Ser	Phe	Gly	Val	
agc	gtc	tgg	acc	tct	ctg	gtg	ccg	gtt	gtg	ctg	atg	gcg	atg	cgt	gcg	720
Ser	Val	Trp	Thr	Ser	Leu	Val	Pro	Val	Val	Leu	Met	Ala	Met	Arg	Ala	
att	gcc	gaa	atg	atc	ctg	ccg	aaa	ggt	cac	gct	ttc	ctg	ccg	gta	gcg	768
Ile	Ala	Glu	Met	Ile	Leu	Pro	Lys	Gly	His	Ala	Phe	Leu	Pro	Val	Ala	
gag	ttc	ctc	ggt	gac	ccg	gta	atg	gca	acg	ctg	att	gcc	gtg	ctg	att	816
Glu	Phe	Leu	Gly	Asp	Pro	Val	Met	Ala	Thr	Leu	Ile	Ala	Val	Leu	Ile	
gcg	atg	ttc	acc	ttt	ggt	ctg	aac	cgt	ggt	cgt	tca	atg	gat	cag	att	864
Ala	Met	Phe	Thr	Phe	Gly	Leu	Asn	Arg	Gly	Arg	Ser	Met	Asp	Gln	Ile	
aac	gac	acg	ctg	gtt	tct	tcc	atc	aaa	atc	att	gcg	atg	atg	ctg	ttg	912
Asn	Asp	Thr	Leu	Val	Ser	Ser	Ile	Lys	Ile	Ile	Ala	Met	Met	Leu	Leu	
atc	atc	ggt	ggt	ggc	ggt	gcg	ttc	aag	cag	gtg	ctg	gta	gac	agc	ggc	960
Ile	Ile	Gly	Gly	Gly	Gly	Ala	Phe	Lys	Gln	Val	Leu	Val	Asp	Ser	Gly	
gtg	gac	aaa	tac	att	gct	tcc	atg	atg	cac	gaa	acc	aac	att	tct	ccg	1008
Val	Asp	Lys	Tyr	Ile	Ala	Ser	Met	Met	His	Glu	Thr	Asn	Ile	Ser	Pro	
ctg	ctg	atg	gcc	tgg	tcg	att	gct	gcc	gta	ctg	cgt	atc	gcg	ctg	ggt	1056
Leu	Leu	Met	Ala	Trp	Ser	Ile	Ala	Ala	Val	Leu	Arg	Ile	Ala	Leu	Gly	
tcc	gca	acc	gtt	gcg	gca	atc	act	gcg	ggt	ggt	atc	gcg	gca	ccg	ctg	1104
Ser	Ala	Thr	Val	Ala	Ala	Ile	Thr	Ala	Gly	Gly	Ile	Ala	Ala	Pro	Leu	
att	gca	acg	acg	ggt	gtt	agc	cca	cag	ctg	atg	gtt	att	gcg	gtg	ggt	1152
Ile	Ala	Thr	Thr	Gly	Val	Ser	Pro	Gln	Leu	Met	Val	Ile	Ala	Val	Gly	
tcc	ggt	agt	gtg	att	ttc	tct	cat	gtg	aac	gat	ccg	ggc	ttc	tgg	ctg	1200
Ser	Gly	Ser	Val	Ile	Phe	Ser	His	Val	Asn	Asp	Pro	Gly	Phe	Trp	Leu	
ttc	aaa	gag	tac	ttt	aac	ctg	act	atc	ggc	gag	acc	atc	aaa	tcc	tgg	1248

PF59083SeqList PF59083.txt

Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Thr	Ile	Gly	Glu	Thr	Ile	Lys	Ser	Trp	
				405					410					415		
tcg	atg	ctg	gaa	acc	att	atc	tcg	gtg	ggc	ctg	gta	ggc	tgt	ctg		1296
Ser	Met	Leu	Glu	Thr	Ile	Ile	Ser	Val	Cys	Gly	Leu	Val	Gly	Cys	Leu	
			420					425					430			
ctg	ctg	aat	atg	gtg	att	tga										1317
Leu	Leu	Asn	Met	Val	Ile											
			435													

<210> 10135
 <211> 438
 <212> PRT
 <213> Shigella flexneri 2a str. 301

<400> 10135

Met	Pro	Leu	Val	Ile	Val	Ala	Ile	Gly	Val	Ile	Leu	Leu	Leu	Leu	Leu	
1				5					10					15		
Met	Ile	Arg	Phe	Lys	Met	Asn	Gly	Phe	Ile	Ala	Leu	Val	Leu	Val	Ala	
			20					25					30			
Leu	Ala	Val	Gly	Leu	Met	Gln	Gly	Met	Pro	Leu	Asp	Lys	Val	Ile	Gly	
		35					40					45				
Ser	Ile	Lys	Ala	Gly	Val	Gly	Gly	Thr	Leu	Gly	Ser	Leu	Ala	Leu	Ile	
	50					55				60						
Met	Gly	Phe	Gly	Ala	Met	Leu	Gly	Lys	Met	Leu	Ala	Asp	Cys	Gly	Gly	
65					70					75					80	
Ala	Gln	Arg	Ile	Ala	Thr	Thr	Leu	Ile	Ala	Lys	Phe	Gly	Lys	Lys	His	
			85						90					95		
Ile	Gln	Trp	Ala	Val	Val	Leu	Thr	Gly	Phe	Thr	Val	Gly	Phe	Ala	Leu	
			100					105					110			
Phe	Tyr	Glu	Val	Gly	Phe	Val	Leu	Met	Leu	Pro	Leu	Val	Phe	Thr	Ile	
		115					120					125				
Ala	Ala	Ser	Ala	Asn	Ile	Pro	Leu	Leu	Tyr	Val	Gly	Val	Pro	Met	Ala	
	130					135				140						
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
145					150					155					160	
Thr	Ala	Ile	Ala	Thr	Ile	Phe	Asn	Ala	Asp	Met	Gly	Lys	Thr	Leu	Leu	
			165					170						175		
Tyr	Gly	Thr	Ile	Leu	Ala	Ile	Pro	Thr	Val	Ile	Leu	Ala	Gly	Pro	Val	
			180					185					190			
Tyr	Ala	Arg	Val	Leu	Lys	Gly	Ile	Asp	Lys	Pro	Ile	Pro	Glu	Gly	Leu	
		195					200					205				
Tyr	Ser	Ala	Lys	Thr	Phe	Ser	Glu	Glu	Glu	Met	Pro	Ser	Phe	Gly	Val	
	210					215					220					
Ser	Val	Trp	Thr	Ser	Leu	Val	Pro	Val	Val	Leu	Met	Ala	Met	Arg	Ala	
225					230					235					240	
Ile	Ala	Glu	Met	Ile	Leu	Pro	Lys	Gly	His	Ala	Phe	Leu	Pro	Val	Ala	
			245						250					255		
Glu	Phe	Leu	Gly	Asp	Pro	Val	Met	Ala	Thr	Leu	Ile	Ala	Val	Leu	Ile	
			260					265					270			
Ala	Met	Phe	Thr	Phe	Gly	Leu	Asn	Arg	Gly	Arg	Ser	Met	Asp	Gln	Ile	
		275					280					285				
Asn	Asp	Thr	Leu	Val	Ser	Ser	Ile	Lys	Ile	Ile	Ala	Met	Met	Leu	Leu	
	290					295					300					
Ile	Ile	Gly	Gly	Gly	Gly	Ala	Phe	Lys	Gln	Val	Leu	Val	Asp	Ser	Gly	
305					310					315					320	
Val	Asp	Lys	Tyr	Ile	Ala	Ser	Met	Met	His	Glu	Thr	Asn	Ile	Ser	Pro	
			325						330					335		
Leu	Leu	Met	Ala	Trp	Ser	Ile	Ala	Ala	Val	Leu	Arg	Ile	Ala	Leu	Gly	
			340					345					350			
Ser	Ala	Thr	Val	Ala	Ala	Ile	Thr	Ala	Gly	Gly	Ile	Ala	Ala	Pro	Leu	
		355					360					365				
Ile	Ala	Thr	Thr	Gly	Val	Ser	Pro	Gln	Leu	Met	Val	Ile	Ala	Val	Gly	
	370					375					380					
Ser	Gly	Ser	Val	Ile	Phe	Ser	His	Val	Asn	Asp	Pro	Gly	Phe	Trp	Leu	
385					390					395					400	
Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Thr	Ile	Gly	Glu	Thr	Ile	Lys	Ser	Trp	
			405						410					415		
Ser	Met	Leu	Glu	Thr	Ile	Ile	Ser	Val	Cys	Gly	Leu	Val	Gly	Cys	Leu	
			420					425					430			

PF59083SeqList PF59083.txt

Leu Leu Asn Met Val Ile
435

<210> 10136
<211> 1344
<212> DNA
<213> Shigella flexneri 2a str. 301

<220>
<221> CDS
<222> (1)..(1344)
<223> transl_table=11

```

<400> 10136
atg cat gtg ctt aac att ctc tgg gtg gta ttc ggc att ggc ctg atg      48
Met His Val Leu Asn Ile Leu Trp Val Val Phe Gly Ile Gly Leu Met
1      5      10      15
ctg ata ctg aat ttg aag ttc aaa atc aat tca atg gtg gct ttg ttg      96
Leu Ile Leu Asn Leu Lys Phe Lys Ile Asn Ser Met Val Ala Leu Leu
20      25      30
gtg gcg gcg ctg tcc gtc ggg atg ctg gca ggc atg gat ttg atg tcg      144
Val Ala Ala Leu Ser Val Gly Met Leu Ala Gly Met Asp Leu Met Ser
35      40      45
ctg ctg cac acc atg aaa gcg ggc ttc ggc aac acg ctg gga gaa ctg      192
Leu Leu His Thr Met Lys Ala Gly Phe Gly Asn Thr Leu Gly Glu Leu
50      55      60
gct atc atc gtg gtg ttc ggt gcg gtc atc ggt aaa ttg atg gtc gac      240
Ala Ile Ile Val Val Phe Gly Ala Val Ile Gly Lys Leu Met Val Asp
65      70      75      80
tcc ggc gcg gct cac cag ata gca cat acg ctg gcg cgt ctc ggt      288
Ser Gly Ala Ala His Gln Ile Ala His Thr Leu Leu Ala Arg Leu Gly
85      90      95
ctg cgc tat gta cag ctg tcg gtg att atc atc ggc ctt att ttc ggt      336
Leu Arg Tyr Val Gln Leu Ser Val Ile Ile Ile Gly Leu Ile Phe Gly
100      105      110
ctg gcg atg ttc tat gaa gtg gcc ttt atc atg tta gcg ccg ctg gtt      384
Leu Ala Met Phe Tyr Glu Val Ala Phe Ile Met Leu Ala Pro Leu Val
115      120      125
att gtt att gcc gcc gaa gct aaa att ccg ttc ctg aaa ctg gcg atc      432
Ile Val Ile Ala Ala Glu Ala Lys Ile Pro Phe Leu Lys Leu Ala Ile
130      135      140
ccg gca gta gca gct gcc act acc gca cat tca ctg ttc cca ccg cag      480
Pro Ala Val Ala Ala Ala Thr Thr Ala His Ser Leu Phe Pro Pro Gln
145      150      155      160
ccg ggt ccg gtg gcg ctg gtg aat gct tat ggc gcg gat atg ggg atg      528
Pro Gly Pro Val Ala Leu Val Asn Ala Tyr Gly Ala Asp Met Gly Met
165      170      175
gtt tat atc tat ggc gta ctg gtg acg atc cca agt gta atc tgc gca      576
Val Tyr Ile Tyr Gly Val Leu Val Thr Ile Pro Ser Val Ile Cys Ala
180      185      190
ggg ctg atc ctg ccg aag ttc ctc ggc aat ctt gag cgc cca acg cca      624
Gly Leu Ile Leu Pro Lys Phe Leu Gly Asn Leu Glu Arg Pro Thr Pro
195      200      205
tca ttc ctg aaa gca gat caa ccg gta gat atg aat aat ctg ccc tct      672
Ser Phe Leu Lys Ala Asp Gln Pro Val Asp Met Asn Asn Leu Pro Ser
210      215      220
ttc ggc gtt tcg att ctg gtg ccg ctg atc ccg gcg atc att atg atc      720
Phe Gly Val Ser Ile Leu Val Pro Leu Ile Pro Ala Ile Ile Met Ile
225      230      235      240
tct acc acc atc gcc aat atc tgg ctg gta gat acc cct gcc tgg      768
Ser Thr Thr Ile Ala Asn Ile Trp Leu Val Lys Asp Thr Pro Ala Trp
245      250      255
gaa gtg gtt aac ttt att ggt tcc tcg ccg att gcg atg ttt att gcg      816
Glu Val Val Asn Phe Ile Gly Ser Ser Pro Ile Ala Met Phe Ile Ala
260      265      270
atg gtg gtt gca ttc gta ctc ttt ggc acc gcg cgt ggt cat gac atg      864
Met Val Val Ala Phe Val Leu Phe Gly Thr Ala Arg Gly His Asp Met
275      280      285
cag tgg gtg atg aac gct ttt gaa agc gcg gtg aag agt att gca atg      912

```

PF59083SeqList PF59083.txt

Gln	Trp	Val	Met	Asn	Ala	Phe	Glu	Ser	Ala	Val	Lys	Ser	Ile	Ala	Met	
290						295					300					
gtg	att	ctg	atc	atc	ggt	gcg	ggt	ggc	gtg	ctg	aag	cag	acc	atc	atc	960
Val	Ile	Leu	Ile	Ile	Gly	Ala	Gly	Gly	Val	Leu	Lys	Gln	Thr	Ile	Ile	
305					310					315					320	
gac	acc	ggc	att	ggc	gac	acc	atc	ggc	atg	ttg	atg	tcc	cac	ggc	aat	1008
Asp	Thr	Gly	Ile	Gly	Asp	Thr	Ile	Gly	Met	Leu	Met	Ser	His	Gly	Asn	
				325					330					335		
atc	tcg	ccc	tac	att	atg	gca	tgg	ctg	atc	act	gtg	cta	att	cgt	ctg	1056
Ile	Ser	Pro	Tyr	Ile	Met	Ala	Trp	Leu	Ile	Thr	Val	Leu	Ile	Arg	Leu	
			340					345					350			
gcg	acg	ggt	cag	ggt	gtc	gtt	tcg	gcg	atg	acc	gcc	gcc	ggg	att	atc	1104
Ala	Thr	Gly	Gln	Gly	Val	Val	Ser	Ala	Met	Thr	Ala	Ala	Gly	Ile	Ile	
		355					360				365					
agt	gct	gca	atc	ctt	gat	cca	gca	acc	ggt	cag	ctg	gtt	ggc	gtg	aat	1152
Ser	Ala	Ala	Ile	Leu	Asp	Pro	Ala	Thr	Gly	Gln	Leu	Val	Gly	Val	Asn	
		370				375					380					
ccg	gcg	ctg	ctg	gta	ctg	gcg	acg	gct	gcg	ggt	tcc	aac	acc	ctc	acc	1200
Pro	Ala	Leu	Leu	Val	Leu	Ala	Thr	Ala	Ala	Gly	Ser	Asn	Thr	Leu	Thr	
385					390					395					400	
cac	att	aat	gat	gca	tct	ttc	tgg	ttg	ttc	aaa	ggt	tac	ttt	gac	ctg	1248
His	Ile	Asn	Asp	Ala	Ser	Phe	Trp	Leu	Phe	Lys	Gly	Tyr	Phe	Asp	Leu	
				405					410					415		
tca	gta	aaa	gac	acg	ttg	aaa	acc	tgg	ggt	ctg	ctg	gag	ctg	gtc	aac	1296
Ser	Val	Lys	Asp	Thr	Leu	Lys	Thr	Trp	Gly	Leu	Leu	Glu	Leu	Val	Asn	
			420					425					430			
tcc	gtg	gtt	ggg	ctg	att	att	gtg	ctg	att	att	agc	atg	gta	gcg		1341
Ser	Val	Val	Gly	Leu	Ile	Ile	Val	Leu	Ile	Ile	Ser	Met	Val	Ala		
		435					440					445				
taa																1344

<210> 10137

<211> 447

<212> PRT

<213> Shigella flexneri 2a str. 301

<400> 10137

Met	His	Val	Leu	Asn	Ile	Leu	Trp	Val	Val	Phe	Gly	Ile	Gly	Leu	Met	
1				5					10					15		
Leu	Ile	Leu	Asn	Leu	Lys	Phe	Lys	Ile	Asn	Ser	Met	Val	Ala	Leu	Leu	
			20					25					30			
Val	Ala	Ala	Leu	Ser	Val	Gly	Met	Leu	Ala	Gly	Met	Asp	Leu	Met	Ser	
		35					40					45				
Leu	Leu	His	Thr	Met	Lys	Ala	Gly	Phe	Gly	Asn	Thr	Leu	Gly	Glu	Leu	
		50				55				60						
Ala	Ile	Ile	Val	Val	Phe	Gly	Ala	Val	Ile	Gly	Lys	Leu	Met	Val	Asp	
65					70				75					80		
Ser	Gly	Ala	Ala	His	Gln	Ile	Ala	His	Thr	Leu	Leu	Ala	Arg	Leu	Gly	
				85					90					95		
Leu	Arg	Tyr	Val	Gln	Leu	Ser	Val	Ile	Ile	Ile	Gly	Leu	Ile	Phe	Gly	
			100					105					110			
Leu	Ala	Met	Phe	Tyr	Glu	Val	Ala	Phe	Ile	Met	Leu	Ala	Pro	Leu	Val	
		115					120					125				
Ile	Val	Ile	Ala	Ala	Glu	Ala	Lys	Ile	Pro	Phe	Leu	Lys	Leu	Ala	Ile	
		130				135					140					
Pro	Ala	Val	Ala	Ala	Ala	Thr	Thr	Ala	His	Ser	Leu	Phe	Pro	Pro	Gln	
145				150						155					160	
Pro	Gly	Pro	Val	Ala	Leu	Val	Asn	Ala	Tyr	Gly	Ala	Asp	Met	Gly	Met	
				165					170					175		
Val	Tyr	Ile	Tyr	Gly	Val	Leu	Val	Thr	Ile	Pro	Ser	Val	Ile	Cys	Ala	
			180					185					190			
Gly	Leu	Ile	Leu	Pro	Lys	Phe	Leu	Gly	Asn	Leu	Glu	Arg	Pro	Thr	Pro	
		195					200					205				
Ser	Phe	Leu	Lys	Ala	Asp	Gln	Pro	Val	Asp	Met	Asn	Asn	Leu	Pro	Ser	
		210				215					220					
Phe	Gly	Val	Ser	Ile	Leu	Val	Pro	Leu	Ile	Pro	Ala	Ile	Ile	Met	Ile	
225					230					235					240	

PF59083SeqList PF59083.txt

Ser Thr Thr Ile Ala Asn Ile Trp Leu Val Lys Asp Thr Pro Ala Trp
 245 250 255
 Glu Val Val Asn Phe Ile Gly Ser Ser Pro Ile Ala Met Phe Ile Ala
 260 265 270
 Met Val Val Ala Phe Val Leu Phe Gly Thr Ala Arg Gly His Asp Met
 275 280 285
 Gln Trp Val Met Asn Ala Phe Glu Ser Ala Val Lys Ser Ile Ala Met
 290 295 300
 Val Ile Leu Ile Ile Gly Ala Gly Gly Val Leu Lys Gln Thr Ile Ile
 305 310 315 320
 Asp Thr Gly Ile Gly Asp Thr Ile Gly Met Leu Met Ser His Gly Asn
 325 330 335
 Ile Ser Pro Tyr Ile Met Ala Trp Leu Ile Thr Val Leu Ile Arg Leu
 340 345 350
 Ala Thr Gly Gln Gly Val Val Ser Ala Met Thr Ala Ala Gly Ile Ile
 355 360 365
 Ser Ala Ala Ile Leu Asp Pro Ala Thr Gly Gln Leu Val Gly Val Asn
 370 375 380
 Pro Ala Leu Leu Val Leu Ala Thr Ala Ala Gly Ser Asn Thr Leu Thr
 385 390 395 400
 His Ile Asn Asp Ala Ser Phe Trp Leu Phe Lys Gly Tyr Phe Asp Leu
 405 410 415
 Ser Val Lys Asp Thr Leu Lys Thr Trp Gly Leu Leu Glu Leu Val Asn
 420 425 430
 Ser Val Val Gly Leu Ile Ile Val Leu Ile Ile Ser Met Val Ala
 435 440 445

<210> 10138

<211> 1398

<212> DNA

<213> Streptomyces coelicolor A3(2)

<220>

<221> CDS

<222> (1)..(1398)

<223> transl_table=11

<400> 10138

gtg acc aga ctc agc gtc gag atg ctg gca gcg gac ccc gtc gag ccg	48
Met Thr Arg Leu Ser Val Glu Met Leu Ala Asp Pro Val Glu Pro	
1 5 10 15	
atc acc tcg gcg ggc cac gcc cag ctg ggc atc gcc gtg ctc ctg ggc	96
Ile Thr Ser Ala Gly His Ala Gln Leu Gly Ile Ala Val Leu Leu Gly	
20 25 30	
atc gcc gtc atc gtc ctg ctc atc acc aag ttc aag ctg cat gcc ttc	144
Ile Ala Val Ile Val Leu Leu Ile Thr Lys Phe Lys Leu His Ala Phe	
35 40 45	
ctg tcg ctg acc atc ggg tcg ctg gcg ctc ggc gcg ttc gcc ggt gcg	192
Leu Ser Leu Thr Ile Gly Ser Leu Ala Leu Gly Ala Phe Ala Gly Ala	
50 55 60	
ccg ctg gac aag gtc atc acc agc ttc acc gcc gga ctc ggc tcc acc	240
Pro Leu Asp Lys Val Ile Thr Ser Phe Thr Ala Gly Leu Gly Ser Thr	
65 70 75 80	
gtc gcg ggc gtc ggc gtc ctg atc gcc ctc ggt gcg atc ctc ggc aag	288
Val Ala Gly Val Gly Val Leu Ile Ala Leu Gly Ala Ile Leu Gly Lys	
85 90 95	
atg ctc gcc gac tcc ggc ggc gcc gac cag atc gtg gac acc atc ctg	336
Met Leu Ala Asp Ser Gly Gly Ala Asp Gln Ile Val Asp Thr Ile Leu	
100 105 110	
gcg aag gcc acg ccc cgt tcg atg ccg tgg acg atg gtg ctg atc gcc	384
Ala Lys Ala Thr Pro Arg Ser Met Pro Trp Thr Met Val Leu Ile Ala	
115 120 125	
tcg gtc atc gga ctg ccg ctg ttc ttc gag gtc ggc atc gtg ctg ctg	432
Ser Val Ile Gly Leu Pro Leu Phe Phe Glu Val Gly Ile Val Leu Leu	
130 135 140	
atc ccg gtc gtc ctg atg gtc gcc aag cgc ggc aac tac tcg ctg atg	480
Ile Pro Val Val Leu Met Val Ala Lys Arg Gly Asn Tyr Ser Leu Met	
145 150 155 160	
cgg atc ggc atc ccg gcg ctg gcc ggt ctg tcc gtg atg cac ggc ctg	528

PF59083SeqList PF59083.txt

Arg	Ile	Gly	Ile	Pro	Ala	Leu	Ala	Gly	Leu	Ser	Val	Met	His	Gly	Leu	
				165					170					175		
gtc	ccg	ccg	cac	ccc	ggc	ccg	ctg	gtc	gcc	atc	gac	gcg	gtg	gac	gcc	576
Val	Pro	Pro	His	Pro	Gly	Pro	Leu	Val	Ala	Ile	Asp	Ala	Val	Asp	Ala	
			180					185					190			
aac	ctc	ggc	gtg	acc	ctg	gag	ctg	ggc	gtg	ctg	atc	gag	atc	ccc	acc	624
Asn	Leu	Gly	Val	Thr	Leu	Ala	Leu	Gly	Val	Leu	Ile	Ala	Ile	Pro	Thr	
		195					200					205				
gtg	atc	atc	gcc	ggc	ccg	gtc	ttc	tcg	aag	tac	gag	gcc	cgc	tgg	gtg	672
Val	Ile	Ile	Ala	Gly	Pro	Val	Phe	Ser	Lys	Tyr	Ala	Ala	Arg	Trp	Val	
	210					215					220					
gac	gtc	ccg	gcc	ccc	gac	cgc	atg	atc	ccg	cag	cgc	gcc	tcc	gag	cgg	720
Asp	Val	Pro	Ala	Pro	Asp	Arg	Met	Ile	Pro	Gln	Arg	Ala	Ser	Glu	Arg	
225					230				235					240		
ctg	gac	aag	cg	ccg	agc	ttc	ggc	gcc	acg	ctg	gcc	acg	atc	ctg	ctg	768
Leu	Asp	Lys	Arg	Pro	Ser	Phe	Gly	Ala	Thr	Leu	Ala	Thr	Ile	Leu	Leu	
				245				250						255		
ccg	gtc	gtg	ctg	atg	ctg	ctc	aag	gcc	ctg	gtc	gac	atc	atc	atc	gac	816
Pro	Val	Val	Leu	Met	Leu	Leu	Lys	Ala	Leu	Val	Asp	Ile	Ile	Ile	Asp	
			260					265					270			
gac	ccc	gac	aac	gtg	gtg	cag	cg	acc	ttc	gac	gtc	atc	ggc	aac	ccg	864
Asp	Pro	Asp	Asn	Val	Val	Gln	Arg	Thr	Phe	Asp	Val	Ile	Gly	Asn	Pro	
		275				280						285				
ctg	atc	gcc	ctg	ctg	gtc	tcg	gtg	atc	gtc	ggc	atc	ttc	acg	ctg	ctg	912
Leu	Ile	Ala	Leu	Leu	Val	Ser	Val	Ile	Val	Gly	Ile	Phe	Thr	Leu	Leu	
	290					295				300						
cg	ccc	gcc	ggg	ttc	ggc	aag	gac	cg	ctc	tcc	ggc	ctg	gtc	gag	aag	960
Arg	Pro	Ala	Gly	Phe	Gly	Lys	Asp	Arg	Leu	Ser	Gly	Leu	Val	Glu	Lys	
305					310			315						320		
ggg	ctg	gag	ccc	atc	ggc	ggc	atc	ctc	ctg	atc	gtc	ggc	gag	ggc	ggc	1008
Gly	Leu	Ala	Pro	Ile	Ala	Gly	Ile	Leu	Leu	Ile	Val	Gly	Ala	Gly	Gly	
				325				330						335		
ggc	ttc	aag	cag	acg	ctg	atc	gac	tcg	ggc	gtg	ggc	cag	atg	gtc	ctg	1056
Gly	Phe	Lys	Gln	Thr	Leu	Ile	Asp	Ser	Gly	Val	Gly	Gln	Met	Val	Leu	
			340					345					350			
gac	atc	tcc	aag	gac	tgg	tcg	atc	ccg	gag	ctg	ctg	ctc	gcc	tgg	ctg	1104
Asp	Ile	Ser	Lys	Asp	Trp	Ser	Ile	Pro	Ala	Leu	Leu	Leu	Ala	Trp	Leu	
		355					360					365				
atc	gag	gtg	gtg	atc	cg	ctg	gag	acc	ggc	tcg	gag	acg	gtg	gag	acc	1152
Ile	Ala	Val	Val	Ile	Arg	Leu	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	Thr	
	370					375					380					
gtc	tcg	gag	gcc	ggc	ctg	gtc	gag	ccg	ctg	gag	gcc	gac	atg	tcg	acc	1200
Val	Ser	Ala	Ala	Gly	Leu	Val	Ala	Pro	Leu	Ala	Ala	Asp	Met	Ser	Thr	
385					390			395						400		
acg	cac	gcc	gcc	ctg	gtc	ctg	gag	atc	ggc	gag	ggc	ggc	tcg	ctc	ttc	1248
Thr	His	Ala	Ala	Leu	Leu	Val	Leu	Ala	Ile	Gly	Ala	Gly	Ser	Leu	Phe	
				405				410						415		
ttc	agt	cac	gtc	aac	gac	ggc	ttc	tgg	ctg	gtg	aag	gag	tac	ttc		1296
Phe	Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Leu	Val	Lys	Glu	Tyr	Phe	
			420				425						430			
ggg	ctg	aac	gtg	ggg	cag	acc	atc	aag	acc	tgg	tcc	gtc	atg	gag	acg	1344
Gly	Leu	Asn	Val	Gly	Gln	Thr	Ile	Lys	Thr	Trp	Ser	Val	Met	Glu	Thr	
		435				440					445					
atc	atc	tcg	gtg	gtc	ggc	ggc	ctg	gtc	ctg	ctg	ttg	tcc	ctg	gtc		1392
Ile	Ile	Ser	Val	Val	Ala	Gly	Ala	Leu	Val	Leu	Leu	Ser	Leu	Val		
	450					455				460						
ata	tag															1398
Ile																
465																

<210> 10139

<211> 465

<212> PRT

<213> Streptomyces coelicolor A3(2)

<400> 10139

Met	Thr	Arg	Leu	Ser	Val	Glu	Met	Leu	Ala	Ala	Asp	Pro	Val	Glu	Pro
1				5					10					15	
Ile	Thr	Ser	Ala	Gly	His	Ala	Gln	Leu	Gly	Ile	Ala	Val	Leu	Leu	Gly

PF59083SeqList PF59083.txt

```

      20      25      30
Ile Ala Val Ile Val Leu Leu Ile Thr Lys Phe Lys Leu His Ala Phe
      35      40      45
Leu Ser Leu Thr Ile Gly Ser Leu Ala Leu Gly Ala Phe Ala Gly Ala
      50      55      60
Pro Leu Asp Lys Val Ile Thr Ser Phe Thr Ala Gly Leu Gly Ser Thr
65      70      75      80
Val Ala Gly Val Gly Val Leu Ile Ala Leu Gly Ala Ile Leu Gly Lys
      85      90      95
Met Leu Ala Asp Ser Gly Gly Ala Asp Gln Ile Val Asp Thr Ile Leu
      100      105      110
Ala Lys Ala Thr Pro Arg Ser Met Pro Trp Thr Met Val Leu Ile Ala
      115      120      125
Ser Val Ile Gly Leu Pro Leu Phe Phe Glu Val Gly Ile Val Leu Leu
      130      135      140
Ile Pro Val Val Leu Met Val Ala Lys Arg Gly Asn Tyr Ser Leu Met
145      150      155      160
Arg Ile Gly Ile Pro Ala Leu Ala Gly Leu Ser Val Met His Gly Leu
      165      170      175
Val Pro Pro His Pro Gly Pro Leu Val Ala Ile Asp Ala Val Asp Ala
      180      185      190
Asn Leu Gly Val Thr Leu Ala Leu Gly Val Leu Ile Ala Ile Pro Thr
      195      200      205
Val Ile Ile Ala Gly Pro Val Phe Ser Lys Tyr Ala Ala Arg Trp Val
210      215      220
Asp Val Pro Ala Pro Asp Arg Met Ile Pro Gln Arg Ala Ser Glu Arg
225      230      235      240
Leu Asp Lys Arg Pro Ser Phe Gly Ala Thr Leu Ala Thr Ile Leu Leu
      245      250      255
Pro Val Val Leu Met Leu Leu Lys Ala Leu Val Asp Ile Ile Ile Asp
      260      265      270
Asp Pro Asp Asn Val Val Gln Arg Thr Phe Asp Val Ile Gly Asn Pro
      275      280      285
Leu Ile Ala Leu Leu Val Ser Val Ile Val Gly Ile Phe Thr Leu Leu
290      295      300
Arg Pro Ala Gly Phe Gly Lys Asp Arg Leu Ser Gly Leu Val Glu Lys
305      310      315      320
Gly Leu Ala Pro Ile Ala Gly Ile Leu Leu Ile Val Gly Ala Gly Gly
      325      330      335
Gly Phe Lys Gln Thr Leu Ile Asp Ser Gly Val Gly Gln Met Val Leu
      340      345      350
Asp Ile Ser Lys Asp Trp Ser Ile Pro Ala Leu Leu Leu Ala Trp Leu
      355      360      365
Ile Ala Val Val Ile Arg Leu Ala Thr Gly Ser Ala Thr Val Ala Thr
      370      375      380
Val Ser Ala Ala Gly Leu Val Ala Pro Leu Ala Ala Asp Met Ser Thr
385      390      395      400
Thr His Ala Ala Leu Leu Val Leu Ala Ile Gly Ala Gly Ser Leu Phe
      405      410      415
Phe Ser His Val Asn Asp Ala Gly Phe Trp Leu Val Lys Glu Tyr Phe
      420      425      430
Gly Leu Asn Val Gly Gln Thr Ile Lys Thr Trp Ser Val Met Glu Thr
      435      440      445
Ile Ile Ser Val Val Ala Gly Ala Leu Val Leu Leu Ser Leu Val
450      455      460
Ile
465

```

<210> 10140
 <211> 1386
 <212> DNA
 <213> Pseudomonas putida KT2440

<220>
 <221> CDS
 <222> (1)..(1386)
 <223> transl_table=11

<400> 10140

PF59083SeqList PF59083.txt																
atg	act	ccc	tta	gat	ata	cag	cta	tta	ctg	acg	gca	ttg	gcc	agt	gtt	48
Met	Thr	Pro	Leu	Asp	Ile	Gln	Leu	Leu	Leu	Thr	Ala	Leu	Ala	Ser	Val	
1				5					10					15		
ctg	gtg	ctg	gtg	gcg	ctc	atc	gtt	tcg	cgc	ctg	aaa	atg	cac	ccg	ctg	96
Leu	Val	Leu	Val	Ala	Leu	Ile	Val	Ser	Arg	Leu	Lys	Met	His	Pro	Leu	
			20					25					30			
ctg	gcc	ttg	ctg	gtg	gtg	tcc	att	ggc	gtg	ggc	ttc	gcg	acg	cat	atg	144
Leu	Ala	Leu	Leu	Val	Val	Ser	Ile	Gly	Val	Gly	Phe	Ala	Thr	His	Met	
		35				40					45					
gcg	cca	ggc	agc	atc	gtc	tcc	cac	ctg	ctc	acc	ggc	gcc	ggc	aag	aca	192
Ala	Pro	Gly	Ser	Ile	Val	Ser	His	Leu	Leu	Thr	Gly	Ala	Gly	Lys	Thr	
	50					55				60						
ctg	ggc	gca	gtg	ggg	gtg	gtg	att	gcg	ctg	ggt	gcg	atg	ctc	ggc	aag	240
Leu	Gly	Ala	Val	Gly	Val	Val	Ile	Ala	Leu	Gly	Ala	Met	Leu	Gly	Lys	
65				70						75				80		
atc	ctg	gct	gac	gct	ggc	gtc	acg	gag	cag	gtc	gcg	gat	gtc	atc	ctc	288
Ile	Leu	Ala	Asp	Ala	Gly	Val	Thr	Glu	Gln	Val	Ala	Asp	Val	Ile	Leu	
			85					90						95		
aag	cgc	acc	ccc	gac	cgc	atg	atc	cct	tgg	gcc	atg	atg	ctg	gtt	gcc	336
Lys	Arg	Thr	Pro	Asp	Arg	Met	Ile	Pro	Trp	Ala	Met	Met	Leu	Val	Ala	
			100					105					110			
ttt	gtc	att	ggc	atc	ccc	atg	ttt	ttc	gaa	gtc	ggc	ctg	gtg	atc	atg	384
Phe	Val	Ile	Gly	Ile	Pro	Met	Phe	Phe	Glu	Val	Gly	Leu	Val	Ile	Met	
		115				120						125				
ctg	ccg	ctg	ata	ttc	agc	gtg	gcg	cgc	aaa	ctg	gaa	agc	aag	gcg	cgc	432
Leu	Pro	Leu	Ile	Phe	Ser	Val	Ala	Arg	Lys	Leu	Glu	Ser	Lys	Ala	Arg	
	130					135					140					
ttc	aaa	ggc	tcg	gcg	tac	gtg	tat	gta	ggt	gtg	ccg	gtc	att	tcg	gcg	480
Phe	Lys	Gly	Ser	Ala	Tyr	Val	Tyr	Val	Gly	Val	Pro	Val	Ile	Ser	Ala	
145				150					155					160		
ctt	gcc	gcc	atg	cac	ggc	atg	gta	ccg	ccg	cac	cca	ggc	ccc	ctg	acc	528
Leu	Ala	Ala	Met	His	Gly	Met	Val	Pro	Pro	His	Pro	Gly	Pro	Leu	Thr	
			165					170					175			
gcc	att	gcc	gtg	ctc	aag	acc	tcg	gtg	ggg	ccc	acc	atg	ctc	tat	ggc	576
Ala	Ile	Ala	Val	Leu	Lys	Thr	Ser	Val	Gly	Pro	Thr	Met	Leu	Tyr	Gly	
		180					185						190			
ttc	ctt	gcc	gcc	att	ccg	gca	atg	atc	ctg	ggc	ggc	ccg	ctg	tac	ggc	624
Phe	Leu	Ala	Ala	Ile	Pro	Ala	Met	Ile	Leu	Gly	Gly	Pro	Leu	Tyr	Gly	
		195				200						205				
atg	ttc	att	tca	ccg	cgc	atg	aac	acg	cgg	ccc	gat	cag	gca	ttg	ctg	672
Met	Phe	Ile	Ser	Pro	Arg	Met	Asn	Thr	Arg	Pro	Asp	Gln	Ala	Leu	Leu	
	210					215					220					
gac	cag	ttc	aca	ctg	gct	gaa	aaa	gcc	gat	ggc	caa	ccc	cgc	ccc	ggg	720
Asp	Gln	Phe	Thr	Leu	Ala	Glu	Lys	Ala	Asp	Gly	Gln	Pro	Arg	Pro	Gly	
225				230						235				240		
gta	atg	gtc	ggc	atg	ctg	gcc	gca	ttg	ctg	ccg	gcc	atc	ctg	atg	ctg	768
Val	Met	Val	Gly	Met	Leu	Ala	Ala	Leu	Leu	Pro	Ala	Ile	Leu	Met	Leu	
		245						250					255			
gtg	cat	gcc	gtc	gcc	gag	atg	ctg	ctg	ccc	aaa	ggc	aat	gcg	ctg	ctg	816
Val	His	Ala	Val	Ala	Glu	Met	Leu	Leu	Pro	Lys	Gly	Asn	Ala	Leu	Leu	
		260					265						270			
gag	atg	gcc	agc	ttc	ctg	ggc	aac	ccg	ctg	atc	gcc	atg	ctg	ctg	ggc	864
Glu	Met	Ala	Ser	Phe	Leu	Gly	Asn	Pro	Leu	Ile	Ala	Met	Leu	Leu	Gly	
		275				280						285				
gtg	ctg	ttc	gcc	ggc	gcc	agc	ctg	gtg	ctt	gcg	cgc	ggc	ggc	gac	gcc	912
Val	Leu	Phe	Ala	Gly	Ala	Ser	Leu	Val	Leu	Ala	Arg	Gly	Gly	Asp	Ala	
	290					295					300					
gaa	cag	ctg	cgc	gat	gca	ctg	ggc	aaa	agc	ctc	aag	ccg	atc	gcc	tcg	960
Glu	Gln	Leu	Arg	Asp	Ala	Leu	Gly	Lys	Ser	Leu	Lys	Pro	Ile	Ala	Ser	
305				310						315				320		
atc	atc	atg	atc	att	gcc	ggt	ggc	ggt	gcc	ttt	caa	gag	atg	ctg	acc	1008
Ile	Ile	Met	Ile	Ile	Ala	Gly	Gly	Gly	Ala	Phe	Gln	Glu	Met	Leu	Thr	
			325					330					335			
agc	gcc	aag	gta	ggc	gat	gcc	att	gtg	cac	ctg	acc	cag	caa	tct	gcc	1056
Ser	Ala	Lys	Val	Gly	Asp	Ala	Ile	Val	His	Leu	Thr	Gln	Gln	Ser	Ala	
		340						345					350			
ttc	cct	ccc	ctg	att	ctg	ggg	tgg	ctg	atc	gcg	atg	ctg	ctc	tcg	gtg	1104
Phe	Pro	Pro	Leu	Ile	Leu	Gly	Trp	Leu	Ile	Ala	Met	Leu	Leu	Ser	Val	
		355					360					365				

PF59083SeqList PF59083.txt

tct	acc	ggt	tcc	gcc	acg	gtc	ggt	atc	gta	ggg	gct	gcc	ggc	ttg	ctg	1152
Ser	Thr	Gly	Ser	Ala	Thr	Val	Gly	Ile	Val	Gly	Ala	Ala	Gly	Leu	Leu	
	370					375					380					
gcg	ccg	ctg	gca	ggt	gca	gac	cca	agc	ctt	aac	ctg	cct	ttg	ctg	gcc	1200
Ala	Pro	Leu	Ala	Gly	Ala	Asp	Pro	Ser	Leu	Asn	Leu	Pro	Leu	Leu	Ala	
385					390					395					400	
ctg	tcc	atc	ggc	tgc	ggt	tcg	ctg	ttc	ttc	aac	tat	gcg	aac	cat	gca	1248
Leu	Ser	Ile	Gly	Cys	Gly	Ser	Leu	Phe	Phe	Asn	Tyr	Ala	Asn	His	Ala	
			405					410						415		
ggc	ttc	tgg	atg	gtg	aaa	gaa	tcc	ttt	ggc	atg	acc	atg	ggc	gaa	gcc	1296
Gly	Phe	Trp	Met	Val	Lys	Glu	Ser	Phe	Gly	Met	Thr	Met	Gly	Glu	Ala	
			420					425					430			
acc	aag	acc	att	tcg	gtg	gtg	cag	tcc	atc	gtg	gcg	gtg	ggt	ggg	ctg	1344
Thr	Lys	Thr	Ile	Ser	Val	Val	Gln	Ser	Ile	Val	Ala	Val	Val	Gly	Leu	
		435					440					445				
atg	gtg	gtg	ttg	atg	ttg	aat	gcc	atc	acc	ata	ggg	tga				1386
Met	Val	Val	Leu	Met	Leu	Asn	Ala	Ala	Ile	Thr	Ile	Gly				
	450					455					460					

<210> 10141

<211> 461

<212> PRT

<213> Pseudomonas putida KT2440

<400> 10141

Met	Thr	Pro	Leu	Asp	Ile	Gln	Leu	Leu	Leu	Thr	Ala	Leu	Ala	Ser	Val	
1				5					10					15		
Leu	Val	Leu	Val	Ala	Leu	Ile	Val	Ser	Arg	Leu	Lys	Met	His	Pro	Leu	
			20					25					30			
Leu	Ala	Leu	Val	Val	Ser	Ile	Gly	Val	Gly	Phe	Ala	Thr	His	Met		
		35				40				45						
Ala	Pro	Gly	Ser	Ile	Val	Ser	His	Leu	Leu	Thr	Gly	Ala	Gly	Lys	Thr	
	50				55					60						
Leu	Gly	Ala	Val	Gly	Val	Ile	Ala	Leu	Gly	Ala	Met	Leu	Gly	Lys		
65				70					75					80		
Ile	Leu	Ala	Asp	Ala	Gly	Val	Thr	Glu	Gln	Val	Ala	Asp	Val	Ile	Leu	
			85					90						95		
Lys	Arg	Thr	Pro	Asp	Arg	Met	Ile	Pro	Trp	Ala	Met	Met	Leu	Val	Ala	
			100					105					110			
Phe	Val	Ile	Gly	Ile	Pro	Met	Phe	Glu	Val	Gly	Leu	Val	Ile	Met		
		115				120				125						
Leu	Pro	Leu	Ile	Phe	Ser	Val	Ala	Arg	Lys	Leu	Glu	Ser	Lys	Ala	Arg	
	130				135					140						
Phe	Lys	Gly	Ser	Ala	Tyr	Val	Tyr	Val	Gly	Val	Pro	Val	Ile	Ser	Ala	
145				150					155					160		
Leu	Ala	Ala	Met	His	Gly	Met	Val	Pro	Pro	His	Pro	Gly	Pro	Leu	Thr	
			165					170						175		
Ala	Ile	Ala	Val	Leu	Lys	Thr	Ser	Val	Gly	Pro	Thr	Met	Leu	Tyr	Gly	
		180					185						190			
Phe	Leu	Ala	Ile	Pro	Ala	Met	Ile	Leu	Gly	Gly	Pro	Leu	Tyr	Gly		
	195				200						205					
Met	Phe	Ile	Ser	Pro	Arg	Met	Asn	Thr	Arg	Pro	Asp	Gln	Ala	Leu	Leu	
	210				215					220						
Asp	Gln	Phe	Thr	Leu	Ala	Glu	Lys	Ala	Asp	Gly	Gln	Pro	Arg	Pro	Gly	
225				230					235					240		
Val	Met	Val	Gly	Met	Leu	Ala	Ala	Leu	Leu	Pro	Ala	Ile	Leu	Met	Leu	
			245					250					255			
Val	His	Ala	Val	Ala	Glu	Met	Leu	Leu	Pro	Lys	Gly	Asn	Ala	Leu	Leu	
		260					265						270			
Glu	Met	Ala	Ser	Phe	Leu	Gly	Asn	Pro	Leu	Ile	Ala	Met	Leu	Leu	Gly	
	275					280						285				
Val	Leu	Phe	Ala	Gly	Ala	Ser	Leu	Val	Leu	Ala	Arg	Gly	Gly	Asp	Ala	
	290				295					300						
Glu	Gln	Leu	Arg	Asp	Ala	Leu	Gly	Lys	Ser	Leu	Lys	Pro	Ile	Ala	Ser	
305				310					315					320		
Ile	Ile	Met	Ile	Ile	Ala	Gly	Gly	Gly	Ala	Phe	Gln	Glu	Met	Leu	Thr	
			325					330						335		
Ser	Ala	Lys	Val	Gly	Asp	Ala	Ile	Val	His	Leu	Thr	Gln	Gln	Ser	Ala	
		340					345						350			

PF59083SeqList PF59083.txt

Phe Pro Pro Leu Ile Leu Gly Trp Leu Ile Ala Met Leu Leu Ser Val
 355 360 365
 Ser Thr Gly Ser Ala Thr Val Gly Ile Val Gly Ala Ala Gly Leu Leu
 370 375 380
 Ala Pro Leu Ala Gly Ala Asp Pro Ser Leu Asn Leu Pro Leu Leu Ala
 385 390 395 400
 Leu Ser Ile Gly Cys Gly Ser Leu Phe Phe Asn Tyr Ala Asn His Ala
 405 410 415
 Gly Phe Trp Met Val Lys Glu Ser Phe Gly Met Thr Met Gly Glu Ala
 420 425 430
 Thr Lys Thr Ile Ser Val Val Gln Ser Ile Val Ala Val Val Gly Leu
 435 440 445
 Met Val Val Leu Met Leu Asn Ala Ala Ile Thr Ile Gly
 450 455 460

<210> 10142
 <211> 1353
 <212> DNA
 <213> Pseudomonas putida KT2440

<220>
 <221> CDS
 <222> (1)..(1353)
 <223> transl_table=11

<400> 10142
 atg ttc gga ctg gct act gat acc ttc ctg ctg ctc gac gcg ctg gtt 48
 Met Phe Gly Leu Ala Thr Asp Thr Phe Leu Leu Leu Asp Ala Leu Val
 1 5 10 15
 acc atc gtc ggg ctg atc ctg ctg atc acc cac ttc aag gtt cac ccc 96
 Thr Ile Val Gly Leu Ile Leu Leu Ile Thr His Phe Lys Val His Pro
 20 25 30
 ttc gtc gcc ctc acc ctc gcg gcc ggc ttc ctg ggc ctg act tcc ggc 144
 Phe Val Ala Leu Thr Leu Ala Ala Gly Phe Leu Gly Leu Thr Ser Gly
 35 40 45
 atg ccg gtg gcc aag gtc atg aaa tcg ttc cag gac ggt ttt ggc ggc 192
 Met Pro Val Ala Lys Val Met Lys Ser Phe Gln Asp Gly Phe Gly Gly
 50 55 60
 gta ctc ggc ttc gtc ggt atc gtg ctc gcc ctg ggc acc atg ctc ggc 240
 Val Leu Gly Phe Val Gly Ile Val Leu Ala Gly Thr Met Leu Gly
 65 70 75 80
 aag ctg atg gcc gac tcc ggt ggt gcc gac cag atc gcg caa acc ctc 288
 Lys Leu Met Ala Asp Ser Gly Gly Ala Asp Gln Ile Ala Gln Thr Leu
 85 90 95
 atc cgc gcc ttc ggc aag aag aac gtg cat tgg gcg atg atg ttc gcc 336
 Ile Arg Ala Phe Gly Lys Lys Asn Val His Trp Ala Met Met Phe Ala
 100 105 110
 gcc ttc ctg gtg ggc atc ccg ctg ttc ttc gaa atc ggc ttt gtg ctg 384
 Ala Phe Leu Val Gly Ile Pro Leu Phe Phe Glu Ile Gly Phe Val Leu
 115 120 125
 ctg att cca ctg gtg ttc atc gtc gcc cgg cgc tcg ggc gtc tcg ttg 432
 Leu Ile Pro Leu Val Phe Ile Val Ala Arg Arg Ser Gly Val Ser Leu
 130 135 140
 gtg aaa atc ggc att ccg ctg ctg gcc ggc ctg tcg gtg gtg cac ggt 480
 Val Lys Ile Gly Ile Pro Leu Leu Ala Gly Ser Val Val His Gly
 145 150 155 160
 ctg gtg cca cca cac ccg ggc ccc ttg ctg gcg atc ggc att ttc cac 528
 Leu Val Pro Pro His Pro Gly Pro Leu Leu Ala Ile Gly Ile Phe His
 165 170 175
 gct gac att ggc aag acc atc ttc tac gcg ctg atc gtc gca ctg ccc 576
 Ala Asp Ile Gly Lys Thr Ile Phe Tyr Gly Leu Ile Val Ala Leu Pro
 180 185 190
 acc gcg atc atc gcc ggc cct ctg ttc ggt aac ttc att tcc cgc tac 624
 Thr Ala Ile Ile Ala Gly Pro Leu Phe Gly Asn Phe Ile Ser Arg Tyr
 195 200 205
 atc ccg ggc aac ccg tcc cag gag ctg atg gac cag atc gcc aag gac 672
 Ile Pro Gly Asn Pro Ser Gln Glu Leu Met Asp Gln Ile Ala Lys Asp
 210 215 220
 tcc gat cag ggc aac ctg cca agc ttc agc att acc ctg gtc act gta 720

PF59083SeqList PF59083.txt

Ser 225	Asp	Gln	Gly	Asn	Leu 230	Pro	Ser	Phe	Ser	Ile 235	Thr	Leu	Val	Thr	Val 240	
ctg	ctg	ccg	gtc	gcg	ttg	atg	ctg	ctg	aaa	acg	ttc	gcc	gac	gtg	gtg	768
Leu	Leu	Pro	Val	Ala 245	Leu	Met	Leu	Leu	Lys 250	Thr	Phe	Ala	Asp	Val 255	Val	
ctg	cct	gcc	gag	cac	atc	gtg	cg	cag	tgg	atg	gac	ctg	atc	ggg	cac	816
Leu	Pro	Ala	Glu	His	Ile	Val	Arg	Gln	Trp	Met	Asp	Leu	Ile	Gly	His	
ccg	atc	acc	gcc	ctg	ctc	gcc	gcc	ctg	tta	ctg	gcc	ttc	tac	acc	ttc	864
Pro	Ile	Thr 275	Ala	Leu	Leu	Ala	Ala 280	Leu	Leu	Leu	Ala	Phe	Tyr	Thr	Phe	
ggc	tcg	gcc	cg	ggc	ttc	aac	cg	cag	cag	atc	atg	aag	atg	ctc	gac	912
Gly	Ser 290	Ala	Arg	Gly	Phe	Asn 295	Arg	Gln	Gln	Ile	Met 300	Lys	Met	Leu	Asp	
cag	agc	ctg	gca	ccg	act	gcc	gcc	atc	gtg	ctg	atc	gtc	ggc	gct	ggc	960
Gln	Ser	Leu	Ala	Pro	Thr 310	Ala	Ala	Ile	Val	Leu 315	Ile	Val	Gly	Ala	Gly	
ggg	ggc	ttc	aag	caa	atg	ctg	gtg	gat	acc	ggc	gta	ggc	aac	gtg	atc	1008
Gly	Gly	Phe	Lys	Gln 325	Met	Leu	Val	Asp	Thr 330	Gly	Val	Gly	Asn	Val 335	Ile	
ggg	cag	atg	gct	gtc	cag	gca	gaa	att	tcg	ccg	atc	atg	ctg	gca	tgg	1056
Gly	Gln	Met	Ala	Val	Gln	Ala	Glu	Ile 345	Ser	Pro	Ile	Met	Leu	Ala	Trp	
ctg	gtg	gcg	gcg	gtg	atc	cg	atc	gcg	acc	ggc	tcc	gcc	acg	gtc	gcc	1104
Leu	Val	Ala 355	Ala	Val	Ile	Arg	Ile 360	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	
acc	atc	acc	ggc	gcg	ggg	atc	gtg	gca	ccg	gtg	atc	gac	ctc	gtg	ccg	1152
Thr	Ile	Thr	Gly	Ala	Gly 375	Ile	Val	Ala	Pro	Val	Ile 380	Asp	Leu	Val	Pro	
ggg	gtg	aac	cg	gag	ctg	ttg	gta	ctg	gcc	acc	ggg	gcc	ggc	tcg	ctg	1200
Gly	Val	Asn	Arg	Glu	Leu 390	Leu	Val	Leu	Ala	Thr 395	Gly	Ala	Gly	Ser	Leu	
atc	ctg	tcg	cat	gtg	aac	gat	gcc	ggg	ttc	tgg	ctg	gtg	aag	cag	tac	1248
Ile	Leu	Ser	His	Val 405	Asn	Asp	Ala	Gly	Phe	Trp	Leu	Val	Lys	Gln 415	Tyr	
ttc	aac	atg	acc	gtg	gca	gaa	acc	ttc	aag	acc	tgg	agc	atg	atg	gag	1296
Phe	Asn	Met	Thr	Val	Ala	Glu	Thr	Phe 425	Lys	Thr	Trp	Ser	Met	Met	Glu	
acg	atc	ctg	tcc	atc	gtc	ggc	atc	att	ttc	atc	atg	ttg	ctg	tcg	ctg	1344
Thr	Ile	Leu 435	Ser	Ile	Val	Gly	Ile 440	Ile	Phe	Ile	Met	Leu	Leu	Ser	Leu	
gtg	gtg	tga														1353
Val	Val															
	450															

<210> 10143

<211> 450

<212> PRT

<213> Pseudomonas putida KT2440

<400> 10143

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

PF59083SeqList PF59083.txt

Val Lys Ile Gly Ile Pro Leu Leu Ala Gly Leu Ser Val Val His Gly
145 150 155 160
Leu Val Pro Pro His Pro Gly Pro Leu Leu Ala Ile Gly Ile Phe His
165 170 175
Ala Asp Ile Gly Lys Thr Ile Phe Tyr Gly Leu Ile Val Ala Leu Pro
180 185 190
Thr Ala Ile Ile Ala Gly Pro Leu Phe Gly Asn Phe Ile Ser Arg Tyr
195 200 205
Ile Pro Gly Asn Pro Ser Gln Glu Leu Met Asp Gln Ile Ala Lys Asp
210 215 220
Ser Asp Gln Gly Asn Leu Pro Ser Phe Ser Ile Thr Leu Val Thr Val
225 230 235 240
Leu Leu Pro Val Ala Leu Met Leu Leu Lys Thr Phe Ala Asp Val Val
245 250 255
Leu Pro Ala Glu His Ile Val Arg Gln Trp Met Asp Leu Ile Gly His
260 265 270
Pro Ile Thr Ala Leu Leu Ala Ala Leu Leu Leu Ala Phe Tyr Thr Phe
275 280 285
Gly Ser Ala Arg Gly Phe Asn Arg Gln Gln Ile Met Lys Met Leu Asp
290 295 300
Gln Ser Leu Ala Pro Thr Ala Ala Ile Val Leu Ile Val Gly Ala Gly
305 310 315 320
Gly Gly Phe Lys Gln Met Leu Val Asp Thr Gly Val Gly Asn Val Ile
325 330 335
Gly Gln Met Ala Val Gln Ala Glu Ile Ser Pro Ile Met Leu Ala Trp
340 345 350
Leu Val Ala Ala Val Ile Arg Ile Ala Thr Gly Ser Ala Thr Val Ala
355 360 365
Thr Ile Thr Gly Ala Gly Ile Val Ala Pro Val Ile Asp Leu Val Pro
370 375 380
Gly Val Asn Arg Glu Leu Leu Val Leu Ala Thr Gly Ala Gly Ser Leu
385 390 395 400
Ile Leu Ser His Val Asn Asp Ala Gly Phe Trp Leu Val Lys Gln Tyr
405 410 415
Phe Asn Met Thr Val Ala Glu Thr Phe Lys Thr Trp Ser Met Met Glu
420 425 430
Thr Ile Leu Ser Ile Val Gly Ile Ile Phe Ile Met Leu Leu Ser Leu
435 440 445
Val Val
450

<210> 10144
<211> 1356
<212> DNA
<213> Lactobacillus plantarum WCFS1

<220>
<221> CDS
<222> (1)..(1356)
<223> transl_table=11

<400> 10144
atg cca ttt gtt gtt ctt aca ctc ggc atc cta cta cta tta cta tta 48
Met Pro Phe Val Val Leu Thr Leu Gly Ile Leu Leu Leu Leu Leu Leu
1 5 10 15
att att aaa ttc aag ctg aat act tat att gca ctg att gtt acg gcc 96
Ile Ile Lys Phe Lys Leu Asn Thr Tyr Ile Ala Leu Ile Val Thr Ala
20 25 30
gtc gtc gtc gga atc gga cta ggg atg cca tta act aag att gct act 144
Val Val Val Gly Ile Gly Leu Met Pro Leu Thr Lys Ile Ala Thr
35 40 45
agt att cag aac ggg att ggc agt caa ctg ggt gag tta gca cta gtc 192
Ser Ile Gln Asn Gly Ile Gly Ser Gln Leu Gly Glu Leu Ala Leu Val
50 55 60
ttc ggc ttc ggt gcc atg ctc ggc cgc tta gta gcc gat gct ggt ggt 240
Phe Gly Phe Gly Ala Met Leu Gly Arg Leu Val Ala Asp Ala Gly Gly
65 70 75 80
gct tac acg att tcc acg aca cta ttg gat att ttc ggg cgc aaa cgg 288
Ala Tyr Thr Ile Ser Thr Thr Leu Leu Asp Ile Phe Gly Arg Lys Arg

PF59083SeqList PF59083.txt

															85																90																95																	
cta	caa	att	gcc	atc	gta	gtc	gcc	tca	ttt	atc	atc	ggg	att	gcc	ctc	336																																																
Leu	Gln	Ile	Ala	Ile	Val	Val	Ala	Ser	Phe	Ile	Ile	Gly	Ile	Ala	Leu																																																	
															100																105																110																	
ttc	ttc	gaa	gtt	ggg	atc	gtc	ttg	ttg	att	cca	atc	gtc	ttt	gcc	att	384																																																
Phe	Phe	Glu	Val	Gly	Ile	Val	Leu	Leu	Ile	Pro	Ile	Val	Phe	Ala	Ile																																																	
															115																120																125																	
gcg	atc	gaa	gca	caa	gtt	ccc	gtt	ctc	tat	ctg	ggg	att	ccc	atg	ggc	432																																																
Ala	Ile	Glu	Ala	Gln	Val	Pro	Val	Leu	Tyr	Leu	Gly	Ile	Pro	Met	Gly																																																	
															130																135																140																	
gcc	gca	tta	tct	gtt	act	cac	gga	ttc	tta	cca	ccg	cac	ccg	gca	cca	480																																																
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Ala	Pro																																																	
															145																150																155																160	
act	gca	att	gcg	acg	acg	cta	aat	gcg	aac	gtg	ggt	cat	gtg	cta	cta	528																																																
Thr	Ala	Ile	Ala	Thr	Thr	Leu	Asn	Ala	Asn	Val	Gly	His	Val	Leu	Leu																																																	
															165																170																175																	
ttc	ggg	atc	att	att	gcg	att	cca	act	gtt	tat	atc	gca	gga	ccg	ctc	576																																																
Phe	Gly	Ile	Ile	Ile	Ala	Ile	Pro	Thr	Val	Tyr	Ile	Ala	Gly	Pro	Leu																																																	
															180																185																190																	
ttt	tca	cgc	tgg	gcg	caa	aag	atg	gtt	cct	gac	gca	ttc	acc	ggt	aaa	624																																																
Phe	Ser	Arg	Trp	Ala	Gln	Lys	Met	Val	Pro	Asp	Ala	Phe	Thr	Gly	Lys																																																	
															195																200																205																	
cca	cac	ctg	cca	ctt	agc	agt	aac	aaa	cgt	caa	ttc	aaa	gta	tct	gaa	672																																																
Pro	His	Leu	Pro	Leu	Ser	Ser	Asn	Lys	Arg	Gln	Phe	Lys	Val	Ser	Glu																																																	
															210																215																220																	
gca	ccc	ggg	ttt	gga	ctc	agt	gtc	tta	acg	gcg	ctc	ttc	ccc	gtg	att	720																																																
Ala	Pro	Gly	Phe	Gly	Leu	Ser	Val	Leu	Thr	Ala	Leu	Phe	Pro	Val	Ile																																																	
															225																230																235																240	
ctg	atg	aca	atc	acc	acc	gtc	tac	gaa	tta	gtc	gtt	gat	cac	ggt	gtg	768																																																
Leu	Met	Thr	Ile	Thr	Val	Tyr	Glu	Leu	Val	Val	Val	Asp	His	Gly	Val																																																	
															245																250																255																	
aca	cct	aaa	aac	ccg	tcg	acc	ctt	gac	caa	atc	att	cgt	ttg	att	ggg	816																																																
Thr	Pro	Lys	Asn	Pro	Ser	Thr	Leu	Asp	Gln	Ile	Ile	Arg	Leu	Ile	Gly																																																	
															260																265																270																	
gca	ccc	gga	att	gcc	atg	tta	att	tca	cta	tta	ttc	gcc	ctc	tgg	tca	864																																																
Ala	Pro	Gly	Ile	Ala	Met	Leu	Ile	Ser	Leu	Leu	Phe	Ala	Leu	Trp	Ser																																																	
															275																280																285																	
atg	ggg	att	cac	caa	cac	aag	acc	aat	aag	gcc	atc	acg	gcc	acc	atc	912																																																
Met	Gly	Ile	His	Gln	His	Lys	Thr	Asn	Lys	Ala	Ile	Thr	Ala	Thr	Ile																																																	
															290																295																300																	
gaa	gat	gcc	act	aag	tca	att	gcc	atg	tta	tta	cta	atc	atc	ggt	ggg	960																																																
Glu	Asp	Ala	Thr	Lys	Ser	Ile	Ala	Met	Leu	Leu	Leu	Ile	Ile	Gly	Gly																																																	
															305																310																315																320	
ggt	ggc	gcc	ttc	aaa	cag	atc	tta	att	gat	ggg	ggt	ggt	ggt	aag	gcc	1008																																																
Gly	Gly	Ala	Phe	Lys	Gln	Ile	Leu	Ile	Asp	Gly	Gly	Val	Gly	Lys	Ala																																																	
															325																330																335																	
gtg	gcc	cag	ttg	ttc	agt	ggc	agc	agc	atc	tca	cca	ctg	att	ctt	ggc	1056																																																
Val	Ala	Gln	Leu	Phe	Ser	Gly	Ser	Ser	Ile	Ser	Pro	Leu	Ile	Leu	Gly																																																	
															340																345																350																	
tgg	cta	gtc	gct	gtc	atc	tta	cgg	gtc	tca	ctc	ggc	tcc	gct	acc	gta	1104																																																
Trp	Leu	Val	Ala	Val	Ile	Leu	Arg	Val	Ser	Leu	Gly	Ser	Ala	Thr	Val																																																	
															355																360																365																	
gcg	gcc	ctc	acg	gca	gcc	ggc	cta	gtt	gcg	ccg	tta	atg	acg	caa	gct	1152																																																
Ala	Ala	Leu	Thr	Ala	Ala	Gly	Leu	Val	Ala	Pro	Leu	Met	Thr	Gln	Ala																																																	
															370																375																380																	
ggt	atc	gac	ccc	gcc	ctg	atg	gta	att	gcc	atc	ggc	tct	ggg	agt	gtc	1200																																																
Gly	Ile	Asp	Pro	Ala	Leu	Met	Val	Ile	Ala	Ile	Gly	Ser	Gly	Ser	Val																																																	
															385																390																395																400	
gcc	gct	tct	cac	gtg	aac	gac	gct	ggt	ttc	tgg	atg	ttc	cgg	gaa	tac	1248																																																
Ala	Ala	Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Met	Phe	Arg	Glu	Tyr																																																	
															405																410																415																	
ttc	gac	ctg	acc	gtc	aag	caa	acg	ctg	ctt	aca	tgg	aca	atg	tta	gaa	1296																																																
Phe	Asp	Leu	Thr	Val	Lys	Gln	Thr	Leu	Leu	Thr	Trp	Thr	Met	Leu	Glu																																																	
															420																425																430																	
acg	atc	atc	gct	gtc	tgc	ggt	ctc	gga	ggc	gtg	ttg	gcg	ctc	aac	gcc	1344																																																
Thr	Ile	Ile	Ala	Val	Cys	Gly	Leu	Gly	Gly	Val	Leu	Ala	Leu	Asn	Ala																																																	
															435																440																445																	
atc	ttc	cat	taa															1356																																														
Ile	Phe	His																																																														

450

<210> 10145

<211> 451

<212> PRT

<213> Lactobacillus plantarum WCFS1

<400> 10145

```

Met Pro Phe Val Val Leu Thr Leu Gly Ile Leu Leu Leu Leu Leu Leu
1      5      10      15
Ile Ile Lys Phe Lys Leu Asn Thr Tyr Ile Ala Leu Ile Val Thr Ala
20      25      30
Val Val Val Gly Ile Gly Leu Gly Met Pro Leu Thr Lys Ile Ala Thr
35      40      45
Ser Ile Gln Asn Gly Ile Gly Ser Gln Leu Gly Glu Leu Ala Leu Val
50      55      60
Phe Gly Phe Gly Ala Met Leu Gly Arg Leu Val Ala Asp Ala Gly Gly
65      70      75      80
Ala Tyr Thr Ile Ser Thr Thr Leu Leu Asp Ile Phe Gly Arg Lys Arg
85      90      95
Leu Gln Ile Ala Ile Val Val Ala Ser Phe Ile Ile Gly Ile Ala Leu
100     105
Phe Phe Glu Val Gly Ile Val Leu Leu Ile Pro Ile Val Phe Ala Ile
115     120     125
Ala Ile Glu Ala Gln Val Pro Val Leu Tyr Leu Gly Ile Pro Met Gly
130     135     140
Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Ala Pro
145     150     155     160
Thr Ala Ile Ala Thr Thr Leu Asn Ala Asn Val Gly His Val Leu Leu
165     170     175
Phe Gly Ile Ile Ile Ala Ile Pro Thr Val Tyr Ile Ala Gly Pro Leu
180     185     190
Phe Ser Arg Trp Ala Gln Lys Met Val Pro Asp Ala Phe Thr Gly Lys
195     200     205
Pro His Leu Pro Leu Ser Ser Asn Lys Arg Gln Phe Lys Val Ser Glu
210     215     220
Ala Pro Gly Phe Gly Leu Ser Val Leu Thr Ala Leu Phe Pro Val Ile
225     230     235     240
Leu Met Thr Ile Thr Thr Val Tyr Glu Leu Val Val Asp His Gly Val
245     250     255
Thr Pro Lys Asn Pro Ser Thr Leu Asp Gln Ile Ile Arg Leu Ile Gly
260     265     270
Ala Pro Gly Ile Ala Met Leu Ile Ser Leu Leu Phe Ala Leu Trp Ser
275     280     285
Met Gly Ile His Gln His Lys Thr Asn Lys Ala Ile Thr Ala Thr Ile
290     295     300
Glu Asp Ala Thr Lys Ser Ile Ala Met Leu Leu Leu Ile Ile Gly Gly
305     310     315     320
Gly Gly Ala Phe Lys Gln Ile Leu Ile Asp Gly Gly Val Gly Lys Ala
325     330     335
Val Ala Gln Leu Phe Ser Gly Ser Ser Ile Ser Pro Leu Ile Leu Gly
340     345     350
Trp Leu Val Ala Val Ile Leu Arg Val Ser Leu Gly Ser Ala Thr Val
355     360     365
Ala Ala Leu Thr Ala Ala Gly Leu Val Ala Pro Leu Met Thr Gln Ala
370     375     380
Gly Ile Asp Pro Ala Leu Met Val Ile Ala Ile Gly Ser Gly Ser Val
385     390     395     400
Ala Ala Ser His Val Asn Asp Ala Gly Phe Trp Met Phe Arg Glu Tyr
405     410     415
Phe Asp Leu Thr Val Lys Gln Thr Leu Leu Thr Trp Thr Met Leu Glu
420     425     430
Thr Ile Ile Ala Val Cys Gly Leu Gly Gly Val Leu Ala Leu Asn Ala
435     440     445
Ile Phe His
450

```

<210> 10146

<211> 1353

PF59083SeqList PF59083.txt

<212> DNA

<213> Pseudomonas syringae pv. tomato str. DC3000

<220>

<221> CDS

<222> (1)..(1353)

<223> transl_table=11

<400> 10146

atg ttc ggt atg acc cat gag acg ttc ctg ctc gtc gat gcg ttg gtg	48
Met Phe Gly Met Thr His Glu Thr Phe Leu Leu Val Asp Ala Leu Val	
1 5 10 15	
acc atc gtc ggc ctt gtg cta ctg atc acc acc ttc aag gtt cac cct	96
Thr Ile Val Gly Leu Val Leu Leu Ile Thr Thr Phe Lys Val His Pro	
20 25 30	
ttc gtc gcg ctg aca ctg gcg gca ggc ttt ctt ggc ctg acg tcg gga	144
Phe Val Ala Leu Thr Leu Ala Ala Gly Phe Leu Gly Leu Thr Ser Gly	
35 40 45	
atg cca gta gaa aaa gtc atg aag tcc ttc cag gag ggc ttc ggc ggc	192
Met Pro Val Glu Lys Val Met Lys Ser Phe Gln Gly Phe Gly Gly	
50 55 60	
gtg ctg ggt ttc gtc ggt atc atc ctt ggc ctg ggc acc atg ctc ggc	240
Val Leu Gly Phe Val Gly Ile Ile Leu Gly Leu Gly Thr Met Leu Gly	
65 70 75 80	
aag ctg atg gcc gat tcg ggg ggt gcg gac cag att gcg cag acc ctg	288
Lys Leu Met Ala Asp Ser Gly Gly Ala Asp Gln Ile Ala Gln Thr Leu	
85 90 95	
atc cgc acc ttt ggt aaa cag aaa gtg cat tgg gca atg atg ttc tcc	336
Ile Arg Thr Phe Gly Lys Gln Lys Val His Trp Ala Met Met Phe Ser	
100 105 110	
gcg ttt ctg gtg ggc atc ccg ctg ttc ttc gag atc ggt ttt gtg ctg	384
Ala Phe Leu Val Gly Ile Pro Leu Phe Phe Glu Ile Gly Phe Val Leu	
115 120 125	
ctg atc ccg ctg gtg ttc atc gtc gcc cgt cgt acc ggc gtg tcc atc	432
Leu Ile Pro Leu Val Phe Ile Val Ala Arg Arg Thr Gly Val Ser Ile	
130 135 140	
gtc aag atc ggc atc ccg ttg ctg gct ggc ctg tcg gcc gta cac ggc	480
Val Lys Ile Gly Ile Pro Leu Leu Ala Gly Leu Ser Ala Val His Gly	
145 150 155 160	
ctg gtt cca ccg cac ccg ggc ccg ctg ctg gcc atc ggc att ttt ggt	528
Leu Val Pro Pro His Pro Gly Pro Leu Leu Ala Ile Gly Ile Phe Gly	
165 170 175	
gct gat atc ggc aag acc att ttt tat ggc ctg atc gtc gcg ctg cca	576
Ala Asp Ile Gly Lys Thr Ile Phe Tyr Gly Leu Ile Val Ala Leu Pro	
180 185 190	
acc gcc atc atc gcg ggt ccc atc tac ggc aac tgg atc tcc aag cgc	624
Thr Ala Ile Ile Ala Gly Pro Ile Tyr Gly Asn Trp Ile Ser Lys Arg	
195 200 205	
atc ccc ggt acg ccg tcg cag gag ttg atg gac cag atc gcc aag gag	672
Ile Pro Gly Thr Pro Ser Gln Glu Leu Met Asp Gln Ile Ala Lys Glu	
210 215 220	
tcg agc act gaa aac ctg ccg ggc ttt ggc atc acg ctg atc acc atc	720
Ser Ser Thr Glu Asn Leu Pro Gly Phe Gly Ile Thr Leu Ile Thr Ile	
225 230 235 240	
ctg ctg cct gtg ttc ctg atg ctg ctc aag acc ttt gct gac gtg gtg	768
Leu Leu Pro Val Phe Leu Met Leu Leu Lys Thr Phe Ala Asp Val Val	
245 250 255	
ttg ccg gaa aac aac atg ttc cgc atc tgg atg gac ctg atc ggt cac	816
Leu Pro Glu Asn Asn Met Phe Arg Ile Trp Met Asp Leu Ile Gly His	
260 265 270	
ccg atc act gcc ctg ctg gca gcg ctg ttg ctg gcg ttc tac acc ttt	864
Pro Ile Thr Ala Leu Leu Ala Ala Leu Leu Leu Ala Phe Tyr Thr Phe	
275 280 285	
ggt gcg gca cgc ggc ttt gac cgc acc aaa atc atg aaa ctg ctg gac	912
Gly Ala Arg Gly Phe Asp Arg Thr Lys Ile Met Lys Leu Leu Asp	
290 295 300 305	
cag agc ctt gca ccg gtt gca gcc atc gtc ctg atc gtc ggc gca ggt	960
Gln Ser Leu Ala Pro Val Ala Ala Ile Val Leu Ile Val Gly Ala Gly	
310 315 320	

PF59083SeqList PF59083.txt

ggc	ggc	ttc	aag	cag	atg	ctg	gtg	gcc	agc	ggg	gtg	ggg	gat	gtc	atc	1008
Gly	Gly	Phe	Lys	Gln	Met	Leu	Val	Ala	Ser	Gly	Val	Gly	Asp	Val	Ile	
			325						330					335		
ggg	cac	atg	gcc	gta	cag	gca	cag	atc	aac	ccg	atc	atg	ctg	gct	tgg	1056
Gly	His	Met	Ala	Val	Gln	Ala	Gln	Ile	Asn	Pro	Ile	Met	Leu	Ala	Trp	
			340					345					350			
ctg	gtg	gcg	gcg	gtg	att	cgc	att	gcg	act	ggg	tcg	gct	acc	gtg	gcg	1104
Leu	Val	Ala	Ala	Val	Ile	Arg	Ile	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	
			355				360					365				
acc	att	acc	ggg	gca	ggg	att	gtg	gcg	cca	gtg	gtt	ggc	ctg	att	cca	1152
Thr	Ile	Thr	Gly	Ala	Gly	Ile	Val	Ala	Pro	Val	Val	Gly	Leu	Ile	Pro	
	370					375					380					
ggc	gtc	aat	cgc	gag	ctg	ctg	gtg	ctg	gcc	acg	ggg	gcc	ggc	tcg	ttg	1200
Gly	Val	Asn	Arg	Glu	Leu	Leu	Val	Leu	Ala	Thr	Gly	Ala	Gly	Ser	Leu	
385					390					395					400	
atc	ctg	tcg	cac	gtc	gat	gcc	ggg	ttc	tgg	ctg	gtt	aaa	cag	tat		1248
Ile	Leu	Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Leu	Val	Lys	Gln	Tyr	
			405					410					415			
ttc	aac	atg	acc	gtt	gcc	gaa	acg	ttc	aag	acc	tgg	aca	gtg	atg	gaa	1296
Phe	Asn	Met	Thr	Val	Ala	Glu	Thr	Phe	Lys	Thr	Trp	Thr	Val	Met	Glu	
			420				425						430			
acc	atc	ctg	tcg	gtg	gtc	ggc	ctg	atc	ttc	atc	atg	ctg	ttg	tcg	atg	1344
Thr	Ile	Leu	Ser	Val	Val	Gly	Leu	Ile	Phe	Ile	Met	Leu	Leu	Ser	Met	
		435					440					445				
gca	ctt	taa														1353
Ala	Leu															
	450															

<210> 10147

<211> 450

<212> PRT

<213> Pseudomonas syringae pv. tomato str. DC3000

<400> 10147

Met	Phe	Gly	Met	Thr	His	Glu	Thr	Phe	Leu	Leu	Val	Asp	Ala	Leu	Val	
1				5					10					15		
Thr	Ile	Val	Gly	Leu	Val	Leu	Leu	Ile	Thr	Thr	Phe	Lys	Val	His	Pro	
			20					25					30			
Phe	Val	Ala	Leu	Thr	Leu	Ala	Ala	Gly	Phe	Leu	Gly	Leu	Thr	Ser	Gly	
		35				40						45				
Met	Pro	Val	Glu	Lys	Val	Met	Lys	Ser	Phe	Gln	Glu	Gly	Phe	Gly	Gly	
	50					55					60					
Val	Leu	Gly	Phe	Val	Gly	Ile	Ile	Leu	Gly	Leu	Gly	Thr	Met	Leu	Gly	
65					70					75				80		
Lys	Leu	Met	Ala	Asp	Ser	Gly	Gly	Ala	Asp	Gln	Ile	Ala	Gln	Thr	Leu	
			85						90					95		
Ile	Arg	Thr	Phe	Gly	Lys	Gln	Lys	Val	His	Trp	Ala	Met	Met	Phe	Ser	
			100					105					110			
Ala	Phe	Leu	Val	Gly	Ile	Pro	Leu	Phe	Phe	Glu	Ile	Gly	Phe	Val	Leu	
		115				120						125				
Leu	Ile	Pro	Leu	Val	Phe	Ile	Val	Ala	Arg	Arg	Thr	Gly	Val	Ser	Ile	
		130				135					140					
Val	Lys	Ile	Gly	Ile	Pro	Leu	Leu	Ala	Gly	Leu	Ser	Ala	Val	His	Gly	
145					150					155				160		
Leu	Val	Pro	Pro	His	Pro	Gly	Pro	Leu	Leu	Ala	Ile	Gly	Ile	Phe	Gly	
			165						170					175		
Ala	Asp	Ile	Gly	Lys	Thr	Ile	Phe	Tyr	Gly	Leu	Ile	Val	Ala	Leu	Pro	
		180						185					190			
Thr	Ala	Ile	Ile	Ala	Gly	Pro	Ile	Tyr	Gly	Asn	Trp	Ile	Ser	Lys	Arg	
		195				200						205				
Ile	Pro	Gly	Thr	Pro	Ser	Gln	Glu	Leu	Met	Asp	Gln	Ile	Ala	Lys	Glu	
		210				215					220					
Ser	Ser	Thr	Glu	Asn	Leu	Pro	Gly	Phe	Gly	Ile	Thr	Leu	Ile	Thr	Ile	
225					230					235					240	
Leu	Leu	Pro	Val	Phe	Leu	Met	Leu	Leu	Lys	Thr	Phe	Ala	Asp	Val	Val	
			245						250					255		
Leu	Pro	Glu	Asn	Asn	Met	Phe	Arg	Ile	Trp	Met	Asp	Leu	Ile	Gly	His	
		260						265					270			
Pro	Ile	Thr	Ala	Leu	Leu	Ala	Ala	Leu	Leu	Leu	Ala	Phe	Tyr	Thr	Phe	

PF59083SeqList PF59083.txt

```

      275      280      285
Gly Ala Ala Arg Gly Phe Asp Arg Thr Lys Ile Met Lys Leu Leu Asp
 290      295      300
Gln Ser Leu Ala Pro Val Ala Ala Ile Val Leu Ile Val Gly Ala Gly
 305      310      315
Gly Gly Phe Lys Gln Met Leu Val Ala Ser Gly Val Gly Asp Val Ile
      325      330      335
Gly His Met Ala Val Gln Ala Gln Ile Asn Pro Ile Met Leu Ala Trp
      340      345      350
Leu Val Ala Ala Val Ile Arg Ile Ala Thr Gly Ser Ala Thr Val Ala
      355      360      365
Thr Ile Thr Gly Ala Gly Ile Val Ala Pro Val Val Gly Leu Ile Pro
      370      375      380
Gly Val Asn Arg Glu Leu Leu Val Leu Ala Thr Gly Ala Gly Ser Leu
 385      390      395
Ile Leu Ser His Val Asn Asp Ala Gly Phe Trp Leu Val Lys Gln Tyr
      405      410      415
Phe Asn Met Thr Val Ala Glu Thr Phe Lys Thr Trp Thr Val Met Glu
      420      425      430
Thr Ile Leu Ser Val Val Gly Leu Ile Phe Ile Met Leu Ser Met
      435      440      445
Ala Leu
 450

```

<210> 10148

<211> 1377

<212> DNA

<213> Vibrio parahaemolyticus RIMD 2210633

<220>

<221> CDS

<222> (1)..(1377)

<223> transl_table=11

<400> 10148

```

atg gag caa tta acc caa gcc cca gat cct acg ttc cta ctg acg att      48
Met Glu Gln Leu Thr Gln Ala Pro Asp Pro Thr Phe Leu Leu Thr Ile
 1      5      10      15
gca ggc ctt gcc att gca gcg tta ctc gtt ctg atc att aaa ctg aaa      96
Ala Gly Leu Ala Ile Ala Ala Leu Val Leu Ile Ile Lys Leu Lys
      20      25      30
gtc cat gct ttt gct tcc ctt act atg gtg agt tta ggc aca gca atc      144
Val His Ala Phe Ala Ser Leu Thr Met Val Ser Leu Gly Thr Ala Ile
      35      40      45
gcc act ggc gtt cct tct gag aaa gtc gta tcg acc atg atg ggc ggc      192
Ala Thr Gly Val Pro Ser Glu Lys Val Val Ser Thr Met Met Gly Gly
      50      55      60
ttc ggc ggc aca ctg gct tcc gtg gca ttg ctg gtt ggt ctt ggt gcg      240
Phe Gly Gly Thr Leu Ala Ser Val Ala Leu Leu Val Gly Leu Gly Ala
      65      70      75      80
atg atc ggt aaa att ctt gaa gtg act ggc ggt gcg aaa gtg ctg gca      288
Met Ile Gly Lys Ile Leu Glu Val Thr Gly Gly Ala Lys Val Leu Ala
      85      90      95
gac act ttg att ggt cgc ttt ggt aaa gag cgc gca cca ttt gct ttg      336
Asp Thr Leu Ile Gly Arg Phe Gly Lys Glu Arg Ala Pro Phe Ala Leu
      100      105      110
ggc gtc gct tca tta ctg ttt ggc ttc cca atc ttc ttc gat gct ggc      384
Gly Val Ala Ser Leu Leu Phe Gly Phe Pro Ile Phe Phe Asp Ala Gly
      115      120      125
ctt gta gtg atg atg cca atc atc cta agt gtg gcg gct cgt ttt ggt      432
Leu Val Val Met Met Pro Ile Ile Leu Ser Val Ala Ala Arg Phe Gly
      130      135      140
ggc tca cca att aaa tac gcg ttg cct gca gct ggt gct ttt gcg gtt      480
Gly Ser Pro Ile Lys Tyr Ala Leu Pro Ala Ala Gly Ala Phe Ala Val
      145      150      155      160
atg cac gcg ttt gtt cca cca cac cca ggt ccg gtt gca gcg gca gaa      528
Met His Ala Phe Val Pro Pro His Pro Gly Pro Val Ala Ala Ala Glu
      165      170      175
ttc ctt ggc gca aac atc ggt ctg cta ttg gtg gtg ggt att ttg gtt      576

```

PF59083SeqList PF59083.txt

Phe	Leu	Gly	Ala	Asn	Ile	Gly	Leu	Leu	Val	Val	Gly	Ile	Leu	Val	
180							185					190			
gct	att	cca	act	tgg	tac	ctt	ggc	gct	tac	cta	ttt	ggt	ttg	tac	gcg
Ala	Ile	Pro	Thr	Trp	Tyr	Leu	Gly	Ala	Tyr	Leu	Phe	Gly	Leu	Tyr	Ala
195							200					205			
ggc	aaa	aaa	ttc	gat	atc	cca	cta	tct	aaa	gcc	ttc	ttt	aat	ggc	gaa
Gly	Lys	Lys	Phe	Asp	Ile	Pro	Leu	Ser	Lys	Ala	Phe	Phe	Asn	Gly	Glu
210						215					220				
gca	atg	gtg	gat	gag	cgc	aac	gca	cca	aaa	ttt	ggc	acg	gtt	atg	acc
Ala	Met	Val	Asp	Glu	Arg	Asn	Ala	Pro	Lys	Phe	Gly	Thr	Val	Met	Thr
225					230					235					240
atc	ctt	gtg	ctg	cca	gtc	ctg	cta	atc	tgt	ttg	gat	acg	gta	ttg	aac
Ile	Leu	Val	Leu	Pro	Val	Leu	Leu	Ile	Cys	Leu	Asp	Thr	Val	Leu	Asn
				245					250					255	
aca	ctg	gcg	gtt	gca	ggg	ttg	att	gat	ggc	aaa	acg	gca	ctg	gtt	gag
Thr	Leu	Ala	Val	Ala	Gly	Leu	Ile	Asp	Gly	Lys	Thr	Ala	Leu	Val	Glu
				260				265						270	
ttc	cta	cgt	atg	cta	ggg	aaa	act	cca	gtc	gcg	ttg	ctg	att	act	ttg
Phe	Leu	Arg	Met	Leu	Gly	Lys	Thr	Pro	Val	Ala	Leu	Leu	Ile	Thr	Leu
		275					280					285			
att	gtc	tgt	ctg	gct	gtg	ttt	gcc	aaa	gac	tac	ggc	atg	gca	aaa	cta
Ile	Val	Cys	Leu	Ala	Val	Phe	Ala	Lys	Asp	Tyr	Gly	Met	Ala	Lys	Leu
		290				295					300				
gaa	aaa	ttg	tgt	ggg	gag	tca	ttg	gct	cca	atc	tgt	ggc	gtt	atc	ctt
Glu	Lys	Leu	Cys	Gly	Glu	Ser	Leu	Ala	Pro	Ile	Cys	Gly	Val	Ile	Leu
305					310					315					320
gta	acg	ggg	gct	ggg	ggc	atg	ttt	ggc	ggc	gta	ctg	cgt	tca	agc	ggc
Val	Thr	Gly	Ala	Gly	Gly	Met	Phe	Gly	Gly	Val	Leu	Arg	Ser	Ser	Gly
				325				330						335	
atc	ggg	gat	gca	ctg	gct	gac	gtt	ctt	aca	gac	aca	ggg	atg	cct	gtg
Ile	Gly	Asp	Ala	Leu	Ala	Asp	Val	Leu	Thr	Asp	Thr	Gly	Met	Pro	Val
			340				345							350	
att	gtg	gcg	gcg	ttt	gtg	att	tca	acc	tgt	ttg	cgt	gtt	gct	caa	ggc
Ile	Val	Ala	Ala	Phe	Val	Ile	Ser	Thr	Cys	Leu	Arg	Val	Ala	Gln	Gly
		355					360					365			
tcg	gca	acc	gta	gcg	cta	acc	act	acg	gcg	gct	ctt	atc	gcg	cca	gtt
Ser	Ala	Thr	Val	Ala	Leu	Thr	Thr	Thr	Ala	Ala	Leu	Ile	Ala	Pro	Val
		370				375					380				
gtg	gct	gca	tca	aca	ggg	ttg	agt	gaa	cta	gac	ctt	tgc	ttt	atc	gta
Val	Ala	Ala	Ser	Thr	Gly	Leu	Ser	Glu	Leu	Asp	Leu	Cys	Phe	Ile	Val
385					390					395					400
atc	gcg	att	gcg	ggg	ggg	gca	acg	gta	ctg	tct	cac	ttc	aat	gac	tct
Ile	Ala	Ile	Ala	Gly	Gly	Ala	Thr	Val	Leu	Ser	His	Phe	Asn	Asp	Ser
				405				410						415	
ggg	ttc	tgg	ttg	gta	tct	cgt	ctg	ctt	gag	atg	gat	gag	aaa	acc	aca
Gly	Phe	Trp	Leu	Val	Ser	Arg	Leu	Leu	Glu	Met	Asp	Glu	Lys	Thr	Thr
				420			425						430		
tta	aaa	act	tgg	acg	gta	atg	gaa	acg	tta	ctt	ggc	ggg	atc	gcg	ttt
Leu	Lys	Thr	Trp	Thr	Val	Met	Glu	Thr	Leu	Leu	Gly	Gly	Ile	Ala	Phe
		435					440					445			
att	atc	gtc	gca	aca	tta	agc	ttt	att	ctt	tag					
Ile	Ile	Val	Ala	Thr	Leu	Ser	Phe	Ile	Leu						
		450				455									

<210> 10149

<211> 458

<212> PRT

<213> Vibrio parahaemolyticus RIMD 2210633

<400> 10149

Met	Glu	Gln	Leu	Thr	Gln	Ala	Pro	Asp	Pro	Thr	Phe	Leu	Leu	Thr	Ile
1				5					10					15	
Ala	Gly	Leu	Ala	Ile	Ala	Ala	Leu	Leu	Val	Leu	Ile	Ile	Lys	Leu	Lys
			20				25						30		
Val	His	Ala	Phe	Ala	Ser	Leu	Thr	Met	Val	Ser	Leu	Gly	Thr	Ala	Ile
		35					40					45			
Ala	Thr	Gly	Val	Pro	Ser	Glu	Lys	Val	Val	Ser	Thr	Met	Met	Gly	Gly
	50					55				60					
Phe	Gly	Gly	Thr	Leu	Ala	Ser	Val	Ala	Leu	Leu	Val	Gly	Leu	Gly	Ala

PF59083SeqList PF59083.txt

```

65      70      75      80
Met Ile Gly Lys Ile Leu Glu Val Thr Gly Gly Ala Lys Val Leu Ala
      85
Asp Thr Leu Ile Gly Arg Phe Gly Lys Glu Arg Ala Pro Phe Ala Leu
      100
Gly Val Ala Ser Leu Leu Phe Gly Phe Pro Ile Phe Phe Asp Ala Gly
      115
Leu Val Val Met Met Pro Ile Ile Leu Ser Val Ala Ala Arg Phe Gly
      130
Gly Ser Pro Ile Lys Tyr Ala Leu Pro Ala Ala Gly Ala Phe Ala Val
      145
Met His Ala Phe Val Pro Pro His Pro Gly Pro Val Ala Ala Ala Glu
      165
Phe Leu Gly Ala Asn Ile Gly Leu Leu Val Val Gly Ile Leu Val
      180
Ala Ile Pro Thr Trp Tyr Leu Gly Ala Tyr Leu Phe Gly Leu Tyr Ala
      195
Gly Lys Lys Phe Asp Ile Pro Leu Ser Lys Ala Phe Phe Asn Gly Glu
      210
Ala Met Val Asp Glu Arg Asn Ala Pro Lys Phe Gly Thr Val Met Thr
      225
Ile Leu Val Leu Pro Val Leu Leu Ile Cys Leu Asp Thr Val Leu Asn
      245
Thr Leu Ala Val Ala Gly Leu Ile Asp Gly Lys Thr Ala Leu Val Glu
      260
Phe Leu Arg Met Leu Gly Lys Thr Pro Val Ala Leu Leu Ile Thr Leu
      275
Ile Val Cys Leu Ala Val Phe Ala Lys Asp Tyr Gly Met Ala Lys Leu
      290
Glu Lys Leu Cys Gly Glu Ser Leu Ala Pro Ile Cys Gly Val Ile Leu
      305
Val Thr Gly Ala Gly Gly Met Phe Gly Gly Val Leu Arg Ser Ser Gly
      325
Ile Gly Asp Ala Leu Ala Asp Val Leu Thr Asp Thr Gly Met Pro Val
      340
Ile Val Ala Ala Phe Val Ile Ser Thr Cys Leu Arg Val Ala Gln Gly
      355
Ser Ala Thr Val Ala Leu Thr Thr Thr Ala Ala Leu Ile Ala Pro Val
      370
Val Ala Ala Ser Thr Gly Leu Ser Glu Leu Asp Leu Cys Phe Ile Val
      385
Ile Ala Ile Ala Gly Gly Ala Thr Val Leu Ser His Phe Asn Asp Ser
      405
Gly Phe Trp Leu Val Ser Arg Leu Leu Glu Met Asp Glu Lys Thr Thr
      420
Leu Lys Thr Trp Thr Val Met Glu Thr Leu Leu Gly Gly Ile Ala Phe
      435
Ile Ile Val Ala Thr Leu Ser Phe Ile Leu
      450
      455

```

<210> 10150

<211> 1398

<212> DNA

<213> Streptomyces avermitilis MA-4680

<220>

<221> CDS

<222> (1)..(1398)

<223> transl_table=11

<400> 10150

```

gtg acc aga ctc agc gtc gag aag ctg gca gcg gac acc gtc gaa ccg
Met Thr Arg Leu Ser Val Glu Lys Leu Ala Ala Asp Thr Val Glu Pro
1      5      10      15
atc acc tcg gcg ggc cac gct caa ctc ggc atc gcg gta ctg gcg ggc
Ile Thr Ser Ala Gly His Ala Gln Leu Gly Ile Ala Val Leu Ala Gly
20      25      30
atc gcc gtc atc gtg ctg ctc atc acc aag ttc aag ctt cac gcg ttc
Ile Ala Val Ile Val Leu Leu Ile Thr Lys Phe Lys Leu His Ala Phe
40      45      50

```

48

96

144

PF59083SeqList PF59083.txt

ctc	gcc	ctg	acc	atc	ggt	tcg	ctc	gcg	ctc	ggc	gcg	ttc	gcc	ggg	gcg	192
Leu	Ala	Leu	Thr	Ile	Gly	Ser	Leu	Ala	Leu	Gly	Ala	Phe	Ala	Gly	Ala	
	50					55				60						
ccg	ctc	gac	aag	acc	atc	gtc	agc	ttc	acg	gcc	ggg	ctc	ggc	tcg	acc	240
Pro	Leu	Asp	Lys	Thr	Ile	Val	Ser	Phe	Thr	Ala	Gly	Leu	Gly	Ser	Thr	
65					70					75					80	
gtc	gcc	ggt	gtg	ggc	gtc	ctg	atc	gcg	ctg	ggc	gcc	atc	ctc	ggc	aag	288
Val	Ala	Gly	Val	Gly	Val	Leu	Ile	Ala	Leu	Gly	Ala	Ile	Leu	Gly	Lys	
				85					90					95		
ctg	ctc	gcc	gac	tcc	ggc	ggc	gcc	gac	cag	atc	gtc	gac	acg	atc	ctc	336
Leu	Leu	Ala	Asp	Ser	Gly	Gly	Ala	Asp	Gln	Ile	Val	Asp	Thr	Ile	Leu	
			100					105					110			
gcg	aag	gcg	ggc	ggg	cgg	gcc	atg	ccg	tgg	gcg	atg	gtg	ctg	atc	gcc	384
Ala	Lys	Ala	Gly	Gly	Arg	Ala	Met	Pro	Trp	Ala	Met	Val	Leu	Ile	Ala	
		115					120					125				
tcc	gtg	atc	ggc	ctg	ccg	ctg	ttc	ttc	gag	gtg	ggc	atc	gtg	ctg	ctc	432
Ser	Val	Ile	Gly	Leu	Pro	Leu	Phe	Phe	Glu	Val	Gly	Ile	Val	Leu	Leu	
130					135					140						
atc	ccg	gtc	gtg	ctg	atg	gtc	gcc	aag	cgc	ggc	aac	tac	tcg	ctg	atg	480
Ile	Pro	Val	Val	Leu	Met	Val	Ala	Lys	Arg	Gly	Asn	Tyr	Ser	Leu	Met	
145					150					155					160	
cgg	atc	ggc	atc	ccg	gcg	ctc	gcg	ggc	ctg	tcc	gtg	atg	cac	ggg	ctg	528
Arg	Ile	Gly	Ile	Pro	Ala	Leu	Ala	Gly	Leu	Ser	Val	Met	His	Gly	Leu	
				165					170					175		
atc	ccg	ccg	cac	ccc	ggc	ccg	ctg	gtc	gcg	atc	gac	gcg	gtc	aag	gcg	576
Ile	Pro	Pro	His	Pro	Gly	Pro	Leu	Val	Ala	Ile	Asp	Ala	Val	Lys	Ala	
			180					185					190			
aac	ctc	ggc	ctc	acg	ctg	gcg	ctc	ggt	gtc	ctc	gtc	gcc	atc	ccg	acg	624
Asn	Leu	Gly	Leu	Thr	Leu	Ala	Leu	Gly	Val	Leu	Val	Ala	Ile	Pro	Thr	
		195					200					205				
gtg	atc	atc	gcg	ggc	ccg	gtg	ttc	tcg	aaa	tac	gca	gcc	cgc	tgg	gtg	672
Val	Ile	Ile	Ala	Gly	Pro	Val	Phe	Ser	Lys	Tyr	Ala	Ala	Arg	Trp	Val	
210					215					220						
gac	gtt	ccg	gct	ccc	gac	cgc	atg	atc	ccc	acc	cgc	gct	tcc	gag	gac	720
Asp	Val	Pro	Ala	Pro	Asp	Arg	Met	Ile	Pro	Thr	Arg	Ala	Ser	Glu	Asp	
225				230						235					240	
ctg	gac	aag	cgc	ccc	ggc	ttc	ggc	gcc	acc	ctc	gcc	acc	atg	ctg	ctg	768
Leu	Asp	Lys	Arg	Pro	Gly	Phe	Gly	Ala	Thr	Leu	Ala	Thr	Met	Leu	Leu	
				245					250					255		
ccg	gtc	gtg	ctg	atg	ctg	gca	aag	gcc	ctg	gtc	gac	atc	atc	gtc	gac	816
Pro	Val	Val	Leu	Met	Leu	Ala	Lys	Ala	Leu	Val	Asp	Ile	Ile	Val	Asp	
			260					265					270			
gac	ccc	acg	cac	cag	gtg	cag	cgc	gtc	ttc	gac	gtc	atc	ggc	gca	ccg	864
Asp	Pro	Thr	His	Gln	Val	Gln	Arg	Val	Phe	Asp	Val	Ile	Gly	Ala	Pro	
		275					280					285				
ctg	atc	gcg	ctg	ctc	gcg	gcc	gtg	atc	gtc	ggt	atg	ttc	acg	ctg	ggc	912
Leu	Ile	Ala	Leu	Leu	Ala	Ala	Val	Ile	Val	Gly	Met	Phe	Thr	Leu	Gly	
290					295					300						
cgc	gcg	gcc	ggc	ttc	acc	aag	gag	cgc	ctc	tcg	acc	gtc	gag	aag		960
Arg	Ala	Ala	Gly	Phe	Thr	Lys	Glu	Arg	Leu	Ser	Thr	Thr	Val	Glu	Lys	
305				310						315				320		
tcc	ctc	gcc	ccg	atc	gcg	ggc	atc	ctg	ctg	atc	gtc	ggc	gcg	ggc	ggt	1008
Ser	Leu	Ala	Pro	Ile	Ala	Gly	Ile	Leu	Leu	Ile	Val	Gly	Ala	Gly	Gly	
				325					330					335		
ggc	ttc	aag	cag	acg	ctg	atc	gac	tcc	ggt	gtg	ggc	cag	atg	atc	ctg	1056
Gly	Phe	Lys	Gln	Thr	Leu	Ile	Asp	Ser	Gly	Val	Gly	Gln	Met	Ile	Leu	
			340					345					350			
gag	atc	tcc	aag	gac	tgg	tcg	atc	ccg	gcg	ctg	ctg	ctg	gcc	tgg	ctg	1104
Glu	Ile	Ser	Lys	Asp	Trp	Ser	Ile	Pro	Ala	Leu	Leu	Leu	Ala	Trp	Leu	
			355				360						365			
atc	gcg	gtg	gcg	atc	cgg	ctc	gcg	acc	ggt	tcg	gcg	acg	gtc	gcg	acc	1152
Ile	Ala	Val	Ala	Ile	Arg	Leu	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	Thr	
					375					380						
atc	tcc	gcg	gcc	ggt	ctc	gtc	gcg	ccc	ctc	gcg	gac	atg	tcg	acc		1200
Ile	Ser	Ala	Ala	Gly	Leu	Val	Ala	Pro	Leu	Ala	Ala	Asp	Met	Ser	Thr	
385				390						395					400	
gcg	cac	acc	tcg	ctc	ctc	gtg	ctg	gcg	atc	ggg	gcg	ggc	tcg	ctc	ttc	1248
Ala	His	Thr	Ser	Leu	Leu	Val	Leu	Ala	Ile	Gly	Ala	Gly	Ser	Leu	Phe	

PF59083SeqList PF59083.txt

				405					410					415				
ttc	agc	cat	gtg	aac	gat	gcc	ggg	ttc	tgg	ctg	gtc	aag	gag	tac	ttc			1296
Phe	Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Leu	Val	Lys	Glu	Tyr	Phe			
			420				425						430					
ggg	ctg	agc	gtc	ggc	cag	acg	gtc	aag	acc	tgg	tcg	atc	atg	gag	acc			1344
Gly	Leu	Ser	Val	Gly	Gln	Thr	Val	Lys	Thr	Trp	Ser	Ile	Met	Glu	Thr			
		435					440					445						
atc	atc	tcg	gtg	gtc	gcc	ggc	gga	ctg	gtc	ctg	ctg	ctg	tcc	ctc	gtg			1392
Ile	Ile	Ser	Val	Val	Ala	Gly	Gly	Leu	Val	Leu	Leu	Leu	Ser	Leu	Val			
	450					455				460								
atc	tag																	1398
Ile																		
465																		

<210> 10151

<211> 465

<212> PRT

<213> Streptomyces avermitilis MA-4680

<400> 10151

Met	Thr	Arg	Leu	Ser	Val	Glu	Lys	Leu	Ala	Ala	Asp	Thr	Val	Glu	Pro			
1				5					10					15				
Ile	Thr	Ser	Ala	Gly	His	Ala	Gln	Leu	Gly	Ile	Ala	Val	Leu	Ala	Gly			
			20					25					30					
Ile	Ala	Val	Ile	Val	Leu	Leu	Ile	Thr	Lys	Phe	Lys	Leu	His	Ala	Phe			
		35					40					45						
Leu	Ala	Leu	Thr	Ile	Gly	Ser	Leu	Ala	Leu	Gly	Ala	Phe	Ala	Gly	Ala			
	50				55					60								
Pro	Leu	Asp	Lys	Thr	Ile	Val	Ser	Phe	Thr	Ala	Gly	Leu	Gly	Ser	Thr			
65				70					75					80				
Val	Ala	Gly	Val	Gly	Val	Leu	Ile	Ala	Leu	Gly	Ala	Ile	Leu	Gly	Lys			
			85				90						95					
Leu	Leu	Ala	Asp	Ser	Gly	Gly	Ala	Asp	Gln	Ile	Val	Asp	Thr	Ile	Leu			
		100					105					110						
Ala	Lys	Ala	Gly	Gly	Arg	Ala	Met	Pro	Trp	Ala	Met	Val	Leu	Ile	Ala			
		115					120					125						
Ser	Val	Ile	Gly	Leu	Pro	Leu	Phe	Phe	Glu	Val	Gly	Ile	Val	Leu	Leu			
	130				135					140								
Ile	Pro	Val	Val	Leu	Met	Val	Ala	Lys	Arg	Gly	Asn	Tyr	Ser	Leu	Met			
145				150					155					160				
Arg	Ile	Gly	Ile	Pro	Ala	Leu	Ala	Gly	Leu	Ser	Val	Met	His	Gly	Leu			
			165				170						175					
Ile	Pro	Pro	His	Pro	Gly	Pro	Leu	Val	Ala	Ile	Asp	Ala	Val	Lys	Ala			
		180					185						190					
Asn	Leu	Gly	Leu	Thr	Leu	Ala	Leu	Gly	Val	Leu	Val	Ala	Ile	Pro	Thr			
		195					200					205						
Val	Ile	Ile	Ala	Gly	Pro	Val	Phe	Ser	Lys	Tyr	Ala	Ala	Arg	Trp	Val			
	210				215					220								
Asp	Val	Pro	Ala	Pro	Asp	Arg	Met	Ile	Pro	Thr	Arg	Ala	Ser	Glu	Asp			
225				230				235						240				
Leu	Asp	Lys	Arg	Pro	Gly	Phe	Gly	Ala	Thr	Leu	Ala	Thr	Met	Leu	Leu			
			245				250						255					
Pro	Val	Val	Leu	Met	Leu	Ala	Lys	Ala	Leu	Val	Asp	Ile	Ile	Val	Asp			
		260					265						270					
Asp	Pro	Thr	His	Gln	Val	Gln	Arg	Val	Phe	Asp	Val	Ile	Gly	Ala	Pro			
		275					280					285						
Leu	Ile	Ala	Leu	Leu	Ala	Ala	Val	Ile	Val	Gly	Met	Phe	Thr	Leu	Gly			
	290				295					300								
Arg	Ala	Ala	Gly	Phe	Thr	Lys	Glu	Arg	Leu	Ser	Thr	Thr	Val	Glu	Lys			
305					310					315				320				
Ser	Leu	Ala	Pro	Ile	Ala	Gly	Ile	Leu	Leu	Ile	Val	Gly	Ala	Gly	Gly			
			325					330					335					
Gly	Phe	Lys	Gln	Thr	Leu	Ile	Asp	Ser	Gly	Val	Gly	Gln	Met	Ile	Leu			
			340				345						350					
Glu	Ile	Ser	Lys	Asp	Trp	Ser	Ile	Pro	Ala	Leu	Leu	Leu	Ala	Trp	Leu			
		355				360						365						
Ile	Ala	Val	Ala	Ile	Arg	Leu	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	Thr			
	370				375					380								
Ile	Ser	Ala	Ala	Gly	Leu	Val	Ala	Pro	Leu	Ala	Ala	Asp	Met	Ser	Thr			

PF59083SeqList PF59083.txt

385 390 395 400
Ala His Thr Ser Leu Leu Val Leu Ala Ile Gly Ala Gly Ser Leu Phe
Phe Ser His Val Asn Asp Ala Gly Phe Trp Leu Val Lys Glu Tyr Phe
Gly Leu Ser Val Gly Gln Thr Val Lys Thr Trp Ser Ile Met Glu Thr
Ile Ile Ser Val Val Ala Gly Gly Leu Val Leu Leu Ser Leu Val
Ile 450 455 460
465

<210> 10152
<211> 1338
<212> DNA
<213> Photorhabdus luminescens subsp. laumondii TT01

<220>
<221> CDS
<222> (1)..(1338)
<223> transl_table=11

<400> 10152
gtg gat tca caa cct tgg gtg att ggt acg tta ctc aca agt att gcg 48
Met Asp Ser Gln Pro Trp Val Ile Gly Thr Leu Leu Thr Ser Ile Ala
1 5 10 15
tta att gta ttt acg ata att aaa tta aaa att cac cct ttt ctt gct 96
Leu Ile Val Phe Thr Ile Ile Lys Leu Lys Ile His Pro Phe Leu Ala
20 25 30
cta ttg tta gcc agt ttt tat gtc ggt gcc tta atg gga atg aac cct 144
Leu Leu Leu Ala Ser Phe Tyr Val Gly Ala Leu Met Gly Met Asn Pro
35 40 45
gtt gaa atg gtg aac gcc att caa ggg gga atc gga gat acg cta ggt 192
Val Glu Met Val Asn Ala Ile Gln Gly Gly Ile Gly Asp Thr Leu Gly
50 55 60
ttt tta gcc gta gtg att ggt ctg ggg acc att ctt ggt aag atg atg 240
Phe Leu Ala Val Val Ile Gly Leu Gly Thr Ile Leu Gly Lys Met Met
65 70 75 80
gag ata tcc ggc gcg gca gag cgg att ggt atc aca ttg caa aaa tgc 288
Glu Ile Ser Gly Ala Ala Glu Arg Ile Gly Ile Thr Leu Gln Lys Cys
85 90 95
cga tgg cta tca cct gat atc att atg gta ctg att ggt ttg gtt tgt 336
Arg Trp Leu Ser Pro Asp Ile Ile Met Val Leu Ile Gly Leu Val Cys
100 105 110
ggt att acg ctg ttt gtt gaa gtc ggg gtg gta ttg tta att cca ttg 384
Gly Ile Thr Leu Phe Val Glu Val Gly Val Val Leu Leu Ile Pro Leu
115 120 125
gca ttt tct att gcc agg aaa acc aat aca tca ttg ctg aaa tta gcg 432
Ala Phe Ser Ile Ala Arg Lys Thr Asn Thr Ser Leu Leu Lys Leu Ala
130 135 140
atc cca tta tgt aca gcg ttg atg gcg gtt cac tgt att att cct ccg 480
Ile Pro Leu Cys Thr Ala Leu Met Ala Val His Cys Ile Ile Pro Pro
145 150 155 160
cac ccg gct gca tta ttt gtg acg aat aaa ctg ggt gcg gat att ggc 528
His Pro Ala Ala Leu Phe Val Thr Asn Lys Leu Gly Ala Asp Ile Gly
165 170 175
tcg gtg att gtt tat ggg ttg ata gtt ggc ctg ttt gcc gct ttg gtg 576
Ser Val Ile Val Tyr Gly Leu Ile Val Gly Leu Phe Ala Ala Leu Val
180 185 190
ggg ggg cca tta ttt ctg aaa ttt ctc ggt agc cgt ctg cct ttt aaa 624
Gly Gly Pro Leu Phe Leu Lys Phe Leu Gly Ser Arg Leu Pro Phe Lys
195 200 205
tcg gtt ccg gct gaa ttt tct gaa att gca gtt cgt caa gaa gag gat 672
Ser Val Pro Ala Glu Phe Ser Glu Ile Ala Val Arg Gln Glu Glu Asp
210 215 220
tta ccc tct tta ggc atg aca ttg ttt act gtg tta ttg cca att ggg 720
Leu Pro Ser Leu Gly Met Thr Leu Phe Thr Val Leu Leu Pro Ile Gly
225 230 235 240
tta atg ttg act aaa acg gct gct gaa tta aat atg gaa aaa ggt acc 768

PF59083SeqList PF59083.txt

Leu	Met	Leu	Thr	Lys	Thr	Ala	Ala	Glu	Leu	Asn	Met	Glu	Lys	Gly	Thr		
				245					250					255			
acg	ttt	tat	acg	gtg	ctg	gaa	ttt	att	ggg	aat	cct	att	aca	gcc	atg	816	
Thr	Phe	Tyr	Thr	Val	Leu	Glu	Phe	Ile	Gly	Asn	Pro	Ile	Thr	Ala	Met		
			260					265					270				
ttc	att	gcc	gcg	ttt	gtt	gcc	tat	tac	acc	ttg	ggc	att	aag	caa	aat	864	
Phe	Ile	Ala	Ala	Phe	Val	Ala	Tyr	Tyr	Thr	Leu	Gly	Ile	Lys	Gln	Asn		
		275					280					285					
atg	gga	atg	agt	aca	ctg	ttg	acg	aag	acg	gaa	gat	tgt	ttc	tct	tct	912	
Met	Gly	Met	Ser	Thr	Leu	Leu	Thr	Lys	Thr	Glu	Asp	Cys	Phe	Ser	Ser		
	290					295				300							
atc	gcc	aat	att	tta	tta	att	atc	ggc	gcg	ggc	ggg	gca	ttt	aat	agt	960	
Ile	Ala	Asn	Ile	Leu	Leu	Ile	Ile	Gly	Ala	Gly	Gly	Ala	Phe	Asn	Ser		
305				310				315							320		
att	tta	aaa	gtc	agt	ggc	ctt	agt	gat	acg	ttg	gcc	gtt	att	ttg	tcg	1008	
Ile	Leu	Lys	Val	Ser	Gly	Leu	Ser	Asp	Thr	Leu	Ala	Val	Ile	Leu	Ser		
			325					330					335				
agt	ctg	gat	atg	cac	cca	att	ctt	ttg	tct	tgg	ttg	gtt	gcc	att	att	1056	
Ser	Leu	Asp	Met	His	Pro	Ile	Leu	Leu	Ser	Trp	Leu	Val	Ala	Ile	Ile		
			340				345						350				
ttg	cat	gcg	gcg	gtt	ggg	tca	gca	acg	gtc	gca	atg	atg	ggg	gca	aca	1104	
Leu	His	Ala	Ala	Val	Gly	Ser	Ala	Thr	Val	Ala	Met	Met	Gly	Ala	Thr		
		355				360						365					
gcg	att	gtt	tcg	cct	atg	ttg	ccg	tta	tat	cca	gat	att	agc	cct	gaa	1152	
Ala	Ile	Val	Ser	Pro	Met	Leu	Pro	Leu	Tyr	Pro	Asp	Ile	Ser	Pro	Glu		
370					375						380						
atc	att	aca	ttg	gcg	att	ggg	tct	ggg	gct	atc	ggc	tgt	act	att	gtg	1200	
Ile	Ile	Thr	Leu	Ala	Ile	Gly	Ser	Gly	Ala	Ile	Gly	Cys	Thr	Ile	Val		
385				390				395							400		
acg	gat	tca	ctg	ttt	tgg	ttg	gtt	aag	caa	tat	tgc	gga	aca	acg	ctc	1248	
Thr	Asp	Ser	Leu	Phe	Trp	Leu	Val	Lys	Gln	Tyr	Cys	Gly	Thr	Thr	Leu		
			405					410					415				
agt	gaa	act	ttt	aag	tat	tat	aca	acc	gca	aca	ttt	att	gcc	tct	gtg	1296	
Ser	Glu	Thr	Phe	Lys	Tyr	Tyr	Thr	Thr	Ala	Thr	Phe	Ile	Ala	Ser	Val		
			420				425						430				
gtt	gcg	ttg	gtt	ggg	acg	ttt	ctt	ctt	tct	acc	atc	gtg	tag			1338	
Val	Ala	Leu	Val	Gly	Thr	Phe	Leu	Leu	Ser	Thr	Ile	Val					
		435					440					445					

<210> 10153

<211> 445

<212> PRT

<213> Photorhabdus luminescens subsp. laumondii TT01

<400> 10153

Met	Asp	Ser	Gln	Pro	Trp	Val	Ile	Gly	Thr	Leu	Leu	Thr	Ser	Ile	Ala		
1				5				10						15			
Leu	Ile	Val	Phe	Thr	Ile	Ile	Lys	Leu	Lys	Ile	His	Pro	Phe	Leu	Ala		
		20					25					30					
Leu	Leu	Leu	Ala	Ser	Phe	Tyr	Val	Gly	Ala	Leu	Met	Gly	Met	Asn	Pro		
		35					40					45					
Val	Glu	Met	Val	Asn	Ala	Ile	Gln	Gly	Gly	Ile	Gly	Asp	Thr	Leu	Gly		
	50			55				60									
Phe	Leu	Ala	Val	Val	Ile	Gly	Leu	Gly	Thr	Ile	Leu	Gly	Lys	Met	Met		
65				70				75						80			
Glu	Ile	Ser	Gly	Ala	Ala	Glu	Arg	Ile	Gly	Ile	Thr	Leu	Gln	Lys	Cys		
			85				90						95				
Arg	Trp	Leu	Ser	Pro	Asp	Ile	Ile	Met	Val	Leu	Ile	Gly	Leu	Val	Cys		
		100					105						110				
Gly	Ile	Thr	Leu	Phe	Val	Glu	Val	Gly	Val	Val	Leu	Leu	Ile	Pro	Leu		
		115				120						125					
Ala	Phe	Ser	Ile	Ala	Arg	Lys	Thr	Asn	Thr	Ser	Leu	Leu	Lys	Leu	Ala		
	130				135						140						
Ile	Pro	Leu	Cys	Thr	Ala	Leu	Met	Ala	Val	His	Cys	Ile	Ile	Pro	Pro		
145				150						155				160			
His	Pro	Ala	Ala	Leu	Phe	Val	Thr	Asn	Lys	Leu	Gly	Ala	Asp	Ile	Gly		
			165				170						175				
Ser	Val	Ile	Val	Tyr	Gly	Leu	Ile	Val	Gly	Leu	Phe	Ala	Ala	Leu	Val		
			180				185						190				

PF59083SeqList PF59083.txt

Gly	Gly	Pro	Leu	Phe	Leu	Lys	Phe	Leu	Gly	Ser	Arg	Leu	Pro	Phe	Lys
		195					200					205			
Ser	Val	Pro	Ala	Glu	Phe	Ser	Glu	Ile	Ala	Val	Arg	Gln	Glu	Glu	Asp
	210					215					220				
Leu	Pro	Ser	Leu	Gly	Met	Thr	Leu	Phe	Thr	Val	Leu	Leu	Pro	Ile	Gly
	225				230					235					240
Leu	Met	Leu	Thr	Lys	Thr	Ala	Ala	Glu	Leu	Asn	Met	Glu	Lys	Gly	Thr
				245					250					255	
Thr	Phe	Tyr	Thr	Val	Leu	Glu	Phe	Ile	Gly	Asn	Pro	Ile	Thr	Ala	Met
			260					265					270		
Phe	Ile	Ala	Ala	Phe	Val	Ala	Tyr	Thr	Leu	Gly	Ile	Lys	Gln	Asn	
		275					280								
Met	Gly	Met	Ser	Thr	Leu	Leu	Thr	Lys	Thr	Glu	Asp	Cys	Phe	Ser	Ser
	290					295					300				
Ile	Ala	Asn	Ile	Leu	Leu	Ile	Ile	Gly	Ala	Gly	Gly	Ala	Phe	Asn	Ser
	305				310					315					320
Ile	Leu	Lys	Val	Ser	Gly	Leu	Ser	Asp	Thr	Leu	Ala	Val	Ile	Leu	Ser
				325					330					335	
Ser	Leu	Asp	Met	His	Pro	Ile	Leu	Leu	Ser	Trp	Leu	Val	Ala	Ile	Ile
			340					345					350		
Leu	His	Ala	Ala	Val	Gly	Ser	Ala	Thr	Val	Ala	Met	Met	Gly	Ala	Thr
		355					360					365			
Ala	Ile	Val	Ser	Pro	Met	Leu	Pro	Leu	Tyr	Pro	Asp	Ile	Ser	Pro	Glu
	370					375					380				
Ile	Ile	Thr	Leu	Ala	Ile	Gly	Ser	Gly	Ala	Ile	Gly	Cys	Thr	Ile	Val
	385				390					395					400
Thr	Asp	Ser	Leu	Phe	Trp	Leu	Val	Lys	Gln	Tyr	Cys	Gly	Thr	Thr	Leu
				405					410					415	
Ser	Glu	Thr	Phe	Lys	Tyr	Tyr	Thr	Thr	Ala	Thr	Phe	Ile	Ala	Ser	Val
			420					425					430		
Val	Ala	Leu	Val	Gly	Thr	Phe	Leu	Leu	Ser	Thr	Ile	Val			
		435					440					445			

<210> 10154
 <211> 1389
 <212> DNA
 <213> Corynebacterium diphtheriae NCTC 13129

<220>
 <221> CDS
 <222> (1)..(1389)
 <223> transl_table=11

<400> 10154	
atg gaa gat tgg gtt ccc acc ctt agt gct ggc ccc tta ttg ggg atc	48
Met Glu Asp Trp Val Pro Thr Leu Ser Ala Gly Pro Leu Leu Gly Ile	
1 5 10 15	
gcc gcc gcg gcg att gca ctc att ttg gtc ctc gtc att gtg ttc aag	96
Ala Ala Ala Ala Ile Ala Leu Ile Leu Val Leu Val Ile Val Phe Lys	
20 25 30	
ctc cac gct ttc ctc aca ctg atc atc gtt tcc gca gct acc gga ctc	144
Leu His Ala Phe Leu Thr Leu Ile Ile Val Ser Ala Ala Thr Gly Leu	
35 40 45	
gcc gcc ggc atc cca ctg gag ggc atc gtg ccc acc atg acc aaa ggc	192
Ala Ala Gly Ile Pro Leu Glu Gly Ile Val Pro Thr Met Thr Lys Gly	
50 55 60	
ttc gga agt aca ctc gcc tca gtt gcc ctc ctc gtc ggc ctc gga gca	240
Phe Gly Ser Thr Leu Ala Ser Val Ala Leu Leu Val Gly Leu Gly Ala	
65 70 75 80	
atg ctc ggc cgg ctt gtc gaa acc tcc ggc ggt gca aaa agc ctc gcc	288
Met Leu Gly Arg Leu Val Glu Thr Ser Gly Gly Ala Lys Ser Leu Ala	
85 90 95	
gaa acc ctc gtc gcc cgc ttc ggt gaa caa cgc gcc ccc ttc gcc ctc	336
Glu Thr Leu Val Ala Arg Phe Gly Glu Gln Arg Ala Pro Phe Ala Leu	
100 105 110	
ggc gta gcc tcc ctg ctg atg ggt ttc ccc atc ttc ttc gac gcc ggc	384
Gly Val Ala Ser Leu Leu Met Gly Phe Pro Ile Phe Phe Asp Ala Gly	
115 120 125	
ctg atc gtc atg ctg ccc gtc atc ttc gcc gtg gca cgc cga ctc aac	432

PF59083SeqList PF59083.txt

Leu	Ile	Val	Met	Leu	Pro	Val	Ile	Phe	Ala	Val	Ala	Arg	Arg	Leu	Asn	
130						135					140					
ggc	ccc	gtc	ctg	gcc	tac	ggc	atc	ccc	gcc	gcc	ggc	gcg	ttc	tcc	gtc	480
Gly	Pro	Val	Leu	Ala	Tyr	Gly	Ile	Pro	Ala	Ala	Gly	Ala	Phe	Ser	Val	
145					150					155					160	
atg	cac	atc	tac	ctg	cca	ccg	cac	cca	ggg	cca	atc	tca	gct	gca	gaa	528
Met	His	Ile	Tyr	Leu	Pro	Pro	His	Pro	Gly	Pro	Ile	Ser	Ala	Ala	Glu	
				165					170					175		
ttc	tac	agc	gca	gac	atc	ggc	ctc	gtc	atg	ctc	ctc	ggc	cta	atc	atc	576
Phe	Tyr	Ser	Ala	Asp	Ile	Gly	Leu	Val	Met	Leu	Leu	Gly	Leu	Ile	Ile	
			180					185					190			
gcg	atc	cct	acc	tgg	ctg	atc	tcc	ggc	ctc	tgg	ctc	ggc	aaa	acc	ctc	624
Ala	Ile	Pro	Thr	Trp	Leu	Ile	Ser	Gly	Leu	Trp	Leu	Gly	Lys	Thr	Leu	
		195					200					205				
ggc	cgc	cgc	tac	cca	ctg	cca	gtt	cct	gac	atc	cta	gcc	ggc	ggc	ccc	672
Gly	Arg	Arg	Tyr	Pro	Leu	Pro	Val	Pro	Asp	Ile	Leu	Ala	Gly	Gly	Pro	
		210				215					220					
caa	gca	acc	gac	gtg	aaa	aac	ccc	gcc	aca	cca	ggg	ctt	atc	gtc	tcc	720
Gln	Ala	Thr	Asp	Val	Lys	Asn	Pro	Ala	Thr	Pro	Gly	Leu	Ile	Val	Ser	
225				230						235					240	
ctc	ttg	ttg	ctt	cct	atg	ctg	ctc	atc	ttc	ggc	aac	acc	agc	atg	ggc	768
Leu	Leu	Leu	Leu	Pro	Met	Leu	Leu	Ile	Phe	Gly	Asn	Thr	Ser	Met	Gly	
				245					250					255		
ctt	gcc	acc	tcc	gca	ggc	tgg	gta	gac	aag	agc	tcg	agc	ctc	gtg	cgc	816
Leu	Ala	Thr	Ser	Ala	Gly	Trp	Val	Asp	Lys	Ser	Ser	Ser	Leu	Val	Arg	
			260					265					270			
gcc	cta	caa	ttc	gtg	ggc	agc	acc	ccc	att	gcc	ttg	ctg	atc	tca	acc	864
Ala	Leu	Gln	Phe	Val	Gly	Ser	Thr	Pro	Ile	Ala	Leu	Leu	Ile	Ser	Thr	
		275					280					285				
ctc	gtg	gcg	ctg	tac	ttc	ctc	ggc	att	cgt	cgc	ggc	cag	ccc	aaa	gct	912
Leu	Val	Ala	Leu	Tyr	Phe	Leu	Gly	Ile	Arg	Arg	Gly	Gln	Pro	Lys	Ala	
	290					295					300					
gac	cta	gaa	aag	ctt	ctc	gac	ggc	gcc	ctc	gga	ccc	atc	tgc	tcc	gtc	960
Asp	Leu	Glu	Lys	Leu	Leu	Asp	Gly	Ala	Leu	Gly	Pro	Ile	Cys	Ser	Val	
				310						315					320	
gta	ttg	atc	acc	ggc	ggc	ggc	ggc	atg	ttc	ggc	gta	ctg	cgc	acc		1008
Val	Leu	Ile	Thr	Gly	Ala	Gly	Gly	Met	Phe	Gly	Gly	Val	Leu	Arg	Thr	
				325					330					335		
tcc	ggc	atc	ggc	gac	gcc	cta	gcc	gac	tcc	atg	tcc	gac	ctc	ggc	gtc	1056
Ser	Gly	Ile	Gly	Asp	Ala	Leu	Ala	Asp	Ser	Met	Ser	Asp	Leu	Gly	Val	
			340					345					350			
ccc	gtc	gtc	ctc	ggc	tgt	tgg	ctc	gtc	gcc	gcc	atc	ctg	cgc	ctc	gcc	1104
Pro	Val	Val	Leu	Gly	Cys	Trp	Leu	Val	Ala	Ala	Ile	Leu	Arg	Leu	Ala	
		355				360						365				
caa	ggc	tcg	gcc	acc	gtg	gca	ctg	acc	acc	gcc	gca	gca	ctg	atg	gca	1152
Gln	Gly	Ser	Ala	Thr	Val	Ala	Leu	Thr	Thr	Ala	Ala	Ala	Leu	Met	Ala	
		370				375					380					
ccc	gcc	gtc	gcc	gcc	ggc	ggc	tac	agc	gaa	ttc	caa	atc	gca	ctc	atg	1200
Pro	Ala	Val	Ala	Ala	Gly	Gly	Tyr	Ser	Glu	Phe	Gln	Ile	Ala	Leu	Met	
					390					395					400	
gtg	ctg	gcc	tcc	gca	gcc	ggc	tcc	gtt	ttc	gca	ggc	cac	gtc	aac	gac	1248
Val	Leu	Ala	Ser	Ala	Ala	Gly	Ser	Val	Phe	Ala	Gly	His	Val	Asn	Asp	
				405					410					415		
tct	ggc	ttc	tgg	ctc	gtc	ggc	cgc	ctc	atg	ggc	atg	gac	gtt	gcc	acg	1296
Ser	Gly	Phe	Trp	Leu	Val	Gly	Arg	Leu	Met	Gly	Met	Asp	Val	Ala	Thr	
			420					425					430			
acc	ctg	cgc	acc	tgg	aca	ctc	aac	caa	gcg	ctc	gtt	gga	gcc	gtg	ggc	1344
Thr	Leu	Arg	Thr	Trp	Thr	Leu	Asn	Gln	Ala	Leu	Val	Gly	Ala	Val	Gly	
		435					440					445				
ttt	gta	ttc	gtc	ctc	gtc	ttc	tac	gga	gtc	agc	ttt	gcc	ttc	taa		1389
Phe	Val	Phe	Val	Leu	Val	Phe	Tyr	Gly	Val	Ser	Phe	Ala	Phe			
	450					455					460					

<210> 10155

<211> 462

<212> PRT

<213> Corynebacterium diphtheriae NCTC 13129

<400> 10155

PF59083SeqList PF59083.txt

```

Met Glu Asp Trp Val Pro Thr Leu Ser Ala Gly Pro Leu Leu Gly Ile
1      5      10      15
Ala Ala Ala Ala Ile Ala Leu Ile Leu Val Leu Val Ile Val Phe Lys
20      25      30
Leu His Ala Phe Leu Thr Leu Ile Ile Val Ser Ala Ala Thr Gly Leu
35      40      45
Ala Ala Gly Ile Pro Leu Glu Gly Ile Val Pro Thr Met Thr Lys Gly
50      55      60
Phe Gly Ser Thr Leu Ala Ser Val Ala Leu Leu Val Gly Leu Gly Ala
65      70      75      80
Met Leu Gly Arg Leu Val Glu Thr Ser Gly Gly Ala Lys Ser Leu Ala
85      90      95
Glu Thr Leu Val Ala Arg Phe Gly Glu Gln Arg Ala Pro Phe Ala Leu
100     105     110
Gly Val Ala Ser Leu Leu Met Gly Phe Pro Ile Phe Phe Asp Ala Gly
115     120     125
Leu Ile Val Met Leu Pro Val Ile Phe Ala Val Ala Arg Arg Leu Asn
130     135     140
Gly Pro Val Leu Ala Tyr Gly Ile Pro Ala Ala Gly Ala Phe Ser Val
145     150     155     160
Met His Ile Tyr Leu Pro Pro His Pro Gly Pro Ile Ser Ala Ala Glu
165     170     175
Phe Tyr Ser Ala Asp Ile Gly Leu Val Met Leu Leu Gly Leu Ile Ile
180     185     190
Ala Ile Pro Thr Trp Leu Ile Ser Gly Leu Trp Leu Gly Lys Thr Leu
195     200     205
Gly Arg Arg Tyr Pro Leu Pro Val Pro Asp Ile Leu Ala Gly Gly Pro
210     215     220
Gln Ala Thr Asp Val Lys Asn Pro Ala Thr Pro Gly Leu Ile Val Ser
225     230     235     240
Leu Leu Leu Leu Pro Met Leu Leu Ile Phe Gly Asn Thr Ser Met Gly
245     250     255
Leu Ala Thr Ser Ala Gly Trp Val Asp Lys Ser Ser Ser Leu Val Arg
260     265     270
Ala Leu Gln Phe Val Gly Ser Thr Pro Ile Ala Leu Leu Ile Ser Thr
275     280     285
Leu Val Ala Leu Tyr Phe Leu Gly Ile Arg Arg Gly Gln Pro Lys Ala
290     295     300
Asp Leu Glu Lys Leu Leu Asp Gly Ala Leu Gly Pro Ile Cys Ser Val
305     310     315     320
Val Leu Ile Thr Gly Ala Gly Gly Met Phe Gly Gly Val Leu Arg Thr
325     330     335
Ser Gly Ile Gly Asp Ala Leu Ala Asp Ser Met Ser Asp Leu Gly Val
340     345     350
Pro Val Val Leu Gly Cys Trp Leu Val Ala Ala Ile Leu Arg Leu Ala
355     360     365
Gln Gly Ser Ala Thr Val Ala Leu Thr Thr Ala Ala Ala Leu Met Ala
370     375     380
Pro Ala Val Ala Ala Gly Tyr Ser Glu Phe Gln Ile Ala Leu Met
385     390     395     400
Val Leu Ala Ser Ala Ala Gly Ser Val Phe Ala Gly His Val Asn Asp
405     410     415
Ser Gly Phe Trp Leu Val Gly Arg Leu Met Gly Met Asp Val Ala Thr
420     425     430
Thr Leu Arg Thr Trp Thr Leu Asn Gln Ala Leu Val Gly Ala Val Gly
435     440     445
Phe Val Phe Val Leu Val Phe Tyr Gly Val Ser Phe Ala Phe
450     455     460

```

<210> 10156

<211> 1350

<212> DNA

<213> Bacillus cereus ATCC 10987

<220>

<221> CDS

<222> (1)..(1350)

<223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 10156
atg gta gtt gga atc gta cta gcg gca gtt gtc ata cta ctt tta ctt 48
Met Val Val Gly Ile Val Leu Ala Ala Val Val Ile Leu Leu Leu Leu
1 5 10 15
att acg gta gta aaa tgg cat ccg ttt gtc gcg tta att tta aca gca 96
Ile Thr Val Val Lys Trp His Pro Phe Val Ala Leu Ile Leu Thr Ala
20 25 30
att ggt gta ggg cta gca atg gga atg cca ttg att gga act tca cca 144
Ile Gly Val Gly Leu Ala Met Gly Met Pro Leu Ile Gly Thr Ser Pro
35 40 45
aaa gat cca ggg att att gat tct att aaa cta ggg ctt ggt aat acg 192
Lys Asp Pro Gly Ile Ile Asp Ser Ile Lys Leu Gly Leu Gly Asn Thr
50 55 60
tta ggg ttt tta gcg ata gtt tta gca tta gga acg atg ctt gga aaa 240
Leu Gly Phe Leu Ala Ile Val Leu Ala Leu Gly Thr Met Leu Gly Lys
65 70 75
atg atg gcc gaa tct ggc ggt gct gaa cga att gct aac aca tta att 288
Met Met Ala Glu Ser Gly Gly Ala Glu Arg Ile Ala Asn Thr Leu Ile
85 90 95
gat cgt ttt ggg aag aaa cgt gtt cac tgg gca atg atg ttt gtt gca 336
Asp Arg Phe Gly Lys Lys Arg Val His Trp Ala Met Met Phe Val Ala
100 105 110
ttt tta gta ggg att ccg gta ttt ttc caa gtt gga ttt gta cta cta 384
Phe Leu Val Gly Ile Pro Val Phe Phe Gln Val Gly Phe Val Leu Leu
115 120 125
att cca ttg gta ttt aca att gca tta gaa aca ggg gta tca ctt att 432
Ile Pro Leu Val Phe Thr Ile Ala Leu Glu Thr Gly Val Ser Leu Ile
130 135 140
aca atc ggt att cca cta gta gca gga tta tcc gtt gta cac gga cta 480
Thr Ile Gly Ile Pro Val Ala Gly Leu Ser Val Val His Gly Leu
145 150 155
gtg cca ccg cat cca gca gcg atg gca gcg gta ggt att ttt aaa gca 528
Val Pro Pro His Pro Ala Ala Met Ala Ala Val Gly Ile Phe Lys Ala
160 165 170
gat gta ggg aag aca att tta tat gcg tta att gtc gga ctt cca act 576
Asp Val Gly Lys Thr Ile Leu Tyr Ala Leu Ile Val Gly Leu Pro Thr
175 180 185
gca att att tca ggt cca ctt tat gga aaa tgg att ggt gct cgt ata 624
Ala Ile Ile Ser Gly Pro Leu Tyr Gly Lys Trp Ile Gly Ala Arg Ile
190 195 200
cat aag gaa gta cca tta gag ata gca gag caa ttt gtt gaa aaa gat 672
His Lys Glu Val Pro Leu Glu Ile Ala Glu Gln Phe Val Glu Lys Asp
205 210 215
aat aaa aaa gag ctt cct agc ttt ggg aat aca ttg ttt aca att tta 720
Asn Lys Lys Glu Leu Pro Ser Phe Gly Asn Thr Leu Phe Thr Ile Leu
220 225 230
ctt cca gta ttt ctt atg ctt ggt gca tca ata gcg gaa gtt gca tta 768
Leu Pro Val Phe Leu Met Leu Gly Ala Ser Ile Ala Glu Val Ala Leu
235 240 245
aat aaa acg agt caa cta gca caa gta tta cac ttt att gga gat ccg 816
Asn Lys Thr Ser Gln Leu Ala Gln Val Leu His Phe Ile Gly Asp Pro
250 255 260
att gtc gct tta tta att gca acc att tac tct ttc ttt agt ctt gga 864
Ile Val Ala Leu Leu Ile Ala Thr Ile Tyr Ser Phe Phe Ser Leu Gly
265 270 275
tat gca aaa ggt ttc tca aaa gat aaa gta tta caa ttt aca aat gat 912
Tyr Ala Lys Gly Phe Ser Lys Asp Lys Val Leu Gln Phe Thr Asn Asp
280 285 290
tgc ctt ggg cca att gca aac ata ttg tta gtg att ggt gca ggc gga 960
Cys Leu Gly Pro Ile Ala Asn Ile Leu Leu Val Ile Gly Ala Gly Gly
300 305 310
gca ttt aat aaa gta tta tta gat tct gga att gga acg aca att gca 1008
Ala Phe Asn Lys Val Leu Leu Asp Ser Gly Ile Gly Thr Thr Ile Ala
315 320 325
gat atg gcg aaa gaa tcg cat att tca cca ata tta tta ggg tgg gga 1056
Asp Met Ala Lys Glu Ser His Ile Ser Pro Ile Leu Leu Gly Trp Gly
330 335 340
att gcg gca cta atc cga atc gca act gga tcg gca act gtt tct atg 1104
Ile Ala Ala Leu Ile Arg Ile Ala Thr Gly Ser Ala Thr Val Ser Met
345 350

```

PF59083SeqList PF59083.txt

355	atg aca gca gct ggt att gtt gca ccg att gca gca agt aca cca ggt	1152
Met Thr Ala Ala Gly Ile Val Ala Pro Ile Ala Ala Ser Thr Pro Gly		
370	gta aat gta gaa tta tta gca ctt gca aca ggt gca ggg tca tta att	1200
Val Asn Val Glu Leu Leu Ala Leu Ala Thr Gly Ala Gly Ser Leu Ile		
385	tta tca cat gta aat gat tct gga ttt tgg atg att aaa gaa tat ttc	1248
Leu Ser His Val Asn Asp Ser Gly Phe Trp Met Ile Lys Glu Tyr Phe		
405	ggg atg act gtg aaa gaa aca tta tta aca tgg acg gca atg gag aca	1296
Gly Met Thr Val Lys Glu Thr Leu Leu Thr Trp Thr Ala Met Glu Thr		
420	ata tta tct gtt gta gca ctt gga ctc att tcg tta tta aat ata ttt	1344
Ile Leu Ser Val Val Ala Leu Gly Leu Ile Ser Leu Leu Asn Ile Phe		
435	gta tag	1350
Val		

<210> 10157

<211> 449

<212> PRT

<213> Bacillus cereus ATCC 10987

<400> 10157

Met Val Val Gly Ile Val Leu Ala Ala Val Val Ile Leu Leu Leu Leu	
1 5 10 15	
Ile Thr Val Val Lys Trp His Pro Phe Val Ala Leu Ile Leu Thr Ala	
20 25 30	
Ile Gly Val Gly Leu Ala Met Gly Met Pro Leu Ile Gly Thr Ser Pro	
35 40 45	
Lys Asp Pro Gly Ile Ile Asp Ser Ile Lys Leu Gly Leu Gly Asn Thr	
50 55 60	
Leu Gly Phe Leu Ala Ile Val Leu Ala Leu Gly Thr Met Leu Gly Lys	
65 70 75 80	
Met Met Ala Glu Ser Gly Gly Ala Glu Arg Ile Ala Asn Thr Leu Ile	
85 90 95	
Asp Arg Phe Gly Lys Lys Arg Val His Trp Ala Met Met Phe Val Ala	
100 105 110	
Phe Leu Val Gly Ile Pro Val Phe Phe Gln Val Gly Phe Val Leu Leu	
115 120 125	
Ile Pro Leu Val Phe Thr Ile Ala Leu Glu Thr Gly Val Ser Leu Ile	
130 135 140	
Thr Ile Gly Ile Pro Leu Val Ala Gly Leu Ser Val Val His Gly Leu	
145 150 155 160	
Val Pro Pro His Pro Ala Ala Met Ala Ala Val Gly Ile Phe Lys Ala	
165 170 175	
Asp Val Gly Lys Thr Ile Leu Tyr Ala Leu Ile Val Gly Leu Pro Thr	
180 185 190	
Ala Ile Ile Ser Gly Pro Leu Tyr Gly Lys Trp Ile Gly Ala Arg Ile	
195 200 205	
His Lys Glu Val Pro Leu Glu Ile Ala Glu Gln Phe Val Glu Lys Asp	
210 215 220	
Asn Lys Lys Glu Leu Pro Ser Phe Gly Asn Thr Leu Phe Thr Ile Leu	
225 230 235 240	
Leu Pro Val Phe Leu Met Leu Gly Ala Ser Ile Ala Glu Val Ala Leu	
245 250 255	
Asn Lys Thr Ser Gln Leu Ala Gln Val Leu His Phe Ile Gly Asp Pro	
260 265 270	
Ile Val Ala Leu Leu Ile Ala Thr Ile Tyr Ser Phe Phe Ser Leu Gly	
275 280 285	
Tyr Ala Lys Gly Phe Ser Lys Asp Lys Val Leu Gln Phe Thr Asn Asp	
290 295 300	
Cys Leu Gly Pro Ile Ala Asn Ile Leu Leu Val Ile Gly Ala Gly Gly	
305 310 315 320	
Ala Phe Asn Lys Val Leu Leu Asp Ser Gly Ile Gly Thr Thr Ile Ala	
325 330 335	
Asp Met Ala Lys Glu Ser His Ile Ser Pro Ile Leu Leu Gly Trp Gly	

PF59083SeqList PF59083.txt

```

      340      345      350
Ile Ala Ala Leu Ile Arg Ile Ala Thr Gly Ser Ala Thr Val Ser Met
      355      360      365
Met Thr Ala Ala Gly Ile Val Ala Pro Ile Ala Ala Ser Thr Pro Gly
      370      375      380
Val Asn Val Glu Leu Leu Ala Leu Ala Thr Gly Ala Gly Ser Leu Ile
      385      390      395
Leu Ser His Val Asn Asp Ser Gly Phe Trp Met Ile Lys Glu Tyr Phe
      400      405      410
Gly Met Thr Val Lys Glu Thr Leu Leu Thr Trp Thr Ala Met Glu Thr
      415      420      425
Ile Leu Ser Val Val Ala Leu Gly Leu Ile Ser Leu Leu Asn Ile Phe
      430      435      440      445
val

```

<210> 10158
 <211> 1284
 <212> DNA
 <213> Yersinia pestis biovar Microtus str. 91001

<220>
 <221> CDS
 <222> (1)..(1284)
 <223> transl_table=11

```

<400> 10158
atg ctg cta tta ctg atg atc cgt tac aaa ctt aac gga ttt atc tcg      48
Met Leu Leu Leu Leu Met Ile Arg Tyr Lys Leu Asn Gly Phe Ile Ser
  1      5      10      15
ctg ata ctg gtc gcg tta gcg gta ggt atc atg caa ggg atg cca atc      96
Leu Ile Leu Val Ala Leu Ala Val Gly Ile Met Gln Gly Met Pro Ile
      20      25      30
gat aaa gtt gtc ggc tcg atc aaa gcg ggt gtc ggc gga aca tta ggt      144
Asp Lys Val Val Gly Ser Ile Lys Ala Gly Val Gly Thr Leu Gly
      35      40      45
agc ctg gcc ttg att atg ggc ttc ggg gcc atg ctc ggt aaa ttg ctg      192
Ser Leu Ala Leu Ile Met Gly Phe Gly Ala Met Leu Gly Lys Leu Leu
      50      55      60
gcc gat tgt ggc ggc gct caa cgt atc gcg acc ttg att gag aaa      240
Ala Asp Cys Gly Gly Ala Gln Arg Ile Ala Thr Thr Leu Ile Glu Lys
      65      70      75
ttt ggt caa aaa cat att caa tgg gcg gtg gta ctg acc ggc ttt act      288
Phe Gly Gln Lys His Ile Gln Trp Ala Val Val Leu Thr Gly Phe Thr
      80      85      90      95
gtg ggt ttt gcc ctg ttt tat gaa gtg ggt ttt gtg ctg tta ttg cca      336
Val Gly Phe Ala Leu Phe Tyr Glu Val Gly Phe Val Leu Leu Leu Pro
      100      105      110
ctg gta ttc agc att gcg gcc tct gcc cgc atc ccc ttg cta tat gtg      384
Leu Val Phe Ser Ile Ala Ala Ser Ala Arg Ile Pro Leu Leu Tyr Val
      115      120      125
ggg gtt ccc atg gcg gcg gcg ctt tct gtc act cat ggt ttt ctg cca      432
Gly Val Pro Met Ala Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro
      130      135      140
cct cac cca ggc ccg acc gcc att gcc acc att ttc aac gcc gat atg      480
Pro His Pro Gly Pro Thr Ala Ile Ala Thr Ile Phe Asn Ala Asp Met
      145      150      155      160
ggc aaa acg ctg ctg tac ggc acg ttg ctg gca atc cca acc gtg att      528
Gly Lys Thr Leu Leu Tyr Gly Thr Leu Leu Ala Ile Pro Thr Val Ile
      165      170      175
ttg gca ggc ccg gtg tac gcc cgc ttt cta aaa gga att gat aag cct      576
Leu Ala Gly Pro Val Tyr Ala Arg Phe Leu Lys Gly Ile Asp Lys Pro
      180      185      190
gtt cct gaa ggg ttg tat aac ccg aaa atc ttt acc gat aaa gag atg      624
Val Pro Glu Gly Leu Tyr Asn Pro Lys Ile Phe Thr Asp Lys Glu Met
      195      200      205      210
cca agc ttt ggg gtc agt gtc agt acg gcg ctg gta ccg gtt att ttg      672
Pro Ser Phe Gly Val Ser Val Ser Thr Ala Leu Val Pro Val Ile Leu
      210      215      220

```

PF59083SeqList PF59083.txt

atg	gca	ttg	cgg	gcc	gta	gca	gag	atg	att	ttg	cct	aaa	ggc	cat	tcg	720
Met	Ala	Leu	Arg	Ala	Val	Ala	Glu	Met	Ile	Leu	Pro	Lys	Gly	His	Ser	
225					230					235					240	
ctg	ctc	ccc	tat	gcc	gag	ttc	ttt	ggg	gat	cct	gta	att	gct	acg	ctg	768
Leu	Leu	Pro	Tyr	Ala	Glu	Phe	Phe	Gly	Asp	Pro	Val	Ile	Ala	Thr	Leu	
				245					250					255		
att	gcc	gtg	tta	att	gca	att	ttc	acc	ttt	ggg	cta	aac	cgg	ggc	cgc	816
Ile	Ala	Val	Leu	Ile	Ala	Ile	Phe	Thr	Phe	Gly	Leu	Asn	Arg	Gly	Arg	
			260					265					270			
tca	gtg	gaa	tcg	gtc	atg	gag	acc	ctg	tct	gat	tcc	atc	aag	atc	atc	864
Ser	Val	Glu	Ser	Val	Met	Glu	Thr	Leu	Ser	Asp	Ser	Ile	Lys	Ile	Ile	
		275					280					285				
gca	atg	atg	ctg	tta	gtt	att	gga	ggg	ggc	ggg	gct	ttc	aag	cag	gtt	912
Ala	Met	Met	Leu	Leu	Val	Ile	Gly	Gly	Gly	Gly	Ala	Phe	Lys	Gln	Val	
290						295					300					
tta	gtc	gat	agc	ggc	ata	gag	caa	tat	att	gct	ggc	atg	atg	ggc	aat	960
Leu	Val	Asp	Ser	Gly	Ile	Glu	Gln	Tyr	Ile	Ala	Gly	Met	Met	Gly	Asn	
305					310					315					320	
agc	ggg	gca	tca	cct	att	ctg	atg	gca	tgg	tcc	atc	gcc	gcc	tta	ctg	1008
Ser	Gly	Ala	Ser	Pro	Ile	Leu	Met	Ala	Trp	Ser	Ile	Ala	Ala	Leu	Leu	
				325					330					335		
cgt	atc	gcc	ctg	ggg	tct	gcg	acg	gtg	gca	gcg	atc	acc	gct	ggg	ggc	1056
Arg	Ile	Ala	Leu	Gly	Ser	Ala	Thr	Val	Ala	Ala	Ile	Thr	Ala	Gly	Gly	
			340					345					350			
att	gtc	gca	ccg	tta	atc	gcg	acc	ggg	gcc	agc	cct	gag	ttg	atg		1104
Ile	Val	Ala	Pro	Leu	Ile	Ala	Thr	Thr	Gly	Ala	Ser	Pro	Glu	Leu	Met	
		355					360					365				
gtc	att	gcc	gtt	ggg	tcc	ggg	agc	gtg	atc	ttc	tct	cac	gtg	aat	gac	1152
Val	Ile	Ala	Val	Gly	Ser	Gly	Ser	Val	Ile	Phe	Ser	His	Val	Asn	Asp	
370					375						380					
cct	ggc	ttc	tgg	cta	ttc	aag	gag	tat	ttc	aac	cta	acc	att	atg	gaa	1200
Pro	Gly	Phe	Trp	Leu	Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Thr	Ile	Met	Glu	
385					390					395					400	
acc	att	aaa	tcg	tgg	tca	gta	ctg	gaa	acc	att	att	tca	gtc	tgc	ggg	1248
Thr	Ile	Lys	Ser	Trp	Ser	Val	Leu	Glu	Thr	Ile	Ile	Ser	Val	Cys	Gly	
				405					410					415		
ttg	atc	ggc	tgt	ttg	ttg	ctg	tct	ctg	gtt	att	tag					1284
Leu	Ile	Gly	Cys	Leu	Leu	Leu	Ser	Leu	Val	Ile						
			420					425								

<210> 10159

<211> 427

<212> PRT

<213> Yersinia pestis biovar Microtus str. 91001

<400> 10159

Met	Leu	Leu	Leu	Leu	Met	Ile	Arg	Tyr	Lys	Leu	Asn	Gly	Phe	Ile	Ser	
1				5					10					15		
Leu	Ile	Leu	Val	Ala	Leu	Ala	Val	Gly	Ile	Met	Gln	Gly	Met	Pro	Ile	
			20					25					30			
Asp	Lys	Val	Val	Gly	Ser	Ile	Lys	Ala	Gly	Val	Gly	Gly	Thr	Leu	Gly	
		35					40					45				
Ser	Leu	Ala	Leu	Ile	Met	Gly	Phe	Gly	Ala	Met	Leu	Gly	Lys	Leu	Leu	
	50					55				60						
Ala	Asp	Cys	Gly	Gly	Ala	Gln	Arg	Ile	Ala	Thr	Thr	Leu	Ile	Glu	Lys	
65					70				75					80		
Phe	Gly	Gln	Lys	His	Ile	Gln	Trp	Ala	Val	Val	Leu	Thr	Gly	Phe	Thr	
				85					90					95		
Val	Gly	Phe	Ala	Leu	Phe	Tyr	Glu	Val	Gly	Phe	Val	Leu	Leu	Leu	Pro	
			100				105						110			
Leu	Val	Phe	Ser	Ile	Ala	Ala	Ser	Ala	Arg	Ile	Pro	Leu	Leu	Tyr	Val	
		115					120					125				
Gly	Val	Pro	Met	Ala	Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	
	130					135					140					
Pro	His	Pro	Gly	Pro	Thr	Ala	Ile	Ala	Thr	Ile	Phe	Asn	Ala	Asp	Met	
145					150					155					160	
Gly	Lys	Thr	Leu	Leu	Tyr	Gly	Thr	Leu	Leu	Ala	Ile	Pro	Thr	Val	Ile	
				165					170					175		
Leu	Ala	Gly	Pro	Val	Tyr	Ala	Arg	Phe	Leu	Lys	Gly	Ile	Asp	Lys	Pro	

PF59083SeqList PF59083.txt

```

180      185      190
Val Pro Glu Gly Leu Tyr Asn Pro Lys Ile Phe Thr Asp Lys Glu Met
195      200      205
Pro Ser Phe Gly Val Ser Val Ser Thr Ala Leu Val Pro Val Ile Leu
210      215      220
Met Ala Leu Arg Ala Val Ala Glu Met Ile Leu Pro Lys Gly His Ser
225      230      235
Leu Leu Pro Tyr Ala Glu Phe Phe Gly Asp Pro Val Ile Ala Thr Leu
240      245      250
Ile Ala Val Leu Ile Ala Ile Phe Thr Phe Gly Leu Asn Arg Gly Arg
255      260      265
Ser Val Glu Ser Val Met Glu Thr Leu Ser Asp Ser Ile Lys Ile Ile
270      275      280
Ala Met Met Leu Leu Val Ile Gly Gly Gly Gly Ala Phe Lys Gln Val
285      290      295
Leu Val Asp Ser Gly Ile Glu Gln Tyr Ile Ala Gly Met Met Gly Asn
300      305      310
Ser Gly Ala Ser Pro Ile Leu Met Ala Trp Ser Ile Ala Ala Leu Leu
315      320      325
Arg Ile Ala Leu Gly Ser Ala Thr Val Ala Ala Ile Thr Ala Gly Gly
330      335      340
Ile Val Ala Pro Leu Ile Ala Thr Thr Gly Ala Ser Pro Glu Leu Met
345      350      355
Val Ile Ala Val Gly Ser Gly Ser Val Ile Phe Ser His Val Asn Asp
360      365      370
Pro Gly Phe Trp Leu Phe Lys Glu Tyr Phe Asn Leu Thr Ile Met Glu
375      380      385
Thr Ile Lys Ser Trp Ser Val Leu Glu Thr Ile Ile Ser Val Cys Gly
390      395      400
Leu Ile Gly Cys Leu Leu Leu Ser Leu Val Ile
405      410      415
420      425

```

<210> 10160
 <211> 1359
 <212> DNA
 <213> Staphylococcus aureus subsp. aureus MRSA252

<220>
 <221> CDS
 <222> (1)..(1359)
 <223> transl_table=11

```

<400> 10160
atg ttt aac gaa ata tgg ccg tta atc agt gtt gtt tta ggt ata att      48
Met Phe Asn Glu Ile Trp Pro Leu Ile Ser Val Val Leu Gly Ile Ile
1      5      10
att tta tta gta tta atc att ggg ttt aaa tta aat aca ttt att tca      96
Ile Leu Leu Val Leu Ile Ile Gly Phe Lys Leu Asn Thr Phe Ile Ser
20      25      30
tta att atc aca tcg atg att aca gcg tta atg cta ggt ata cca ttg      144
Leu Ile Ile Thr Ser Met Ile Thr Ala Leu Met Leu Gly Ile Pro Leu
35      40      45
act aaa att atg gag acg att gag aaa ggg atg ggc agt acg ctc ggc      192
Thr Lys Ile Met Glu Thr Ile Glu Lys Gly Met Gly Ser Thr Leu Gly
50      55      60
cac att gca ctg ata ttc ggt tta ggt gcc ata ctt ggg aaa tta ctt      240
His Ile Ala Leu Ile Phe Gly Leu Gly Ala Ile Leu Gly Lys Leu Leu
65      70      75
gct gat ggt ggt ggt gca act cga att gca gac acg ttg att caa aaa      288
Ala Asp Gly Gly Gly Ala Thr Arg Ile Ala Asp Thr Leu Ile Gln Lys
80      85      90
ttt ggt caa aaa cat gta caa tgg gca atg ctt gtt gca gca ttt atc      336
Phe Gly Gln Lys His Val Gln Trp Ala Met Leu Val Ala Ala Phe Ile
95      100      105
gtc ggg att gca ttg ttc ttt gaa gta ggt tta gtc tta ctg att cca      384
Val Gly Ile Ala Leu Phe Phe Glu Val Gly Leu Val Leu Leu Ile Pro
110      115      120
tta gta ttt aca gta gca aaa cgc gca aat gtt tca gtg tta aaa cta      432
Leu Val Phe Thr Val Ala Lys Arg Ala Asn Val Ser Val Leu Lys Leu
125

```

PF59083SeqList PF59083.txt

130	gga tta cct atg gta	135	aca gct tta tca gtg	140	aca cat ggc ttt tta cca	480
Gly Leu Pro Met Val	Thr Ala Leu Ser Val	Thr His Gly Phe Leu Pro				
145	cca cat cca gga ccg gta	150	gtc atc gca aaa gaa	155	tta aag gcg aat gta	528
Pro His Pro Gly Pro	Val Val Ile Ala Lys	Glu Leu Lys Ala Asn Val				
165	gga gat gta tta cta tac	170	ggt atg att att gcc	175	att cca gtt aca ctc	576
Gly Asp Val Leu Leu Tyr	Gly Met Ile Ile Ala	Ile Ile Pro Val Thr Leu				
180	att gca gga cct ata ttt	185	aac aaa gtt gca caa	190	aaa atg att ccg tct	624
Ile Ala Gly Pro Ile Phe	Asn Lys Val Ala Gln	Lys Met Ile Pro Ser				
195	gcg tat aca cga gaa ggc	200	gat att tca gcg tta	205	ggt gca caa aaa gaa	672
Ala Tyr Thr Arg Glu Gly	Asp Ile Ser Ala Leu	Gly Ala Gln Lys Glu				
210	ttt acg gat caa gag atg	215	cca gga ttt ggt atg	220	agt tta tta aca gca	720
Phe Thr Asp Gln Glu Met	Pro Gly Phe Gly Met	Ser Leu Leu Thr Ala				
225	aca tta cca gtc ata tta	230	atg tta gtg tct ata	235	acg caa ctt gta	768
Thr Leu Pro Val Ile Leu	Met Leu Val Ser Thr	Ile Thr Gln Leu Val				
245	acc ggg cac gac aaa cct	250	aca aat cta ttt gaa	255	tct atc att tat atg	816
Thr Gly His Asp Lys Pro	Thr Asn Leu Phe Glu	Ser Ile Ile Tyr Met				
260	atc gga aca gca ggg aca	265	gcc atg cta ata gca	270	gta tta ttt gca atc	864
Ile Gly Thr Ala Gly Thr	Ala Met Leu Ile Ala	Val Leu Phe Ala Ile				
275	gtt acg atg gga tta atg	280	aga aaa cgt aag atg	285	aat cat att atg gaa	912
Val Thr Met Gly Leu Met	Arg Lys Arg Lys Met	Asn His Ile Met Glu				
290	tca gtg acg aat gcg att	295	tat cca atc gga atg	300	atg tta ttg att att	960
Ser Val Thr Asn Ala Ile	Tyr Pro Ile Gly Met	Met Met Leu Leu Ile				
305	ggc ggt ggc ggt aca ttt	310	aaa caa gta tta att	315	gac ggt ggt gtc gga	1008
Gly Gly Gly Gly Thr Phe	Lys Gln Val Leu Ile	Asp Gly Gly Val Gly				
325	aat aca att gct aaa atg	330	ttt gaa ggt aca gag	335	atg tct ccg att tta	1056
Asn Thr Ile Ala Lys Met	Phe Glu Gly Thr Glu	Met Ser Pro Ile Leu				
340	cta gct tgg att gtt gca	345	gct gtg cta cgt atc	350	gca tta ggt tcg gct	1104
Leu Ala Trp Ile Val Ala	Ala Val Leu Arg Ile	Ala Leu Gly Ser Ala				
355	aca gta gct gcg att tca	360	act aca ggt att gtc	365	tta cca tta tta caa	1152
Thr Val Ala Ala Ile Ser	Thr Gly Ile Val Leu	Pro Leu Leu Gln				
370	tca tca gat gta aat gtt	375	gca tta gtt gta cta	380	gcg att ggt gca ggt	1200
Ser Ser Asp Val Asn Val	Ala Leu Val Val Leu	Ala Ile Gly Ala Gly				
385	agt gtg att ttg tct cat	390	ggt aat gac gca gga	395	ttc tgg atg ttt aaa	1248
Ser Val Ile Leu Ser His	Val Asn Asp Ala Gly	Phe Trp Met Phe Lys				
405	gaa tat ttt ggt tta act	410	gta aaa gaa aca ttc	415	cta aca tgg tca tta	1296
Glu Tyr Phe Gly Leu Thr	Val Lys Glu Thr Phe	Leu Thr Trp Ser Leu				
420	tta gaa acg att att tcc	425	ggt atc atc ttc att	430	tta ttc atc	1344
Leu Glu Thr Ile Ile Ser	Val Ser Gly Ile Ile	Phe Ile Leu Phe Ile				
435	agc tta ttt gtt taa	440		445		1359
Ser Leu Phe Val						
450						

<210> 10161

<211> 452

<212> PRT

<213> Staphylococcus aureus subsp. aureus MRSA252

<400> 10161

Met Phe Asn Glu Ile Trp Pro Leu Ile Ser Val Val Leu Gly Ile Ile

PF59083SeqList PF59083.txt

```

1           5           10           15
Ile Leu Leu Val Leu Ile Ile Gly Phe Lys Leu Asn Thr Phe Ile Ser
                20
Leu Ile Ile Thr Ser Met Ile Thr Ala Leu Met Leu Gly Ile Pro Leu
                35
Thr Lys Ile Met Glu Thr Ile Glu Lys Gly Met Gly Ser Thr Leu Gly
                50
His Ile Ala Leu Ile Phe Gly Leu Gly Ala Ile Leu Gly Lys Leu Leu
65                70
Ala Asp Gly Gly Gly Ala Thr Arg Ile Ala Asp Thr Leu Ile Gln Lys
                85
Phe Gly Gln Lys His Val Gln Trp Ala Met Leu Val Ala Ala Phe Ile
                100
Val Gly Ile Ala Leu Phe Phe Glu Val Gly Leu Val Leu Ile Pro
115
Leu Val Phe Thr Val Ala Lys Arg Ala Asn Val Ser Val Leu Lys Leu
130
Gly Leu Pro Met Val Thr Ala Leu Ser Val Thr His Gly Phe Leu Pro
145
Pro His Pro Gly Pro Val Val Ile Ala Lys Glu Leu Lys Ala Asn Val
165
Gly Asp Val Leu Leu Tyr Gly Met Ile Ile Ala Ile Pro Val Thr Leu
180
Ile Ala Gly Pro Ile Phe Asn Lys Val Ala Gln Lys Met Ile Pro Ser
195
Ala Tyr Thr Arg Glu Gly Asp Ile Ser Ala Leu Gly Ala Gln Lys Glu
210
Phe Thr Asp Gln Glu Met Pro Gly Phe Gly Met Ser Leu Leu Thr Ala
225
Thr Leu Pro Val Ile Leu Met Leu Val Ser Thr Ile Thr Gln Leu Val
245
Thr Gly His Asp Lys Pro Thr Asn Leu Phe Glu Ser Ile Ile Tyr Met
260
Ile Gly Thr Ala Gly Thr Ala Met Leu Ile Ala Val Leu Phe Ala Ile
275
Val Thr Met Gly Leu Met Arg Lys Arg Lys Met Asn His Ile Met Glu
290
Ser Val Thr Asn Ala Ile Tyr Pro Ile Gly Met Met Leu Leu Ile Ile
305
Gly Gly Gly Gly Thr Phe Lys Gln Val Leu Ile Asp Gly Gly Val Gly
325
Asn Thr Ile Ala Lys Met Phe Glu Gly Thr Glu Met Ser Pro Ile Leu
340
Leu Ala Trp Ile Val Ala Ala Val Leu Arg Ile Ala Leu Gly Ser Ala
355
Thr Val Ala Ala Ile Ser Thr Thr Gly Ile Val Leu Pro Leu Leu Gln
370
Ser Ser Asp Val Asn Val Ala Leu Val Val Leu Ala Ile Gly Ala Gly
385
Ser Val Ile Leu Ser His Val Asn Asp Ala Gly Phe Trp Met Phe Lys
405
Glu Tyr Phe Gly Leu Thr Val Lys Glu Thr Phe Leu Thr Trp Ser Leu
420
Leu Glu Thr Ile Ile Ser Val Ser Gly Ile Ile Phe Ile Leu Phe Ile
435
Ser Leu Phe Val
450

```

<210> 10162
 <211> 1338
 <212> DNA
 <213> Acinetobacter sp. ADP1

<220>
 <221> CDS
 <222> (1)..(1338)
 <223> transl_table=11

<400> 10162

PF59083SeqList PF59083.txt																
atg	ttg	ctt	att	tat	act	gta	gtc	gcg	att	gtt	gct	ttg	gtc	gtg	atg	48
Met	Leu	Leu	Ile	Tyr	Thr	Val	Val	Ala	Ile	Val	Ala	Leu	Val	Val	Met	
1				5					10					15		
atc	gcg	aag	ttt	aga	att	tat	cca	ttt	ctg	gtt	ctt	att	att	gtc	tcg	96
Ile	Ala	Lys	Phe	Arg	Ile	Tyr	Pro	Phe	Leu	Val	Leu	Ile	Ile	Val	Ser	
			20					25					30			
ctt	ggt	ttg	gct	tta	gct	gtt	ggg	atg	cca	atg	ggt	gat	atc	gtt	aaa	144
Leu	Gly	Leu	Ala	Leu	Ala	Val	Gly	Met	Pro	Met	Gly	Asp	Ile	Val	Lys	
		35					40					45				
tca	tac	gaa	gct	ggt	act	ggt	aaa	acc	ttg	ggc	cat	ctt	gca	att	gta	192
Ser	Tyr	Glu	Ala	Gly	Thr	Gly	Lys	Thr	Leu	Gly	His	Leu	Ala	Ile	Val	
	50					55					60					
att	gca	ctc	ggg	acc	atg	ctc	gga	aag	atg	atg	gca	gag	tcg	ggc	ggg	240
Ile	Ala	Leu	Gly	Thr	Met	Leu	Gly	Lys	Met	Met	Ala	Glu	Ser	Gly	Gly	
65					70					75					80	
gca	gaa	cg	att	gcg	att	acc	tta	att	caa	tg	ttt	gga	gag	aaa	aat	288
Ala	Glu	Arg	Ile	Ala	Ile	Thr	Leu	Ile	Gln	Trp	Phe	Gly	Glu	Lys	Asn	
			85						90					95		
atc	cat	tgg	gcc	atg	atg	ttt	att	ggt	ctt	gtg	gtt	ggg	tta	cct	gtg	336
Ile	His	Trp	Ala	Met	Met	Phe	Ile	Gly	Leu	Val	Val	Gly	Leu	Pro	Val	
			100					105					110			
ttt	ttt	gaa	gtg	ggt	ttt	gtg	ctg	ctc	att	cca	att	gta	ttt	aac	att	384
Phe	Phe	Glu	Val	Gly	Phe	Val	Leu	Leu	Ile	Pro	Ile	Val	Phe	Asn	Ile	
		115					120					125				
gct	aaa	cgt	aca	ggt	aag	tca	tta	atc	gtg	ggt	ttg	cca	atg	ctg		432
Ala	Lys	Arg	Thr	Gly	Lys	Ser	Leu	Leu	Ile	Val	Gly	Leu	Pro	Met	Leu	
	130					135					140					
gca	ggc	ttg	tcg	gta	gtg	cat	ggt	tta	att	ccg	ccc	cat	cca	gca	gcg	480
Ala	Gly	Leu	Ser	Val	Val	His	Gly	Leu	Ile	Pro	Pro	His	Pro	Ala	Ala	
145					150					155					160	
ctg	ctc	gct	gta	cag	gcc	tac	aat	gct	gat	att	gga	aca	acg	att	gcc	528
Leu	Leu	Ala	Val	Gln	Ala	Tyr	Asn	Ala	Asp	Ile	Gly	Thr	Thr	Ile	Ala	
			165					170						175		
tac	agc	ctc	ttg	gtg	ggg	gtg	cca	acc	gcc	gtt	gtt	gca	ggg	ccg	tta	576
Tyr	Ser	Leu	Leu	Val	Gly	Val	Pro	Thr	Ala	Val	Val	Ala	Gly	Pro	Leu	
			180				185						190			
tat	gca	ctc	tgg	atc	aat	aaa	tac	gtc	aaa	ttg	cct	gaa	aat	aat	cca	624
Tyr	Ala	Leu	Trp	Ile	Asn	Lys	Tyr	Val	Lys	Leu	Pro	Glu	Asn	Asn	Pro	
			195				200					205				
tta	gca	aag	cag	ttt	gtt	gaa	gat	aca	aac	aga	aat	cgt	gag	cta		672
Leu	Ala	Lys	Gln	Phe	Val	Glu	Ala	Asp	Thr	Asn	Arg	Asn	Arg	Glu	Leu	
	210					215					220					
ccc	agc	ttt	aga	att	act	tta	ttc	acg	atc	atg	ttg	cct	gtg	gtc	ttg	720
Pro	Ser	Phe	Arg	Ile	Thr	Leu	Phe	Thr	Ile	Met	Leu	Pro	Val	Val	Leu	
225					230					235					240	
atg	ttg	gtg	ggg	agc	tgg	gca	gat	tta	ttc	ttt	gca	ccc	caa	acc	ttt	768
Met	Leu	Val	Gly	Ser	Trp	Ala	Asp	Leu	Phe	Phe	Ala	Pro	Gln	Thr	Phe	
			245					250					255			
gcc	aat	gat	ttg	ctg	cgt	ttt	att	ggc	acc	tct	gat	atc	gcg	ttg	tta	816
Ala	Asn	Asp	Leu	Leu	Arg	Phe	Ile	Gly	Thr	Ser	Asp	Ile	Ala	Leu	Leu	
			260					265					270			
att	gca	gta	ctg	gtg	agc	ttt	gtt	acc	ttt	ggg	act	atg	caa	ggt	ttt	864
Ile	Ala	Val	Leu	Val	Ser	Phe	Val	Thr	Phe	Gly	Thr	Met	Gln	Gly	Phe	
		275					280					285				
acc	cgt	gta	caa	att	gaa	aaa	ttc	tgt	ggt	ggc	tgc	ttg	gct	tcg	att	912
Thr	Arg	Val	Gln	Ile	Glu	Lys	Phe	Cys	Gly	Gly	Cys	Leu	Ala	Ser	Ile	
	290					295					300					
gct	gga	atc	atg	ctg	att	gtg	ggt	gct	ggt	ggt	ggt	ttt	ggg	ggt	att	960
Ala	Gly	Ile	Met	Leu	Ile	Val	Gly	Ala	Gly	Gly	Gly	Phe	Gly	Gly	Ile	
305					310					315					320	
tta	cgt	gat	agc	ggt	att	tct	gat	gag	att	gtt	tct	aca	gcc	tta	aag	1008
Leu	Arg	Asp	Ser	Gly	Ile	Ser	Asp	Glu	Ile	Val	Ser	Thr	Ala	Leu	Lys	
			325					330					335			
gcc	aat	cta	tcg	ccg	tta	ttg	ctg	ggc	tgg	ttt	gtt	gca	gca	ttg	att	1056
Ala	Asn	Leu	Ser	Pro	Leu	Leu	Leu	Gly	Trp	Phe	Val	Ala	Ala	Leu	Ile	
			340					345					350			
cgt	ttg	gca	aca	ggt	tcg	gca	act	gtt	gcg	atg	gcc	aca	gcc	tgt	agt	1104
Arg	Leu	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	Met	Ala	Thr	Ala	Cys	Ser	
		355					360					365				

PF59083SeqList PF59083.txt

att	gtc	gca	ccg	att	gcg	gcg	aca	gcg	ggc	gtc	gtt	gtt	aga	cca	gaa	1152
Ile	Val	Ala	Pro	Ile	Ala	Ala	Thr	Ala	Gly	Val	Val	Val	Arg	Pro	Glu	
	370					375					380					
ctc	ttg	gta	ctt	gcc	aca	ggt	tca	ggc	tca	ctg	gtg	ttt	tcg	cat	gtc	1200
Leu	Leu	Val	Leu	Ala	Thr	Gly	Ser	Gly	Ser	Leu	Val	Phe	Ser	His	Val	
385					390					395					400	
aat	gat	gca	ggc	ttt	tgg	ctg	atc	aaa	gaa	tat	ttc	ggg	atg	acg	gtg	1248
Asn	Asp	Ala	Gly	Phe	Trp	Leu	Ile	Lys	Glu	Tyr	Phe	Gly	Met	Thr	Val	
				405				410						415		
gga	caa	aca	ctt	aaa	acc	tgg	tct	gta	ctg	gaa	acc	att	att	tcg	gtg	1296
Gly	Gln	Thr	Leu	Lys	Thr	Trp	Ser	Val	Leu	Glu	Thr	Ile	Ile	Ser	Val	
			420					425					430			
ctg	ggt	ttg	tct	ttt	acg	ctg	cta	ctg	agc	gct	atc	tta	taa			1338
Leu	Gly	Leu	Ser	Phe	Thr	Leu	Leu	Leu	Ser	Ala	Ile	Leu				
		435					440					445				

<210> 10163

<211> 445

<212> PRT

<213> Acinetobacter sp. ADP1

<400> 10163

Met	Leu	Leu	Ile	Tyr	Thr	Val	Val	Ala	Ile	Val	Ala	Leu	Val	Val	Met	
1			5						10					15		
Ile	Ala	Lys	Phe	Arg	Ile	Tyr	Pro	Phe	Leu	Val	Leu	Ile	Ile	Val	Ser	
			20					25					30			
Leu	Gly	Leu	Ala	Leu	Ala	Val	Gly	Met	Pro	Met	Gly	Asp	Ile	Val	Lys	
		35					40					45				
Ser	Tyr	Glu	Ala	Gly	Thr	Gly	Lys	Thr	Leu	Gly	His	Leu	Ala	Ile	Val	
	50					55					60					
Ile	Ala	Leu	Gly	Thr	Met	Leu	Gly	Lys	Met	Met	Ala	Glu	Ser	Gly	Gly	
65					70				75						80	
Ala	Glu	Arg	Ile	Ala	Ile	Thr	Leu	Ile	Gln	Trp	Phe	Gly	Glu	Lys	Asn	
				85					90					95		
Ile	His	Trp	Ala	Met	Met	Phe	Ile	Gly	Leu	Val	Val	Gly	Leu	Pro	Val	
			100					105					110			
Phe	Phe	Glu	Val	Gly	Phe	Val	Leu	Leu	Ile	Pro	Ile	Val	Phe	Asn	Ile	
		115					120					125				
Ala	Lys	Arg	Thr	Gly	Lys	Ser	Leu	Leu	Ile	Val	Gly	Leu	Pro	Met	Leu	
	130					135					140					
Ala	Gly	Leu	Ser	Val	Val	His	Gly	Leu	Ile	Pro	Pro	His	Pro	Ala	Ala	
145					150				155						160	
Leu	Leu	Ala	Val	Gln	Ala	Tyr	Asn	Ala	Asp	Ile	Gly	Thr	Thr	Ile	Ala	
				165					170					175		
Tyr	Ser	Leu	Leu	Val	Gly	Val	Pro	Thr	Ala	Val	Val	Ala	Gly	Pro	Leu	
			180					185					190			
Tyr	Ala	Leu	Trp	Ile	Asn	Lys	Tyr	Val	Lys	Leu	Pro	Glu	Asn	Asn	Pro	
		195					200					205				
Leu	Ala	Lys	Gln	Phe	Val	Glu	Ala	Asp	Thr	Asn	Arg	Asn	Arg	Glu	Leu	
	210					215					220					
Pro	Ser	Phe	Arg	Ile	Thr	Leu	Phe	Thr	Ile	Met	Leu	Pro	Val	Val	Leu	
225					230				235						240	
Met	Leu	Val	Gly	Ser	Trp	Ala	Asp	Leu	Phe	Phe	Ala	Pro	Gln	Thr	Phe	
				245				250						255		
Ala	Asn	Asp	Leu	Arg	Phe	Ile	Gly	Thr	Ser	Asp	Ile	Ala	Leu	Leu		
			260				265					270				
Ile	Ala	Val	Leu	Val	Ser	Phe	Val	Thr	Phe	Gly	Thr	Met	Gln	Gly	Phe	
		275					280					285				
Thr	Arg	Val	Gln	Ile	Glu	Lys	Phe	Cys	Gly	Gly	Cys	Leu	Ala	Ser	Ile	
	290					295					300					
Ala	Gly	Ile	Met	Leu	Ile	Val	Gly	Ala	Gly	Gly	Gly	Phe	Gly	Gly	Ile	
305					310				315						320	
Leu	Arg	Asp	Ser	Gly	Ile	Ser	Asp	Glu	Ile	Val	Ser	Thr	Ala	Leu	Lys	
				325				330						335		
Ala	Asn	Leu	Ser	Pro	Leu	Leu	Leu	Gly	Trp	Phe	Val	Ala	Ala	Leu	Ile	
			340					345				350				
Arg	Leu	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	Met	Ala	Thr	Ala	Cys	Ser	
		355					360					365				
Ile	Val	Ala	Pro	Ile	Ala	Ala	Thr	Ala	Gly	Val	Val	Arg	Pro	Glu		

PF59083SeqList PF59083.txt

370 375 380
 Leu Leu Val Leu Ala Thr Gly Ser Gly Ser Leu Val Phe Ser His Val
 385 390 395 400
 Asn Asp Ala Gly Phe Trp Leu Ile Lys Glu Tyr Phe Gly Met Thr Val
 405 410 415
 Gly Gln Thr Leu Lys Thr Trp Ser Val Leu Glu Thr Ile Ile Ser Val
 420 425 430
 Leu Gly Leu Ser Phe Thr Leu Leu Leu Ser Ala Ile Leu
 435 440 445

<210> 10164
 <211> 1335
 <212> DNA
 <213> Erwinia carotovora subsp. atroseptica SCRI1043

<220>
 <221> CDS
 <222> (1)..(1335)
 <223> transl_table=11

<400> 10164
 atg cca tta atc atc gta gca att ggg gtt gcc ctg ctg ctg ctg ctg 48
 Met Pro Leu Ile Ile Val Ala Ile Gly Val Ala Leu Leu Leu Leu Leu
 1 5 10 15
 atg atc cgt tgt aaa ttg aac ggg ttc att tca ttg att ctg gtg tcg 96
 Met Ile Arg Cys Lys Leu Asn Gly Phe Ile Ser Leu Ile Leu Val Ser
 20 25 30
 ctg gcc gtc ggc ttg gcg ttg ggt tac acc act cag ggg gga ttt aac 144
 Leu Ala Val Gly Leu Ala Leu Gly Tyr Thr Thr Gln Gly Gly Phe Asn
 35 40 45
 gtc aat ggc gtg atc act tct atc aaa aat ggg gtt ggc ggc acg ctg 192
 Val Asn Gly Val Ile Thr Ser Ile Lys Asn Gly Val Gly Gly Thr Leu
 50 55 60
 ggc agc ctg gcc ctg atc atg ggg ttt ggc gcc atg ttg ggc aaa ctg 240
 Gly Ser Leu Ala Leu Ile Met Gly Phe Gly Ala Met Leu Gly Lys Leu
 65 70 75 80
 cta gca gat tgc ggc ggc gcc cag cgt att gcg acg acg ctt atc gat 288
 Leu Ala Asp Cys Gly Gly Ala Gln Arg Ile Ala Thr Thr Leu Ile Asp
 85 90 95
 aaa ttt ggt aag gac cgt atc cag tgg gca gtg gtc tta acc ggt ttt 336
 Lys Phe Gly Lys Asp Arg Ile Gln Trp Ala Val Val Leu Thr Gly Phe
 100 105 110
 act gtc ggt ttt gcg ctg ttt tat gaa gtt ggt ttt gtg ttg ctg ctg 384
 Thr Val Gly Phe Ala Leu Phe Tyr Glu Val Gly Phe Val Leu Leu Leu
 115 120 125
 ccg ctg gtg ttt acc att gct gcc gca gcg caa att cca ttg ctg ttt 432
 Pro Leu Val Phe Thr Ile Ala Ala Ala Ala Gln Ile Pro Leu Leu Phe
 130 135 140
 atc ggt gtg ccg atg gct gcc gcg tta tcg gta acc cat gcg ttg ttg 480
 Ile Gly Val Pro Met Ala Ala Leu Ser Val Thr His Ala Leu Leu
 145 150 155 160
 cct ccg cat ccg ggc ccg acc gct atc gct att ctg ttc aaa gcc gat 528
 Pro Pro His Pro Gly Pro Thr Ala Ile Ala Ile Leu Phe Lys Ala Asp
 165 170 175
 atg ggt aaa acc ctg ctt tac gga acc ttg att gct atc cct act gtg 576
 Met Gly Lys Thr Leu Leu Tyr Gly Thr Leu Ile Ala Ile Pro Thr Val
 180 185 190
 att ttg gcg ggg ccg gtc tat gcg cgt ttc ctg aaa agt atc gat aaa 624
 Ile Leu Ala Gly Pro Val Tyr Ala Arg Phe Leu Lys Ser Ile Asp Lys
 195 200 205
 cct att cct gct gga ttg cac aat cca aaa gtg ttt gcc gac cat gag 672
 Pro Ile Pro Ala Gly Leu His Asn Pro Lys Val Phe Ala Asp His Glu
 210 215 220
 atg ccg agc ttt ggt atc agc gta ttc act acc ctg att ccg gtt att 720
 Met Pro Ser Phe Gly Ile Ser Val Phe Thr Thr Leu Ile Pro Val Ile
 225 230 235 240
 ctg atg acg ggc cgt gca gtg gca gaa atg acg ctg caa aaa ggc cac 768
 Leu Met Thr Gly Arg Ala Val Ala Glu Met Thr Leu Gln Lys Gly His
 245 250 255

PF59083SeqList PF59083.txt

ccg	gtg	ctg	ggt	tac	gcg	gag	ttt	ttg	ggc	gac	ccg	ggt	atg	gcg	acc	816
Pro	Val	Leu	Gly	Tyr	Ala	Glu	Phe	Leu	Gly	Asp	Pro	Val	Met	Ala	Thr	
			260				265						270			
ctg	att	tcc	ggt	atc	gtg	gcg	atc	ttt	acc	ttc	ggg	ctt	aat	cg	ggt	864
Leu	Ile	Ser	Val	Ile	Val	Ala	Ile	Phe	Thr	Phe	Gly	Leu	Asn	Arg	Gly	
		275					280						285			
cgt	agc	atg	gat	cag	gta	atg	gat	acc	gtt	agc	gat	tcc	atc	aag	atc	912
Arg	Ser	Met	Asp	Gln	Val	Met	Asp	Thr	Val	Ser	Asp	Ser	Ile	Lys	Ile	
	290					295					300					
atc	gcc	atg	atg	ttg	atg	gtt	atc	ggg	ggc	ggc	ggt	gcg	ttc	aaa	caa	960
Ile	Ala	Met	Met	Leu	Met	Val	Ile	Gly	Gly	Gly	Gly	Ala	Phe	Lys	Gln	
	305				310				315						320	
att	ctg	gtg	gac	ggg	ggc	gtt	gcg	aag	tat	atc	gaa	acg	ctg	atg	gcg	1008
Ile	Leu	Val	Asp	Gly	Gly	Val	Ala	Lys	Tyr	Ile	Glu	Thr	Leu	Met	Ala	
			325						330					335		
ggc	agt	acg	ctg	tcg	ccg	tta	ctg	atg	gga	tgg	gcg	att	gcc	gcg	gca	1056
Gly	Ser	Thr	Leu	Ser	Pro	Leu	Leu	Met	Gly	Trp	Ala	Ile	Ala	Ala	Ala	
			340					345					350			
ttg	cgt	ctg	gct	ctg	ggc	tca	gcg	acc	gtt	gcg	gcc	atg	acc	gca	ggc	1104
Leu	Arg	Leu	Ala	Leu	Gly	Ser	Ala	Thr	Val	Ala	Ala	Met	Thr	Ala	Gly	
		355				360							365			
ggg	att	gtt	gcg	ccg	ttg	ctg	acc	atc	act	ggg	gtg	agt	cct	gag	ctg	1152
Gly	Ile	Val	Ala	Pro	Leu	Leu	Thr	Ile	Thr	Gly	Val	Ser	Pro	Glu	Leu	
	370				375						380					
atg	gtg	ctg	gct	gtg	ggg	tcc	ggc	agc	gtg	att	ttc	tct	cac	gtg	aac	1200
Met	Val	Leu	Ala	Val	Gly	Ser	Gly	Ser	Val	Ile	Phe	Ser	His	Val	Asn	
	385				390					395					400	
gat	ccg	ggt	ttc	tgg	ctg	ttt	aaa	gag	tat	ttc	aac	ctg	act	att	gtc	1248
Asp	Pro	Gly	Phe	Trp	Leu	Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Thr	Ile	Val	
			405						410					415		
gaa	acc	atg	aag	tcc	tgg	tct	gcg	ttg	gaa	acc	att	att	gcg	gtg	tgt	1296
Glu	Thr	Met	Lys	Ser	Trp	Ser	Ala	Leu	Glu	Thr	Ile	Ile	Ala	Val	Cys	
		420						425					430			
ggc	ctg	att	ggc	tgt	ctg	ctg	ctg	aat	atg	gtg	att	taa				1335
Gly	Leu	Ile	Gly	Cys	Leu	Leu	Leu	Asn	Met	Val	Ile					
		435					440									

<210> 10165

<211> 444

<212> PRT

<213> Erwinia carotovora subsp. atroseptica SCRI1043

<400> 10165

Met	Pro	Leu	Ile	Ile	Val	Ala	Ile	Gly	Val	Ala	Leu	Leu	Leu	Leu	Leu	
1				5					10					15		
Met	Ile	Arg	Cys	Lys	Leu	Asn	Gly	Phe	Ile	Ser	Leu	Ile	Leu	Val	Ser	
			20					25					30			
Leu	Ala	Val	Gly	Leu	Ala	Leu	Gly	Tyr	Thr	Thr	Gln	Gly	Gly	Phe	Asn	
		35					40					45				
Val	Asn	Gly	Val	Ile	Thr	Ser	Ile	Lys	Asn	Gly	Val	Gly	Gly	Thr	Leu	
	50					55					60					
Gly	Ser	Leu	Ala	Leu	Ile	Met	Gly	Phe	Gly	Ala	Met	Leu	Gly	Lys	Leu	
	65				70				75					80		
Leu	Ala	Asp	Cys	Gly	Ala	Gln	Arg	Ile	Ala	Thr	Thr	Leu	Ile	Asp		
			85					90					95			
Lys	Phe	Gly	Lys	Asp	Arg	Ile	Gln	Trp	Ala	Val	Val	Leu	Thr	Gly	Phe	
			100					105					110			
Thr	Val	Gly	Phe	Ala	Leu	Phe	Tyr	Glu	Val	Gly	Phe	Val	Leu	Leu	Leu	
		115					120					125				
Pro	Leu	Val	Phe	Thr	Ile	Ala	Ala	Ala	Gln	Ile	Pro	Leu	Leu	Phe		
	130					135										
Ile	Gly	Val	Pro	Met	Ala	Ala	Ala	Leu	Ser	Val	Thr	His	Ala	Leu	Leu	
	145				150				155					160		
Pro	Pro	His	Pro	Gly	Pro	Thr	Ala	Ile	Ala	Ile	Leu	Phe	Lys	Ala	Asp	
			165					170						175		
Met	Gly	Lys	Thr	Leu	Leu	Tyr	Gly	Thr	Leu	Ile	Ala	Ile	Pro	Thr	Val	
			180					185					190			
Ile	Leu	Ala	Gly	Pro	Val	Tyr	Ala	Arg	Phe	Leu	Lys	Ser	Ile	Asp	Lys	
		195					200						205			

PF59083SeqList PF59083.txt

```

Pro Ile Pro Ala Gly Leu His Asn Pro Lys Val Phe Ala Asp His Glu
210 215 220
Met Pro Ser Phe Gly Ile Ser Val Phe Thr Thr Leu Ile Pro Val Ile
225 230 235 240
Leu Met Thr Gly Arg Ala Val Ala Glu Met Thr Leu Gln Lys Gly His
245 250 255
Pro Val Leu Gly Tyr Ala Glu Phe Leu Gly Asp Pro Val Met Ala Thr
260 265 270
Leu Ile Ser Val Ile Val Ala Ile Phe Thr Phe Gly Leu Asn Arg Gly
275 280 285
Arg Ser Met Asp Gln Val Met Asp Thr Val Ser Asp Ser Ile Lys Ile
290 295 300
Ile Ala Met Met Leu Met Val Ile Gly Gly Gly Gly Ala Phe Lys Gln
305 310 315 320
Ile Leu Val Asp Gly Gly Val Ala Lys Tyr Ile Glu Thr Leu Met Ala
325 330 335
Gly Ser Thr Leu Ser Pro Leu Leu Met Gly Trp Ala Ile Ala Ala Ala
340 345 350
Leu Arg Leu Ala Leu Gly Ser Ala Thr Val Ala Ala Met Thr Ala Gly
355 360 365
Gly Ile Val Ala Pro Leu Leu Thr Ile Thr Gly Val Ser Pro Glu Leu
370 375 380
Met Val Leu Ala Val Gly Ser Gly Ser Val Ile Phe Ser His Val Asn
385 390 395 400
Asp Pro Gly Phe Trp Leu Phe Lys Glu Tyr Phe Asn Leu Thr Ile Val
405 410 415
Glu Thr Met Lys Ser Trp Ser Ala Leu Glu Thr Ile Ile Ala Val Cys
420 425 430
Gly Leu Ile Gly Cys Leu Leu Leu Asn Met Val Ile
435 440

```

<210> 10166

<211> 1371

<212> DNA

<213> Propionibacterium acnes KPA171202

<220>

<221> CDS

<222> (1)..(1371)

<223> transl_table=11

<400> 10166

```

atg ccc gtc atc ctc gaa acc gca gcc agt acc ggc caa ctg att atg      48
Met Pro Val Ile Leu Glu Thr Ala Ala Ser Thr Gly Gln Leu Ile Met
1 5 10 15
gcc acc ctc atc ggc ttc gcc acc atc gtt gcc ctt ata acc aag ttc      96
Ala Thr Leu Ile Gly Phe Ala Thr Ile Val Ala Leu Ile Thr Lys Phe
20 25 30
aaa ctc cac ccc ttc ctc tcc ttg acg atc ggt tct tta gtt gtc gga      144
Lys Leu His Pro Phe Leu Ser Leu Thr Ile Gly Ser Leu Val Val Gly
35 40 45
gct atc gca aag ctg tcc ctg tcg gag ata ttg gcg tcc tat tcc aaa      192
Ala Ile Ala Lys Leu Ser Leu Ser Glu Ile Leu Ala Ser Tyr Ser Lys
50 55 60
gga gtc ggg tcg acg gtc gct tct gtc gga gtc ctc atc gcc cta gga      240
Gly Val Gly Ser Thr Val Ala Ser Val Gly Val Leu Ile Ala Leu Gly
65 70 75 80
gcg att atc ggc aag ttg tta gca gat tcc ggt ggc gcc gac gaa atc      288
Ala Ile Ile Gly Lys Leu Leu Ala Asp Ser Gly Gly Ala Asp Glu Ile
85 90 95
gtc gac acc cta gtc tct cag gct tct ccc gcc acc ttg cca tgg gcg      336
Val Asp Thr Leu Val Ser Gln Ala Ser Pro Ala Thr Leu Pro Trp Ala
100 105 110
atg gcc ctc att ggc gct gtc att gga ctg ccc atg ttc ttc gag atc      384
Met Ala Leu Ile Gly Ala Val Ile Gly Leu Pro Met Phe Phe Glu Ile
115 120 125
ggg ctc gtc ctg ctc gtt ccg gtc atc ctg ctg gta acc cgc cgt tcc      432
Gly Leu Val Leu Leu Val Pro Val Ile Leu Leu Val Thr Arg Arg Ser
130 135 140

```

PF59083SeqList PF59083.txt

aag	ctg	ccc	ctc	atg	aga	gta	gct	atc	ccg	gcc	ctg	gct	ggc	cta	tcg	480
Lys	Leu	Pro	Leu	Met	Arg	Val	Ala	Ile	Pro	Ala	Leu	Ala	Gly	Leu	Ser	145
acg	atg	cat	gcc	ctt	gtt	cca	cct	cat	ccg	ggc	cca	ttg	gcc	gcc	att	528
Thr	Met	His	Ala	Val	Val	Pro	Pro	His	Pro	Gly	Pro	Leu	Ala	Ala	Ile	155
ggg	ctg	ctc	aaa	gca	gac	ctc	ggc	atc	acc	ctc	ggg	ttc	ggt	gtc	ctt	576
Gly	Leu	Leu	Lys	Ala	Asp	Leu	Gly	Ile	Thr	Leu	Gly	Phe	Gly	Val	Leu	165
att	gcc	ata	ccg	acg	gtt	att	gct	gct	ggc	ccg	ctg	ttc	tcg	cgg	ctc	180
Ile	Ala	Ile	Pro	Thr	Val	Ile	Ala	Ala	Gly	Pro	Leu	Phe	Ser	Arg	Leu	185
gca	gct	cgg	tgg	gtg	ccc	gtt	gat	gcg	cct	gac	ctc	ttc	ctt	aat	tct	624
Ala	Ala	Arg	Trp	Val	Pro	Val	Asp	Ala	Pro	Asp	Leu	Phe	Leu	Asn	Ser	195
gac	gag	aat	ggc	cgt	tgc	ggt	att	gcc	cct	ggt	cgc	cca	agg	ttc	tcc	200
Asp	Glu	Asn	Gly	Arg	Cys	Gly	Ile	Ala	Pro	Gly	Arg	Pro	Arg	Phe	Ser	210
gtc	acc	ttg	atg	acc	gtc	ctg	cta	cct	gtc	gtc	ctc	atg	atg	ggc	aag	225
Val	Thr	Leu	Met	Thr	Val	Leu	Leu	Pro	Val	Val	Leu	Met	Met	Gly	Lys	230
gcc	ctc	gcc	gat	atc	ttc	gct	ctc	aaa	ggc	acc	gcc	gtc	cgc	agt	atc	768
Ala	Leu	Ala	Asp	Ile	Phe	Ala	Leu	Lys	Gly	Thr	Ala	Val	Arg	Ser	Ile	245
ttg	gat	ttc	ctt	ggc	gag	ccg	atg	ttt	gct	ttg	ctg	ctg	aca	acc	ctg	260
Leu	Asp	Phe	Leu	Gly	Glu	Pro	Met	Phe	Ala	Leu	Leu	Leu	Thr	Thr	Leu	265
ctg	gcg	atc	ttt	acc	ctg	ggc	aag	gct	tcc	ggc	atc	aac	cgg	gac	gct	816
Leu	Ala	Ile	Phe	Thr	Leu	Gly	Lys	Ala	Ser	Gly	Ile	Asn	Arg	Asp	Ala	270
atg	aac	aac	agt	gtg	ggg	gca	gcg	ctg	ccc	cca	atc	gct	ggc	atc	tta	864
Met	Asn	Asn	Ser	Val	Gly	Ala	Ala	Leu	Pro	Pro	Ile	Ala	Gly	Ile	Leu	285
ctc	atc	gtc	gcc	gcc	ggc	ggt	ggg	ttt	aag	cag	atc	ctc	gtc	gac	act	912
Leu	Ile	Val	Ala	Ala	Gly	Gly	Gly	Phe	Lys	Gln	Ile	Leu	Val	Asp	Thr	300
ggt	att	gcc	aag	cta	cta	ggc	aac	ggc	att	acc	cag	tcc	tcg	atc	tcc	960
Gly	Ile	Ala	Lys	Leu	Leu	Gly	Asn	Gly	Ile	Thr	Gln	Ser	Ser	Ile	Ser	310
ccg	cta	ctg	atg	gcc	tgg	ctc	gtc	gct	gtc	gtc	atc	cgg	ttg	gcg	acc	1008
Pro	Leu	Leu	Met	Ala	Trp	Leu	Val	Ala	Val	Val	Ile	Arg	Leu	Ala	Thr	315
ggc	tca	gcg	acg	gtg	gca	acc	gtc	acc	gcg	gcc	ggc	atc	ctg	gaa	ccg	1056
Gly	Ser	Ala	Thr	Val	Ala	Thr	Val	Thr	Ala	Ala	Gly	Ile	Leu	Glu	Pro	340
gtg	gca	gcc	agc	ttg	ccg	ccc	gcc	cat	gcg	gca	ttg	ctg	gtt	cta	gcg	1104
Val	Ala	Ala	Ser	Leu	Pro	Pro	Ala	His	Ala	Ala	Leu	Leu	Val	Leu	Ala	350
atc	ggc	tgc	ggt	tcg	gtt	ttc	ttc	tca	cac	gtc	aat	gac	gcc	ggt	ttc	1152
Ile	Gly	Cys	Gly	Ser	Val	Phe	Phe	Ser	His	Val	Asn	Asp	Ala	Gly	Phe	365
tgg	ctc	atc	aag	gaa	tac	ttc	ggt	atc	tcg	gtg	gga	caa	acc	att	aag	1200
Trp	Leu	Ile	Lys	Glu	Tyr	Phe	Gly	Ile	Ser	Val	Gly	Gln	Thr	Ile	Lys	370
agt	tgg	tcg	ctc	atg	gag	acg	gcg	ctg	tca	gtc	tgc	gga	gtg	ctc	ctg	1248
Ser	Trp	Ser	Leu	Met	Glu	Thr	Ala	Leu	Ser	Val	Cys	Gly	Val	Leu	Leu	380
gtg	ctg	ctg	gtc	tcc	gtc	atc	gtc	tga								1296
Val	Leu	Leu	Val	Ser	Val	Ile	Val									400

<210> 10167

<211> 456

<212> PRT

<213> Propionibacterium acnes KPA171202

<400> 10167

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

PF59083SeqList PF59083.txt

Ala Thr Leu Ile Gly Phe Ala Thr Ile Val Ala Leu Ile Thr Lys Phe
 20 25 30
 Lys Leu His Pro Phe Leu Ser Leu Thr Ile Gly Ser Leu Val Val Gly
 35 40 45
 Ala Ile Ala Lys Leu Ser Leu Ser Glu Ile Leu Ala Ser Tyr Ser Lys
 50 55 60
 Gly Val Gly Ser Thr Val Ala Ser Val Gly Val Leu Ile Ala Leu Gly
 65 70 75 80
 Ala Ile Ile Gly Lys Leu Leu Ala Asp Ser Gly Gly Ala Asp Glu Ile
 85 90 95
 Val Asp Thr Leu Val Ser Gln Ala Ser Pro Ala Thr Leu Pro Trp Ala
 100 105 110
 Met Ala Leu Ile Gly Ala Val Ile Gly Leu Pro Met Phe Phe Glu Ile
 115 120 125
 Gly Leu Val Leu Leu Val Pro Val Ile Leu Leu Val Thr Arg Arg Ser
 130 135 140
 Lys Leu Pro Leu Met Arg Val Ala Ile Pro Ala Leu Ala Gly Leu Ser
 145 150 155 160
 Thr Met His Ala Leu Val Pro Pro His Pro Gly Pro Leu Ala Ala Ile
 165 170 175
 Gly Leu Leu Lys Ala Asp Leu Gly Ile Thr Leu Gly Phe Gly Val Leu
 180 185 190
 Ile Ala Ile Pro Thr Val Ile Ala Ala Gly Pro Leu Phe Ser Arg Leu
 195 200 205
 Ala Ala Arg Trp Val Pro Val Asp Ala Pro Asp Leu Phe Leu Asn Ser
 210 215 220
 Asp Glu Asn Gly Arg Cys Gly Ile Ala Pro Gly Arg Pro Arg Phe Ser
 225 230 235 240
 Val Thr Leu Met Thr Val Leu Leu Pro Val Val Leu Met Met Gly Lys
 245 250 255
 Ala Leu Ala Asp Ile Phe Ala Leu Lys Gly Thr Ala Val Arg Ser Ile
 260 265 270
 Leu Asp Phe Leu Gly Glu Pro Met Phe Ala Leu Leu Leu Thr Thr Leu
 275 280 285
 Leu Ala Ile Phe Thr Leu Gly Lys Ala Ser Gly Ile Asn Arg Asp Ala
 290 295 300
 Met Asn Asn Ser Val Gly Ala Ala Leu Pro Pro Ile Ala Gly Ile Leu
 305 310 315 320
 Leu Ile Val Ala Ala Gly Gly Gly Phe Lys Gln Ile Leu Val Asp Thr
 325 330 335
 Gly Ile Ala Lys Leu Leu Gly Asn Gly Ile Thr Gln Ser Ser Ile Ser
 340 345 350
 Pro Leu Leu Met Ala Trp Leu Val Ala Val Val Ile Arg Leu Ala Thr
 355 360 365
 Gly Ser Ala Thr Val Ala Thr Val Thr Ala Ala Gly Ile Leu Glu Pro
 370 375 380
 Val Ala Ala Ser Leu Pro Pro Ala His Ala Ala Leu Leu Val Leu Ala
 385 390 395 400
 Ile Gly Cys Gly Ser Val Phe Phe Ser His Val Asn Asp Ala Gly Phe
 405 410 415
 Trp Leu Ile Lys Glu Tyr Phe Gly Ile Ser Val Gly Gln Thr Ile Lys
 420 425 430
 Ser Trp Ser Leu Met Glu Thr Ala Leu Ser Val Cys Gly Val Leu Leu
 435 440 445
 Val Leu Leu Val Ser Val Ile Val
 450 455

<210> 10168

<211> 1317

<212> DNA

<213> Yersinia pseudotuberculosis IP 32953

<220>

<221> CDS

<222> (1)..(1317)

<223> transl_table=11

<400> 10168

atg cca tta atc atc gtc gcg gtt ggc gtt gcc atg ctg cta tta ctg
 Seite 10760

PF59083SeqList PF59083.txt

Met	Pro	Leu	Ile	Ile	Val	Ala	Val	Gly	Val	Ala	Met	Leu	Leu	Leu	Leu	
1				5					10					15		
atg	atc	cgt	tac	aaa	ctt	aac	gga	ttt	atc	tcg	ctg	ata	ctg	gtc	gcg	96
Met	Ile	Arg	Tyr	Lys	Leu	Asn	Gly	Phe	Ile	Ser	Leu	Ile	Leu	Val	Ala	
			20					25					30			
tta	gcg	gta	ggg	atc	atg	caa	ggg	atg	cca	atc	gat	aaa	ggt	gtc	ggc	144
Leu	Ala	Val	Gly	Ile	Met	Gln	Gly	Met	Pro	Ile	Asp	Lys	Val	Val	Gly	
		35					40					45				
tcg	atc	aaa	gcg	ggg	gtc	ggc	gga	aca	tta	ggg	agc	ctg	gcc	ttg	att	192
Ser	Ile	Lys	Ala	Gly	Val	Gly	Gly	Thr	Leu	Gly	Ser	Leu	Ala	Leu	Ile	
		50				55					60					
atg	ggc	ttc	ggg	gcc	atg	ctc	ggg	aaa	ttg	ctg	gcc	gat	tgt	ggc	ggc	240
Met	Gly	Phe	Gly	Ala	Met	Leu	Gly	Lys	Leu	Leu	Ala	Asp	Cys	Gly	Gly	
65				70				75						80		
gct	caa	cgt	atc	gcg	acc	acc	tta	att	gag	aag	ttt	ggg	caa	aaa	cat	288
Ala	Gln	Arg	Ile	Ala	Thr	Thr	Leu	Ile	Glu	Lys	Phe	Gly	Gln	Lys	His	
			85					90						95		
att	caa	tgg	gct	gtg	gta	ctg	acc	ggc	ttt	act	gtg	ggg	ttt	gcc	ctg	336
Ile	Gln	Trp	Ala	Val	Val	Leu	Thr	Gly	Phe	Thr	Val	Gly	Phe	Ala	Leu	
			100					105					110			
ttt	tat	gaa	gtg	ggg	ttt	gtg	ctg	tta	ttg	ccg	ctg	gta	ttc	agc	att	384
Phe	Tyr	Glu	Val	Gly	Phe	Val	Leu	Leu	Leu	Pro	Leu	Val	Phe	Ser	Ile	
		115					120					125				
gcg	gcc	tct	gcc	cgc	att	ccc	ttg	cta	tat	gtg	ggg	ggt	ccc	atg	gcg	432
Ala	Ala	Ser	Ala	Arg	Ile	Pro	Leu	Leu	Tyr	Val	Gly	Val	Pro	Met	Ala	
		130				135					140					
gcg	gcg	ctt	tct	gtc	act	cat	ggg	ttt	ctg	cca	cct	cac	cca	ggc	ccg	480
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
145				150				155						160		
aca	gcc	att	gcc	acc	att	ttc	agc	gcc	gat	atg	ggc	aaa	acg	ctg	ctg	528
Thr	Ala	Ile	Ala	Thr	Ile	Phe	Ser	Ala	Asp	Met	Gly	Lys	Thr	Leu	Leu	
			165					170						175		
tac	ggc	aca	ttg	ctg	gca	atc	cca	acc	gtg	att	ttg	gca	ggc	ccg	gtc	576
Tyr	Gly	Thr	Leu	Leu	Ala	Ile	Pro	Thr	Val	Ile	Leu	Ala	Gly	Pro	Val	
			180					185					190			
tac	gct	cgc	ttt	cta	aaa	gga	att	gat	aag	cct	ggt	cct	gaa	ggg	ctg	624
Tyr	Ala	Arg	Phe	Leu	Lys	Gly	Ile	Asp	Lys	Pro	Val	Pro	Glu	Gly	Leu	
		195					200					205				
tat	aac	ccg	aaa	atc	ttt	acc	gat	aaa	gag	atg	cca	agc	ttt	gga	gtc	672
Tyr	Asn	Pro	Lys	Ile	Phe	Thr	Asp	Lys	Glu	Met	Pro	Ser	Phe	Gly	Val	
		210				215					220					
agt	gtc	agt	acg	gcg	ctg	gta	ccg	ggt	att	ttg	atg	gca	ttg	cgg	gcc	720
Ser	Val	Ser	Thr	Ala	Leu	Val	Pro	Val	Ile	Leu	Met	Ala	Leu	Arg	Ala	
225				230				235						240		
gta	gca	gag	atg	att	ttg	cct	aaa	ggc	cat	tcg	ctg	ctc	ccc	tat	gcc	768
Val	Ala	Glu	Met	Ile	Leu	Pro	Lys	Gly	His	Ser	Leu	Leu	Pro	Tyr	Ala	
			245					250						255		
gag	ttc	ttt	ggg	gat	cca	gta	att	gct	acg	ctg	att	gcc	gtg	tta	att	816
Glu	Phe	Phe	Gly	Asp	Pro	Val	Ile	Ala	Thr	Leu	Ile	Ala	Val	Leu	Ile	
			260					265					270			
gca	att	ttc	acc	ttt	ggg	cta	aac	cgg	ggc	cgc	tca	gtg	gaa	tcg	gtc	864
Ala	Ile	Phe	Thr	Phe	Gly	Leu	Asn	Arg	Gly	Arg	Ser	Val	Glu	Ser	Val	
			275			280						285				
atg	gag	acc	ctg	tct	gat	tcc	atc	aag	atc	atc	gca	atg	atg	ctg	tta	912
Met	Glu	Thr	Leu	Ser	Asp	Ser	Ile	Lys	Ile	Ile	Ala	Met	Met	Leu	Leu	
		290			295						300					
gtt	att	gga	ggc	ggc	ggg	gct	ttc	aag	cag	gtt	tta	gtc	gat	agc	ggc	960
Val	Ile	Gly	Gly	Gly	Gly	Ala	Phe	Lys	Gln	Val	Leu	Val	Asp	Ser	Gly	
305				310						315					320	
ata	gag	caa	tat	att	gct	ggc	atg	atg	ggc	aat	agc	ggg	gca	tcg	cct	1008
Ile	Glu	Gln	Tyr	Ile	Ala	Gly	Met	Met	Gly	Asn	Ser	Gly	Ala	Ser	Pro	
			325					330						335		
att	ctg	atg	gca	tgg	tcc	atc	gcc	gcc	tta	ctg	cgt	atc	gcc	ctg	ggg	1056
Ile	Leu	Met	Ala	Trp	Ser	Ile	Ala	Ala	Leu	Leu	Arg	Ile	Ala	Leu	Gly	
			340				345						350			
tct	gcg	acg	gta	gca	gcg	atc	acc	gct	ggg	ggc	att	gtc	gca	ccg	tta	1104
Ser	Ala	Thr	Val	Ala	Ala	Ile	Thr	Ala	Gly	Gly	Ile	Val	Ala	Pro	Leu	
		355					360					365				
atc	gcg	acc	acc	ggg	gcc	agc	cct	gag	ttg	atg	gtc	att	gcc	gtt	ggg	1152

Seite 10761

PF59083SeqList PF59083.txt

Ile	Ala	Thr	Thr	Gly	Ala	Ser	Pro	Glu	Leu	Met	Val	Ile	Ala	Val	Gly	
370						375					380					
tcc	ggt	agc	gtg	atc	ttc	tct	cac	gtg	aat	gac	cct	ggt	ttc	tgg	cta	1200
Ser	Gly	Ser	Val	Ile	Phe	Ser	His	Val	Asn	Asp	Pro	Gly	Phe	Trp	Leu	
385					390					395					400	
ttc	aag	gag	tat	ttc	aac	cta	acc	att	atg	gaa	acc	att	aaa	tcg	tgg	1248
Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Thr	Ile	Met	Glu	Thr	Ile	Lys	Ser	Trp	
				405					410					415		
tca	gta	ctg	gaa	acc	att	att	tca	gtc	tgc	ggg	ttg	atc	ggc	tgt	ttg	1296
Ser	Val	Leu	Glu	Thr	Ile	Ile	Ser	Val	Cys	Gly	Leu	Ile	Gly	Cys	Leu	
			420					425					430			
ttg	ctg	tct	ctg	ggt	att	tag										1317
Leu	Leu	Ser	Leu	Val	Ile											
		435														

<210> 10169

<211> 438

<212> PRT

<213> *Yersinia pseudotuberculosis* IP 32953

<400> 10169

Met	Pro	Leu	Ile	Ile	Val	Ala	Val	Gly	Val	Ala	Met	Leu	Leu	Leu	Leu	
1				5					10					15		
Met	Ile	Arg	Tyr	Lys	Leu	Asn	Gly	Phe	Ile	Ser	Leu	Ile	Leu	Val	Ala	
			20					25					30			
Leu	Ala	Val	Gly	Ile	Met	Gln	Gly	Met	Pro	Ile	Asp	Lys	Val	Val	Gly	
		35					40					45				
Ser	Ile	Lys	Ala	Gly	Val	Gly	Gly	Thr	Leu	Gly	Ser	Leu	Ala	Leu	Ile	
	50					55					60					
Met	Gly	Phe	Gly	Ala	Met	Leu	Gly	Lys	Leu	Leu	Ala	Asp	Cys	Gly	Gly	
65					70					75					80	
Ala	Gln	Arg	Ile	Ala	Thr	Thr	Leu	Ile	Glu	Lys	Phe	Gly	Gln	Lys	His	
			85						90					95		
Ile	Gln	Trp	Ala	Val	Val	Leu	Thr	Gly	Phe	Thr	Val	Gly	Phe	Ala	Leu	
			100					105					110			
Phe	Tyr	Glu	Val	Gly	Phe	Val	Leu	Leu	Pro	Leu	Val	Phe	Ser	Ile		
		115					120				125					
Ala	Ala	Ser	Ala	Arg	Ile	Pro	Leu	Leu	Tyr	Val	Gly	Val	Pro	Met	Ala	
	130					135					140					
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
145					150					155					160	
Thr	Ala	Ile	Ala	Thr	Ile	Phe	Ser	Ala	Asp	Met	Gly	Lys	Thr	Leu	Leu	
			165						170					175		
Tyr	Gly	Thr	Leu	Ala	Ile	Pro	Thr	Val	Ile	Leu	Ala	Gly	Pro	Val		
			180					185					190			
Tyr	Ala	Arg	Phe	Leu	Lys	Gly	Ile	Asp	Lys	Pro	Val	Pro	Glu	Gly	Leu	
		195						200				205				
Tyr	Asn	Pro	Lys	Ile	Phe	Thr	Asp	Lys	Glu	Met	Pro	Ser	Phe	Gly	Val	
	210					215					220					
Ser	Val	Ser	Thr	Ala	Leu	Val	Pro	Val	Ile	Leu	Met	Ala	Leu	Arg	Ala	
225					230					235					240	
Val	Ala	Glu	Met	Ile	Leu	Pro	Lys	Gly	His	Ser	Leu	Leu	Pro	Tyr	Ala	
			245						250					255		
Glu	Phe	Phe	Gly	Asp	Pro	Val	Ile	Ala	Thr	Leu	Ile	Ala	Val	Leu	Ile	
			260					265					270			
Ala	Ile	Phe	Thr	Phe	Gly	Leu	Asn	Arg	Gly	Arg	Ser	Val	Glu	Ser	Val	
			275				280					285				
Met	Glu	Thr	Leu	Ser	Asp	Ser	Ile	Lys	Ile	Ile	Ala	Met	Met	Leu	Leu	
	290					295					300					
Val	Ile	Gly	Gly	Gly	Gly	Ala	Phe	Lys	Gln	Val	Leu	Val	Asp	Ser	Gly	
305					310					315					320	
Ile	Glu	Gln	Tyr	Ile	Ala	Gly	Met	Met	Gly	Asn	Ser	Gly	Ala	Ser	Pro	
			325						330					335		
Ile	Leu	Met	Ala	Trp	Ser	Ile	Ala	Ala	Leu	Leu	Arg	Ile	Ala	Leu	Gly	
			340					345					350			
Ser	Ala	Thr	Val	Ala	Ala	Ile	Thr	Ala	Gly	Gly	Ile	Val	Ala	Pro	Leu	
		355					360					365				
Ile	Ala	Thr	Thr	Gly	Ala	Ser	Pro	Glu	Leu	Met	Val	Ile	Ala	Val	Gly	
	370					375					380					

PF59083SeqList PF59083.txt

Ser Gly Ser Val Ile Phe Ser His Val Asn Asp Pro Gly Phe Trp Leu
 385 390 395 400
 Phe Lys Glu Tyr Phe Asn Leu Thr Ile Met Glu Thr Ile Lys Ser Trp
 405 410 415
 Ser Val Leu Glu Thr Ile Ile Ser Val Cys Gly Leu Ile Gly Cys Leu
 420 425 430
 Leu Leu Ser Leu Val Ile
 435

<210> 10170
 <211> 1377
 <212> DNA
 <213> Symbiobacterium thermophilum IAM 14863

<220>
 <221> CDS
 <222> (1)..(1377)
 <223> transl_table=11

<400> 10170
 atg gcg tca gca gtc tcg ggc tcc cag atg ctc ctg gcc ctg ctg atc 48
 Met Ala Ser Ala Val Ser Gly Ser Gln Met Leu Leu Ala Leu Leu Ile
 1 5 10 15
 ggc atc gtc gtc ctc gtc ttc ctg atc ctg aag acc aag atc cac gcc 96
 Gly Ile Val Val Leu Val Phe Leu Ile Leu Lys Thr Lys Ile His Ala
 20 25 30
 ttc ccg gcc ctg atc atc gcc gcc gcc ctg atc ggc ctc gtc ggc ggc 144
 Phe Pro Ala Leu Ile Ile Ala Ala Ala Leu Ile Gly Leu Val Gly Gly
 35 40 45
 atg gac ccg gtg gac gtc agc tcc gcg atc acg acc gga ttc ggc aac 192
 Met Asp Pro Val Asp Val Ser Ser Ala Ile Thr Thr Gly Phe Gly Asn
 50 55 60
 acc ctc gcc agc atc ggc atc gtc atc ggc ttc ggc gtg atg atg ggc 240
 Thr Leu Ala Ser Ile Gly Ile Val Ile Gly Phe Gly Val Met Met Gly
 65 70 75 80
 cgc atc ctg gag atc tcc ggc gcc gcg gag cgc atg gcc acc ttc ttc 288
 Arg Ile Leu Glu Ile Ser Gly Ala Ala Glu Arg Met Ala Thr Phe Phe
 85 90 95
 ctg aag cac ctg agc cgc cgg cgc ccg gag tgg gcc ctg gcc atc acc 336
 Leu Lys His Leu Ser Arg Arg Arg Pro Glu Trp Ala Leu Ala Ile Thr
 100 105 110
 ggc tac ttc acc tcg atc ccc atc ttc tgt gac tcc ggc tac gtc atc 384
 Gly Tyr Phe Thr Ser Ile Pro Ile Phe Cys Asp Ser Gly Tyr Val Ile
 115 120 125
 ctg gcc ccg ctg gcc aag gcg ctc tcc cgg cag agc ggc aag tcc gtg 432
 Leu Ala Pro Leu Ala Lys Ala Leu Ser Arg Gln Ser Gly Lys Ser Val
 130 135 140
 gtg acc ctg ggc atc tcc ctg gcc gtg ggc ctc gtc tcc acc cac cac 480
 Val Thr Leu Gly Ile Ser Leu Ala Val Gly Leu Val Ser Thr His His
 145 150 155 160
 ctg gtg ccg ccg acc ccg ggc ccg ctg ggc acc gcc ggc atc ttc ggc 528
 Leu Val Pro Pro Thr Pro Gly Pro Leu Gly Thr Ala Gly Ile Phe Gly
 165 170 175
 gcg gac atc ggc aag atg atc ctc tgg ggc atc ctc ttc gcc gtt ccg 576
 Ala Asp Ile Gly Lys Met Ile Leu Trp Gly Ile Leu Phe Ala Val Pro
 180 185 190
 gtc acc atc gtc ggc gtc ctc tac gcc gtc tgg ctg ggc cgg agg atc 624
 Val Thr Ile Val Gly Val Leu Tyr Ala Val Trp Leu Gly Arg Arg Ile
 195 200 205
 tac cag gtg ccc gcc gcc gac ggc gag ggc tgg gag cgc aag gag tgg 672
 Tyr Gln Val Pro Ala Ala Asp Gly Glu Gly Trp Glu Arg Lys Glu Trp
 210 215 220
 aag gcg gag ctg gag cag gcc atc gag atc gtc gag cgg aag gac ctg 720
 Lys Ala Glu Leu Glu Gln Ala Ile Glu Ile Val Glu Arg Lys Asp Leu
 225 230 235 240
 ccc ggc acc gcg ctc tcc ttc gcg ccg atc ctg gtg ccc atc ctg ctg 768
 Pro Gly Thr Ala Leu Ser Phe Ala Pro Ile Leu Val Pro Ile Leu Leu
 245 250 255
 atc ctg ctc aac acc acc ctg tct gcc gtc ggc gcc ggc ggc gcc tgg 816
 10763

PF59083SeqList PF59083.txt

Ile	Leu	Leu	Asn	Thr	Thr	Leu	Ser	Ala	Val	Gly	Ala	Gly	Gly	Ala	Trp	
			260					265					270			
gcc	cgg	ttc	ctg	atc	ttc	ctg	ggc	cag	ccc	atc	atc	gcc	gtg	ctg	gtc	864
Ala	Arg	Phe	Leu	Ile	Phe	Leu	Gly	Gln	Pro	Ile	Ile	Ala	Val	Leu	Val	
		275					280					285				
ggc	ctg	ctg	atc	gcc	atc	tac	ggc	ctg	ggc	gcc	aag	atg	acc	cgg	ccg	912
Gly	Leu	Leu	Ile	Ala	Ile	Tyr	Gly	Leu	Gly	Ala	Lys	Met	Thr	Arg	Pro	
		290				295					300					
gag	gtc	ttg	aag	gag	atg	gag	aag	ggc	gtc	cag	tcc	gcg	ggc	atc	atc	960
Glu	Val	Leu	Lys	Glu	Met	Glu	Lys	Gly	Val	Gln	Ser	Ala	Gly	Ile	Ile	
		305			310					315					320	
atg	ctg	gtc	acc	ggc	gcc	ggc	ggc	gcc	ctg	ggc	cag	gtg	atc	cgg	gcc	1008
Met	Leu	Val	Thr	Gly	Ala	Gly	Gly	Ala	Leu	Gly	Gln	Val	Ile	Arg	Ala	
			325					330						335		
agc	ggc	gcg	ggc	gac	tac	gtg	gcc	cag	gcc	ctg	gcg	aac	agc	gcc	ctg	1056
Ser	Gly	Ala	Gly	Asp	Tyr	Val	Ala	Gln	Ala	Leu	Ala	Asn	Ser	Ala	Leu	
			340					345					350			
ccg	gcg	atc	ctg	ctg	ccc	ttc	gtg	atc	gcc	acc	ggc	ctg	cgg	ctg	atc	1104
Pro	Ala	Ile	Leu	Leu	Pro	Phe	Val	Ile	Ala	Thr	Gly	Leu	Arg	Leu	Ile	
		355				360						365				
cag	ggc	tcc	ggc	acc	acc	gcc	atg	ctg	acc	gcc	gcg	tcc	atc	acc	gcc	1152
Gln	Gly	Ser	Gly	Thr	Thr	Ala	Met	Leu	Thr	Ala	Ala	Ser	Ile	Thr	Ala	
		370				375					380					
ccg	atc	ctg	gcc	ccg	ctg	ggc	atc	gac	ccg	gtc	ttc	gcg	gcc	atg	tcc	1200
Pro	Ile	Leu	Ala	Pro	Leu	Gly	Ile	Asp	Pro	Val	Phe	Ala	Ala	Met	Ser	
		385			390					395					400	
gcc	tcc	atg	ggc	gcc	ttc	gtc	ttc	agc	tac	ttc	aac	gac	tcc	ttc	tac	1248
Ala	Ser	Met	Gly	Ala	Phe	Val	Phe	Ser	Tyr	Phe	Asn	Asp	Ser	Phe	Tyr	
			405					410						415		
tgg	gtc	gtc	aac	cgt	ttc	atc	ggc	atc	gag	gac	gtg	aag	gag	cag	atc	1296
Trp	Val	Val	Asn	Arg	Phe	Ile	Gly	Ile	Glu	Asp	Val	Lys	Glu	Gln	Ile	
			420					425					430			
cag	gtc	tgg	tgc	gtg	ccc	acg	acc	ctg	gcc	tgg	ctc	acc	ccg	ggc	atc	1344
Gln	Val	Trp	Ser	Val	Pro	Thr	Thr	Leu	Ala	Trp	Leu	Thr	Pro	Gly	Ile	
		435				440						445				
tgc	ctg	gtg	atc	gcc	aac	acc	ctg	ttc	gga	tag						1377
Cys	Leu	Val	Ile	Ala	Asn	Thr	Leu	Phe	Gly							
		450				455										

<210> 10171

<211> 458

<212> PRT

<213> Symbiobacterium thermophilum IAM 14863

<400> 10171

Met	Ala	Ser	Ala	Val	Ser	Gly	Ser	Gln	Met	Leu	Leu	Ala	Leu	Leu	Ile	
1				5				10						15		
Gly	Ile	Val	Val	Leu	Val	Phe	Leu	Ile	Leu	Lys	Thr	Lys	Ile	His	Ala	
		20					25						30			
Phe	Pro	Ala	Leu	Ile	Ile	Ala	Ala	Leu	Ile	Gly	Leu	Val	Gly	Gly		
		35				40					45					
Met	Asp	Pro	Val	Asp	Val	Ser	Ser	Ala	Ile	Thr	Thr	Gly	Phe	Gly	Asn	
	50					55				60						
Thr	Leu	Ala	Ser	Ile	Gly	Ile	Val	Ile	Gly	Phe	Gly	Val	Met	Met	Gly	
				70						75					80	
Arg	Ile	Leu	Glu	Ile	Ser	Gly	Ala	Ala	Glu	Arg	Met	Ala	Thr	Phe	Phe	
			85				90							95		
Leu	Lys	His	Leu	Ser	Arg	Arg	Arg	Pro	Glu	Trp	Ala	Leu	Ala	Ile	Thr	
		100					105						110			
Gly	Tyr	Phe	Thr	Ser	Ile	Pro	Ile	Phe	Cys	Asp	Ser	Gly	Tyr	Val	Ile	
		115				120						125				
Leu	Ala	Pro	Leu	Ala	Lys	Ala	Leu	Ser	Arg	Gln	Ser	Gly	Lys	Ser	Val	
	130				135					140						
Val	Thr	Leu	Gly	Ile	Ser	Leu	Ala	Val	Gly	Leu	Val	Ser	Thr	His	His	
				150						155					160	
Leu	Val	Pro	Pro	Thr	Pro	Gly	Pro	Leu	Gly	Thr	Ala	Gly	Ile	Phe	Gly	
			165					170						175		
Ala	Asp	Ile	Gly	Lys	Met	Ile	Leu	Trp	Gly	Ile	Leu	Phe	Ala	Val	Pro	
			180				185						190			

PF59083SeqList PF59083.txt

Val Thr Ile Val Gly Val Leu Tyr Ala Val Trp Leu Gly Arg Arg Ile
 195 200 205
 Tyr Gln Val Pro Ala Ala Asp Gly Glu Gly Trp Glu Arg Lys Glu Trp
 210 215 220
 Lys Ala Glu Leu Glu Gln Ala Ile Glu Ile Val Glu Arg Lys Asp Leu
 225 230 235 240
 Pro Gly Thr Ala Leu Ser Phe Ala Pro Ile Leu Val Pro Ile Leu Leu
 245 250 255
 Ile Leu Leu Asn Thr Thr Leu Ser Ala Val Gly Ala Gly Gly Ala Trp
 260 265 270
 Ala Arg Phe Leu Ile Phe Leu Gly Gln Pro Ile Ile Ala Val Leu Val
 275 280 285
 Gly Leu Leu Ile Ala Ile Tyr Gly Leu Gly Ala Lys Met Thr Arg Pro
 290 295 300
 Glu Val Leu Lys Glu Met Glu Lys Gly Val Gln Ser Ala Gly Ile Ile
 305 310 315 320
 Met Leu Val Thr Gly Ala Gly Gly Ala Leu Gly Gln Val Ile Arg Ala
 325 330 335
 Ser Gly Ala Gly Asp Tyr Val Ala Gln Ala Leu Ala Asn Ser Ala Leu
 340 345 350
 Pro Ala Ile Leu Leu Pro Phe Val Ile Ala Thr Gly Leu Arg Leu Ile
 355 360 365
 Gln Gly Ser Gly Thr Thr Ala Met Leu Thr Ala Ala Ser Ile Thr Ala
 370 375 380
 Pro Ile Leu Ala Pro Leu Gly Ile Asp Pro Val Phe Ala Ala Met Ser
 385 390 395 400
 Ala Ser Met Gly Ala Phe Val Phe Ser Tyr Phe Asn Asp Ser Phe Tyr
 405 410 415
 Trp Val Val Asn Arg Phe Ile Gly Ile Glu Asp Val Lys Glu Gln Ile
 420 425 430
 Gln Val Trp Ser Val Pro Thr Thr Leu Ala Trp Leu Thr Pro Gly Ile
 435 440 445
 Cys Leu Val Ile Ala Asn Thr Leu Phe Gly
 450 455

<210> 10172

<211> 1386

<212> DNA

<213> Mannheimia succiniciproducens MBEL55E

<220>

<221> CDS

<222> (1)..(1386)

<223> transl_table=11

<400> 10172

atg gaa act gca gct agt atg tcg caa atg ctt atc ggt ttg gct atc	48
Met Glu Thr Ala Ala Ser Met Ser Gln Met Leu Ile Gly Leu Ala Ile	
1 5 10 15	
ggt att gca ctt ctc tta ata ctg gca atg aag aca aga atc cat gtc	96
Gly Ile Ala Leu Leu Ile Leu Ala Met Lys Thr Arg Ile His Val	
20 25 30	
ttt gtt gct tta att ctc gcc tcg tta acc acc ggt ctg ata ggc ggt	144
Phe Val Ala Leu Ile Leu Ala Ser Leu Thr Thr Gly Leu Ile Gly Gly	
35 40 45	
tta cct ttt gcc gaa gtg att agt tca gtc act aaa ggt ttc ggt agt	192
Leu Pro Phe Ala Glu Val Ile Ser Ser Val Thr Lys Gly Phe Gly Ser	
50 55 60	
acg ctg ggc agt acc ggt att att atc ggt ctc ggc gtc atg atg ggc	240
Thr Leu Gly Ser Thr Gly Ile Ile Ile Gly Leu Gly Val Met Met Gly	
65 70 75 80	
gca att tta gaa aaa tcc ggc gct gcc gaa caa atg gct ttc tct att	288
Ala Ile Leu Glu Lys Ser Gly Ala Ala Glu Gln Met Ala Phe Ser Ile	
85 90 95	
atc aaa ttg att ggt aaa gcc aag gaa gaa tgg gct tta gcc tta aca	336
Ile Lys Leu Ile Gly Lys Ala Lys Glu Glu Trp Ala Leu Ala Leu Thr	
100 105 110	
ggc tat gtg gtt gcc att ccc gtt ttt gcc gat tcc ggt ttg att att	384
Gly Tyr Val Val Ala Ile Pro Val Phe Ala Asp Ser Gly Leu Ile Ile	

PF59083SeqList PF59083.txt

tta	acc	ccg	ctt	gcc	aga	tcc	tta	tcc	cgt	atg	act	ggg	aaa	agc	gtt	432
Leu	Thr	Pro	Leu	Ala	Arg	Ser	Leu	Ser	Arg	Met	Thr	Gly	Lys	Ser	Val	
130						135					140					
atc	ggg	ctc	ggg	tta	gcc	atg	gca	acc	ggg	ctg	caa	tta	gcg	cac	gta	480
Ile	Gly	Leu	Gly	Leu	Ala	Met	Ala	Thr	Gly	Leu	Gln	Leu	Ala	His	Val	
145					150					155					160	
ttt	att	ccg	ccg	aca	ccg	ggg	ccg	tta	gcg	gtt	gcc	ggg	att	tta	gat	528
Phe	Ile	Pro	Pro	Thr	Pro	Gly	Pro	Leu	Ala	Val	Ala	Gly	Ile	Leu	Asp	
				165					170					175		
atc	gat	atg	ggg	atg	atg	att	att	tgg	ggg	atg	ata	tta	acg	gtt	ccg	576
Ile	Asp	Met	Gly	Met	Met	Ile	Ile	Trp	Gly	Met	Ile	Leu	Thr	Val	Pro	
			180					185					190			
act	ttg	gta	atg	tct	acg	cta	tac	gca	aaa	tgg	ctc	ggg	aaa	aaa	atc	624
Thr	Leu	Val	Met	Ser	Thr	Leu	Tyr	Ala	Lys	Trp	Leu	Gly	Lys	Lys	Ile	
			195				200						205			
tat	cag	att	cct	aac	gaa	gac	ggg	acc	gac	ttt	gaa	cgc	aag	gaa	ttt	672
Tyr	Gln	Ile	Pro	Asn	Glu	Asp	Gly	Thr	Asp	Phe	Glu	Arg	Lys	Glu	Phe	
	210					215					220					
aaa	gag	gaa	tac	att	aaa	tcc	att	gaa	aat	gta	gaa	cag	att	tat	aaa	720
Lys	Glu	Glu	Tyr	Ile	Lys	Ser	Ile	Glu	Asn	Val	Glu	Gln	Ile	Tyr	Lys	
225					230					235					240	
gat	aag	aat	ctg	ccg	ggg	gcc	gga	ctg	tca	ttt	tca	cct	atc	gta	att	768
Asp	Lys	Asn	Leu	Pro	Gly	Ala	Gly	Leu	Ser	Phe	Ser	Pro	Ile	Val	Ile	
				245				250						255		
cct	tta	att	ttg	att	tta	ggg	aat	acc	acc	gtt	aat	ttc	ctg	aaa	atc	816
Pro	Leu	Ile	Leu	Ile	Leu	Gly	Asn	Thr	Thr	Val	Asn	Phe	Leu	Lys	Ile	
			260					265					270			
gaa	aat	ggg	ttt	gcc	gat	ttg	tta	aaa	ata	gta	ggc	cat	cca	att	att	864
Glu	Asn	Gly	Phe	Ala	Asp	Leu	Leu	Lys	Ile	Val	Gly	His	Pro	Ile	Ile	
		275				280						285				
gca	ttg	atc	atc	ggg	ctt	tta	atc	gct	ctt	tat	ggg	tta	ggg	cgc	cgt	912
Ala	Leu	Ile	Ile	Gly	Leu	Leu	Ile	Ala	Leu	Tyr	Gly	Leu	Gly	Arg	Arg	
	290					295				300						
ctt	tct	aaa	gcg	gaa	acc	aac	aaa	gcc	att	gaa	gac	gga	gta	aaa	tcc	960
Leu	Ser	Lys	Ala	Glu	Thr	Asn	Lys	Ala	Ile	Glu	Asp	Gly	Val	Lys	Ser	
305					310					315					320	
aca	ggg	atg	att	tta	ttc	atc	acc	ggg	gcg	ggc	ggg	gcg	tta	ggg	tat	1008
Thr	Gly	Met	Ile	Leu	Phe	Ile	Thr	Gly	Ala	Gly	Gly	Ala	Leu	Gly	Tyr	
				325						330				335		
gtt	gtg	cgc	gat	gcc	ggg	atc	ggg	aat	gcc	tta	ggg	gaa	gcg	gtt	ctg	1056
Val	Val	Arg	Asp	Ala	Gly	Ile	Gly	Asn	Ala	Leu	Gly	Glu	Ala	Val	Leu	
			340				345					350				
acc	gtc	ggg	atc	ccg	ggg	att	ttg	att	cca	ttt	gta	att	gcc	gcg	cta	1104
Thr	Val	Gly	Ile	Pro	Gly	Ile	Leu	Ile	Pro	Phe	Val	Ile	Ala	Ala	Leu	
		355					360					365				
atg	cgt	att	gcg	ctg	ggg	agc	gcc	acc	gtc	gct	tta	att	aca	gcc	gca	1152
Met	Arg	Ile	Ala	Leu	Gly	Ser	Ala	Thr	Val	Ala	Leu	Ile	Thr	Ala	Ala	
	370					375					380					
acc	ctg	gcc	gcc	ccg	ctt	gta	ccg	caa	tta	ggg	tta	aat	ccg	act	tta	1200
Thr	Leu	Ala	Ala	Pro	Leu	Val	Pro	Gln	Leu	Gly	Leu	Asn	Pro	Thr	Leu	
385					390					395					400	
gtt	gcc	atg	tca	acc	tgt	gcc	ggg	gcg	gta	tct	ttc	agt	tac	ttc	aat	1248
Val	Ala	Met	Ser	Thr	Cys	Ala	Gly	Ala	Val	Ser	Phe	Ser	Tyr	Phe	Asn	
				405					410					415		
gac	agc	ggg	ttc	tgg	gta	ttc	aat	ggg	cta	tac	ggg	ttg	aaa	gaa	gta	1296
Asp	Ser	Gly	Phe	Trp	Val	Phe	Asn	Gly	Leu	Tyr	Gly	Leu	Lys	Glu	Val	
			420					425					430			
aaa	gat	caa	ttt	atg	gct	aaa	acc	atg	gtt	tcg	ttt	atc	ggg	gct	ttc	1344
Lys	Asp	Gln	Phe	Met	Ala	Lys	Thr	Met	Val	Ser	Phe	Ile	Gly	Ala	Phe	
		435					440					445				
tcc	tgt	ttg	gcg	ctg	gta	ctg	atc	ttt	aat	atc	ttt	atg	taa			1386
Ser	Cys	Leu	Ala	Leu	Val	Leu	Ile	Phe	Asn	Ile	Phe	Met				
	450					455					460					

<210> 10173

<211> 461

<212> PRT

<213> Mannheimia succiniciproducens MBEL55E

PF59083SeqList PF59083.txt

```

<400> 10173
Met Glu Thr Ala Ala Ser Met Ser Gln Met Leu Ile Gly Leu Ala Ile
1      5      10      15
Gly Ile Ala Leu Leu Ile Leu Ala Met Lys Thr Arg Ile His Val
20      25      30
Phe Val Ala Leu Ile Leu Ala Ser Leu Thr Thr Gly Leu Ile Gly Gly
35      40      45
Leu Pro Phe Ala Glu Val Ile Ser Ser Val Thr Lys Gly Phe Gly Ser
50      55      60
Thr Leu Gly Ser Thr Gly Ile Ile Ile Gly Leu Gly Val Met Met Gly
65      70      75      80
Ala Ile Leu Glu Lys Ser Gly Ala Ala Glu Gln Met Ala Phe Ser Ile
85      90      95
Ile Lys Leu Ile Gly Lys Ala Lys Glu Trp Ala Leu Ala Leu Thr
100     105     110
Gly Tyr Val Val Ala Ile Pro Val Phe Ala Asp Ser Gly Leu Ile Ile
115     120     125
Leu Thr Pro Leu Ala Arg Ser Leu Ser Arg Met Thr Gly Lys Ser Val
130     135     140
Ile Gly Leu Gly Leu Ala Met Ala Thr Gly Leu Gln Leu Ala His Val
145     150     155     160
Phe Ile Pro Pro Thr Pro Gly Pro Leu Ala Val Ala Gly Ile Leu Asp
165     170     175
Ile Asp Met Gly Met Met Ile Ile Trp Gly Met Ile Leu Thr Val Pro
180     185     190
Thr Leu Val Met Ser Thr Leu Tyr Ala Lys Trp Leu Gly Lys Lys Ile
195     200     205
Tyr Gln Ile Pro Asn Glu Asp Gly Thr Asp Phe Glu Arg Lys Glu Phe
210     215     220
Lys Glu Glu Tyr Ile Lys Ser Ile Glu Asn Val Glu Gln Ile Tyr Lys
225     230     235     240
Asp Lys Asn Leu Pro Gly Ala Gly Leu Ser Phe Ser Pro Ile Val Ile
245     250     255
Pro Leu Ile Leu Ile Leu Gly Asn Thr Val Asn Phe Leu Lys Ile
260     265     270
Glu Asn Gly Phe Ala Asp Leu Leu Lys Ile Val Gly His Pro Ile Ile
275     280     285
Ala Leu Ile Ile Gly Leu Leu Ile Ala Leu Tyr Gly Leu Gly Arg Arg
290     295     300
Leu Ser Lys Ala Glu Thr Asn Lys Ala Ile Glu Asp Gly Val Lys Ser
305     310     315     320
Thr Gly Met Ile Leu Phe Ile Thr Gly Ala Gly Gly Ala Leu Gly Tyr
325     330     335
Val Val Arg Asp Ala Gly Ile Gly Asn Ala Leu Gly Glu Ala Val Leu
340     345     350
Thr Val Gly Ile Pro Gly Ile Leu Ile Pro Phe Val Ile Ala Ala Leu
355     360     365
Met Arg Ile Ala Leu Gly Ser Ala Thr Val Ala Leu Ile Thr Ala Ala
370     375     380
Thr Leu Ala Ala Pro Leu Val Pro Gln Leu Gly Leu Asn Pro Thr Leu
385     390     395     400
Val Ala Met Ser Thr Cys Ala Gly Ala Val Ser Phe Ser Tyr Phe Asn
405     410     415
Asp Ser Gly Phe Trp Val Phe Asn Gly Leu Tyr Gly Leu Lys Glu Val
420     425     430
Lys Asp Gln Phe Met Ala Lys Thr Met Val Ser Phe Ile Gly Ala Phe
435     440     445
Ser Cys Leu Ala Leu Val Leu Ile Phe Asn Ile Phe Met
450     455     460

```

```

<210> 10174
<211> 1341
<212> DNA
<213> Burkholderia mallei ATCC 23344

```

```

<220>
<221> CDS
<222> (1)..(1341)

```

<223> transl_table=11

<400> 10174

atg	ctg	ctg	att	tac	acc	gtg	atc	gcg	atc	gcg	gtg	ctg	atc	ctg	atg	48
Met	Leu	Leu	Ile	Tyr	Thr	Val	Ile	Ala	Ile	Ala	Val	Leu	Ile	Leu	Met	
1				5				10						15		
atc	gcg	cgc	tac	aag	gtg	tat	ccg	ttc	ctt	gtg	ctg	atc	atc	gtg	tcg	96
Ile	Ala	Arg	Tyr	Lys	Val	Tyr	Pro	Phe	Leu	Val	Leu	Ile	Ile	Val	Ser	
			20					25					30			
ctc	ggt	ctc	ggc	ctc	gcg	gtc	ggc	atg	ccg	atg	gac	aag	atc	gtg	aaa	144
Leu	Gly	Leu	Gly	Leu	Ala	Val	Gly	Met	Pro	Met	Asp	Lys	Ile	Val	Lys	
			35				40					45				
tcg	ttc	gag	ggg	ggc	acg	ggc	ggc	acg	ctc	ggc	cac	atc	gcg	atc	gtc	192
Ser	Phe	Glu	Gly	Gly	Thr	Gly	Gly	Thr	Leu	Gly	His	Ile	Ala	Ile	Val	
	50					55					60					
gtc	ggc	ctc	ggc	acg	atg	ctc	ggc	aag	atg	atg	gcc	gaa	tcg	ggc	ggc	240
Val	Gly	Leu	Gly	Thr	Met	Leu	Gly	Lys	Met	Met	Ala	Glu	Ser	Gly	Gly	
					70				75						80	
gcc	gag	cgg	atc	gcg	acc	acg	ctg	atc	gac	tgg	ttc	ggc	gag	aag	aac	288
Ala	Glu	Arg	Ile	Ala	Thr	Thr	Leu	Ile	Asp	Trp	Phe	Gly	Glu	Lys	Asn	
				85					90					95		
atc	cac	tgg	gcg	atg	atg	ttc	gtc	gcg	atc	atc	gtc	ggg	ctg	ccg	gtg	336
Ile	His	Trp	Ala	Met	Met	Phe	Val	Ala	Ile	Ile	Val	Gly	Leu	Pro	Val	
			100					105					110			
ttc	ttc	gaa	gtc	ggc	ttc	gtg	ctg	atc	ccg	atc	gcg	ttc	aac	gtc		384
Phe	Phe	Glu	Val	Gly	Phe	Val	Leu	Leu	Ile	Pro	Ile	Ala	Phe	Asn	Val	
		115					120					125				
gcg	aaa	cgc	acc	ggc	aag	tcg	ctg	ctc	gtc	gtc	ggg	ctg	ccg	atg	gtg	432
Ala	Lys	Arg	Thr	Gly	Lys	Ser	Leu	Leu	Val	Val	Gly	Leu	Pro	Met	Val	
	130					135					140					
gcg	ggc	ctg	tcg	gtc	gtg	cac	ggg	ctg	att	ccg	ccg	cac	ccg	gcg	gcg	480
Ala	Gly	Leu	Ser	Val	Val	His	Gly	Leu	Ile	Pro	Pro	His	Pro	Ala	Ala	
	145			150				155						160		
ctc	ctc	gcc	gtt	cag	caa	tac	ggc	gcc	gac	atc	ggc	aag	acg	atc	gcg	528
Leu	Leu	Ala	Val	Gln	Gln	Tyr	Gly	Ala	Asp	Ile	Gly	Lys	Thr	Ile	Ala	
				165				170						175		
tac	ggc	ctc	atc	gtc	ggc	gtg	ccg	acc	gcg	atc	gtc	gcg	ggg	ccg	ctg	576
Tyr	Gly	Leu	Ile	Val	Gly	Val	Pro	Thr	Ala	Ile	Val	Ala	Gly	Pro	Leu	
			180				185					190				
ttc	gcg	ctc	acg	atc	tcg	aag	ttc	gtg	aag	ctg	ccg	gag	cac	aat	ccg	624
Phe	Ala	Leu	Thr	Ile	Ser	Lys	Phe	Val	Lys	Leu	Pro	Glu	His	Asn	Pro	
		195				200						205				
ctc	gcg	tcg	cag	ttc	gtc	gag	acg	cgc	gcg	gcg	ggc	gag	acg	cgc	gcg	672
Leu	Ala	Ser	Gln	Phe	Val	Glu	Thr	Arg	Ala	Ala	Gly	Glu	Thr	Arg	Ala	
		210				215					220					
ctg	ccg	agc	ttc	ggc	atc	acg	ctg	ttc	acg	atc	ctg	ctg	ccc	gtc	gtg	720
Leu	Pro	Ser	Phe	Gly	Ile	Thr	Leu	Phe	Thr	Ile	Leu	Leu	Pro	Val	Val	
				230				235						240		
ctg	atg	ctc	gtc	ggc	agc	tgg	gcc	gat	ctc	gtg	ttc	gcg	ccg	aaa	tcg	768
Leu	Met	Leu	Val	Gly	Ser	Trp	Ala	Asp	Leu	Val	Phe	Ala	Pro	Lys	Ser	
				245				250						255		
ctg	ccg	aac	agc	ctg	ctg	cgc	ttc	gcc	ggc	aat	tcg	gat	gtc	gcg	ctc	816
Leu	Pro	Asn	Ser	Leu	Leu	Arg	Phe	Ala	Gly	Asn	Ser	Asp	Val	Ala	Leu	
			260			265						270				
ctg	atc	gct	gtg	ctc	gtg	agc	ttc	ttc	acg	ttc	ggc	aag	ctg	cag	ggc	864
Leu	Ile	Ala	Val	Leu	Val	Ser	Phe	Phe	Thr	Phe	Gly	Lys	Leu	Gln	Gly	
		275				280					285					
ttc	aat	cgc	gag	cag	atc	cag	aag	ttc	tgc	ggc	gat	tgc	ctc	gcg	ccg	912
Phe	Asn	Arg	Glu	Gln	Ile	Gln	Lys	Phe	Cys	Gly	Asp	Cys	Leu	Ala	Pro	
		290				295					300					
atc	gcg	ggc	atc	acg	ctg	atc	gtc	ggc	gcg	ggc	ggc	ggc	ttc	ggc	ggt	960
Ile	Ala	Gly	Ile	Thr	Leu	Ile	Val	Gly	Ala	Gly	Gly	Gly	Phe	Gly	Gly	
				310				315						320		
att	ctg	cgc	gac	agc	ggc	atc	tcg	cag	cag	atc	gtc	gcg	acc	gcg	acg	1008
Ile	Leu	Arg	Asp	Ser	Gly	Ile	Ser	Gln	Gln	Ile	Val	Ala	Thr	Ala	Thr	
				325				330						335		
cac	gcg	cat	ctg	tcg	ccg	ctg	ctg	ctc	ggc	tgg	ttc	gtc	gcg	gcg	ctg	1056
His	Ala	His	Leu	Ser	Pro	Leu	Leu	Leu	Gly	Trp	Phe	Val	Ala	Ala	Leu	
			340					345					350			

PF59083SeqList PF59083.txt

atc	cgt	ctc	gcc	acg	ggt	tcg	gcc	acc	gtc	gcg	atg	acg	acc	gcc	tgc	1104
Ile	Arg	Leu	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	Met	Thr	Thr	Ala	Cys	
		355					360					365				
ggg	atc	gtc	gcg	ccg	atc	gcc	gcg	gcc	tcg	ggc	gtc	acg	gtg	cgc	ccg	1152
Gly	Ile	Val	Ala	Pro	Ile	Ala	Ala	Ala	Ser	Gly	Val	Thr	Val	Arg	Pro	
		370					375					380				
gag	ctg	ctc	gtg	ctc	gcg	acg	ggc	tcg	ggc	tcg	ctc	atc	ttc	tcg	cac	1200
Glu	Leu	Leu	Val	Leu	Ala	Thr	Gly	Ser	Gly	Ser	Leu	Ile	Phe	Ser	His	
		385				390				395					400	
gtg	aac	gac	ggc	ggc	ttc	tgg	ctg	atc	aag	gaa	tat	ttc	ggg	atg	acc	1248
Val	Asn	Asp	Gly	Gly	Phe	Trp	Leu	Ile	Lys	Glu	Tyr	Phe	Gly	Met	Thr	
				405					410					415		
gtg	ggg	cag	acg	ttc	aag	acg	tgg	acg	ctg	ctc	gaa	acg	atc	atc	tcg	1296
Val	Gly	Gln	Thr	Phe	Lys	Thr	Trp	Thr	Leu	Leu	Glu	Thr	Ile	Ile	Ser	
			420					425					430			
gtg	ctc	ggt	ctc	acc	ttc	acg	ctg	gcg	ctg	agc	gcg	gtt	ctg	taa		1341
Val	Leu	Gly	Leu	Thr	Phe	Thr	Leu	Ala	Leu	Ser	Ala	Val	Leu			
		435					440					445				

<210> 10175

<211> 446

<212> PRT

<213> Burkholderia mallei ATCC 23344

<400> 10175

Met	Leu	Leu	Ile	Tyr	Thr	Val	Ile	Ala	Ile	Ala	Val	Leu	Ile	Leu	Met	
1				5					10					15		
Ile	Ala	Arg	Tyr	Lys	Val	Tyr	Pro	Phe	Leu	Val	Leu	Ile	Ile	Val	Ser	
			20					25					30			
Leu	Gly	Leu	Gly	Leu	Ala	Val	Gly	Met	Pro	Met	Asp	Lys	Ile	Val	Lys	
		35					40					45				
Ser	Phe	Glu	Gly	Gly	Thr	Gly	Gly	Thr	Leu	Gly	His	Ile	Ala	Ile	Val	
	50					55					60					
Val	Gly	Leu	Gly	Thr	Met	Leu	Gly	Lys	Met	Met	Ala	Glu	Ser	Gly	Gly	
65					70					75					80	
Ala	Glu	Arg	Ile	Ala	Thr	Thr	Leu	Ile	Asp	Trp	Phe	Gly	Glu	Lys	Asn	
			85						90					95		
Ile	His	Trp	Ala	Met	Met	Phe	Val	Ala	Ile	Ile	Val	Gly	Leu	Pro	Val	
			100					105					110			
Phe	Phe	Glu	Val	Gly	Phe	Val	Leu	Ile	Pro	Ile	Ala	Phe	Asn	Val		
		115					120				125					
Ala	Lys	Arg	Thr	Gly	Lys	Ser	Leu	Leu	Val	Val	Gly	Leu	Pro	Met	Val	
	130					135					140					
Ala	Gly	Leu	Ser	Val	Val	His	Gly	Leu	Ile	Pro	His	Pro	Ala	Ala		
145					150					155				160		
Leu	Leu	Ala	Val	Gln	Gln	Tyr	Gly	Ala	Asp	Ile	Gly	Lys	Thr	Ile	Ala	
			165						170					175		
Tyr	Gly	Leu	Ile	Val	Gly	Val	Pro	Thr	Ala	Ile	Val	Ala	Gly	Pro	Leu	
		180						185					190			
Phe	Ala	Leu	Thr	Ile	Ser	Lys	Phe	Val	Lys	Leu	Pro	Glu	His	Asn	Pro	
		195					200					205				
Leu	Ala	Ser	Gln	Phe	Val	Glu	Thr	Arg	Ala	Ala	Gly	Glu	Thr	Arg	Ala	
	210					215					220					
Leu	Pro	Ser	Phe	Gly	Ile	Thr	Leu	Phe	Thr	Ile	Leu	Leu	Pro	Val	Val	
225					230					235					240	
Leu	Met	Leu	Val	Gly	Ser	Trp	Ala	Asp	Leu	Val	Phe	Ala	Pro	Lys	Ser	
			245						250					255		
Leu	Pro	Asn	Ser	Leu	Leu	Arg	Phe	Ala	Gly	Asn	Ser	Asp	Val	Ala	Leu	
		260						265					270			
Leu	Ile	Ala	Val	Leu	Val	Ser	Phe	Thr	Phe	Gly	Lys	Leu	Gln	Gly		
		275					280					285				
Phe	Asn	Arg	Glu	Gln	Ile	Gln	Lys	Phe	Cys	Gly	Asp	Cys	Leu	Ala	Pro	
	290					295					300					
Ile	Ala	Gly	Ile	Thr	Leu	Ile	Val	Gly	Ala	Gly	Gly	Gly	Phe	Gly	Gly	
305					310					315					320	
Ile	Leu	Arg	Asp	Ser	Gly	Ile	Ser	Gln	Gln	Ile	Val	Ala	Thr	Ala	Thr	
			325						330					335		
His	Ala	His	Leu	Ser	Pro	Leu	Leu	Leu	Gly	Trp	Phe	Val	Ala	Ala	Leu	
			340					345					350			

PF59083SeqList PF59083.txt
Ile Arg Leu Ala Thr Gly Ser Ala Thr Val Ala Met Thr Thr Ala Cys
355 360 365
Gly Ile Val Ala Pro Ile Ala Ala Ala Ser Gly Val Thr Val Arg Pro
370 375 380
Glu Leu Leu Val Leu Ala Thr Gly Ser Gly Ser Leu Ile Phe Ser His
385 390 395 400
Val Asn Asp Gly Gly Phe Trp Leu Ile Lys Glu Tyr Phe Gly Met Thr
405 410 415
Val Gly Gln Thr Phe Lys Thr Trp Thr Leu Leu Glu Thr Ile Ile Ser
420 425 430
Val Leu Gly Leu Thr Phe Thr Leu Ala Leu Ser Ala Val Leu
435 440 445

<210> 10176
<211> 1386
<212> DNA
<213> Neisseria gonorrhoeae FA 1090

<220>
<221> CDS
<222> (1)..(1386)
<223> transl_table=11

<400> 10176
atg gac ggc cgg aca cag acg ctg tcc gcg caa acc ttg ttg ggc att 48
Met Asp Gly Arg Thr Gln Thr Leu Ser Ala Gln Thr Leu Leu Gly Ile
1 5 10 15
tcg gcg gcg gca atc atc ctc att ctg att tta atc gtc aaa ttc cgc 96
Ser Ala Ala Ala Ile Ile Leu Ile Leu Ile Leu Ile Val Lys Phe Arg
20 25 30
atc cgc gcg ctg ctg aca ctg gtc atc gcc agc ctg ctg acg gct ttg 144
Ile Arg Ala Leu Leu Thr Leu Val Ile Ala Ser Leu Leu Thr Ala Leu
35 40 45
gca acc ggt ttg ccc aca ggc agc atc gtc aac gac gta ctg gtc aaa 192
Ala Thr Gly Leu Pro Thr Gly Ser Ile Val Asn Asp Val Leu Val Lys
50 55 60
aac ttc ggc ggc acg ctc ggc ggc gtg gcg ctt ctg gtc ggt ctg ggc 240
Asn Phe Gly Gly Thr Leu Gly Gly Val Ala Leu Leu Val Gly Leu Gly
65 70 75 80
gca atg ctc gga cgt ttg gta gaa aca tcc ggc ggc gca cag tcg ctg 288
Ala Met Leu Gly Arg Leu Val Glu Thr Ser Gly Gly Ala Gln Ser Leu
85 90 95
gcg gac gcg ctg atc cgg atg ttc ggc gaa aaa cgc gca ccg ttc gct 336
Ala Asp Ala Leu Ile Arg Met Phe Gly Glu Lys Arg Ala Pro Phe Ala
100 105 110
ccg ggc gtt gcc tcg ctg att ttc ggc ttc ccg att ttc ttc gat gcc 384
Pro Gly Val Ala Ser Leu Ile Phe Gly Phe Pro Ile Phe Phe Asp Ala
115 120 125
gga cta atc gtc atg ctg ccc atc gta ttc gcc acc gca ccg cgc atg 432
Gly Leu Ile Val Met Leu Pro Ile Val Phe Ala Thr Ala Arg Arg Met
130 135 140
aaa cag gac gta ctg ccc ttc gcg ctt gcc tcc gtc ggc gca ttt tcc 480
Lys Gln Asp Val Leu Pro Phe Ala Leu Ala Ser Val Gly Ala Phe Ser
145 150 155 160
gtc atg cac gtc ttc ctg ccg ccc cat ccg ggc ccg att gcc gct tcc 528
Val Met His Val Phe Leu Pro Pro His Pro Gly Pro Ile Ala Ala Ser
165 170 175
gaa ttt tac ggc gcg aac atc ggc cag gtt ttg att ttg ggt ctg ccg 576
Glu Phe Tyr Gly Ala Asn Ile Gly Gln Val Leu Ile Leu Gly Leu Pro
180 185 190
acc gcc ttc atc aca tgg tat ttc agc ggc tat atg ctc ggc aaa gtg 624
Thr Ala Phe Ile Thr Trp Tyr Phe Ser Gly Tyr Met Leu Gly Lys Val
195 200 205
ttg ggg cgc gcc atc cat gtt ccc gtt ccc gaa ctg ctc agc ggc ggc 672
Leu Gly Arg Ala Ile His Val Pro Val Pro Glu Leu Leu Ser Gly Gly
210 215 220
acg caa gac agc gac ccg ccg aaa gaa cct gcc aaa gca gga acg gtc 720
Thr Gln Asp Ser Asp Pro Pro Lys Glu Pro Ala Lys Ala Gly Thr Val
225 230 235 240

PF59083SeqList PF59083.txt

gtc	gcc	gtc	atg	ctg	att	ccc	atg	ctg	ctg	att	ttc	ctg	aat	acc	ggc	768
Val	Ala	Val	Met	Leu	Ile	Pro	Met	Leu	Leu	Ile	Phe	Leu	Asn	Thr	Gly	
				245					250					255		
gta	tca	gcc	ctc	atc	agc	gaa	aaa	ctc	gta	agt	gcg	gac	gaa	act	tgg	816
Val	Ser	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Val	Ser	Ala	Asp	Glu	Thr	Trp	
			260					265					270			
gtt	cag	acg	gca	aaa	atg	atc	ggg	tcg	aca	cct	gtc	gcc	ctt	ctg	att	864
Val	Gln	Thr	Ala	Lys	Met	Ile	Gly	Ser	Thr	Pro	Val	Ala	Leu	Leu	Ile	
			275				280					285				
tcc	gta	ttg	gcc	gca	ctg	ttg	gtc	ttg	gga	cgc	aaa	cgc	ggc	gaa	agc	912
Ser	Val	Leu	Ala	Ala	Leu	Leu	Val	Leu	Gly	Arg	Lys	Arg	Gly	Glu	Ser	
			290			295					300					
ggc	agc	acg	ttg	gaa	aaa	acc	gtg	gac	ggc	gca	ctc	gcc	ccc	gcc	tgt	960
Gly	Ser	Thr	Leu	Glu	Lys	Thr	Val	Asp	Gly	Ala	Leu	Ala	Pro	Ala	Cys	
305					310					315					320	
tcc	gtg	att	ctg	att	acc	ggc	gcg	ggc	ggg	atg	ttc	ggc	ggc	gtt	ttg	1008
Ser	Val	Ile	Leu	Ile	Thr	Gly	Ala	Gly	Gly	Met	Phe	Gly	Gly	Val	Leu	
			325					330						335		
cgc	gct	tcc	ggc	atc	ggc	aag	gca	ctc	gcc	gac	agc	atg	gcg	gat	ttg	1056
Arg	Ala	Ser	Gly	Ile	Gly	Lys	Ala	Leu	Ala	Asp	Ser	Met	Ala	Asp	Leu	
			340				345						350			
ggc	att	ccc	gtc	ctt	ttg	ggc	tgc	ttc	ctt	gtc	gcc	ttg	gca	ctg	cgt	1104
Gly	Ile	Pro	Val	Leu	Leu	Gly	Cys	Phe	Leu	Val	Ala	Leu	Ala	Leu	Arg	
			355				360					365				
atc	gcg	caa	ggg	tcg	gca	acc	gtc	gcc	ctg	acc	aca	gcc	gcc	gcg	ctg	1152
Ile	Ala	Gln	Gly	Ser	Ala	Thr	Val	Ala	Leu	Thr	Thr	Ala	Ala	Ala	Leu	
			370			375					380					
atg	gct	cct	gcc	ggt	gcc	gcc	gcc	ggc	ttt	acc	gac	tgg	cag	ctc	gcc	1200
Met	Ala	Pro	Ala	Val	Ala	Ala	Ala	Gly	Phe	Thr	Asp	Trp	Gln	Leu	Ala	
385				390						395				400		
tgt	atc	gta	ttg	gca	acg	gcg	gca	ggg	tcg	gtc	ggg	tgc	agc	cac	ttc	1248
Cys	Ile	Val	Leu	Ala	Thr	Ala	Ala	Gly	Ser	Val	Gly	Cys	Ser	His	Phe	
			405					410						415		
aac	gac	tcc	ggc	ttc	tgg	ctg	gtc	ggc	cgc	ctc	ttg	gat	atg	gac	gta	1296
Asn	Asp	Ser	Gly	Phe	Trp	Leu	Val	Gly	Arg	Leu	Leu	Asp	Met	Asp	Val	
			420				425						430			
ccg	acc	acg	ctg	aaa	acc	tgg	acg	gtc	aac	caa	acc	ctc	atc	gca	ttc	1344
Pro	Thr	Thr	Leu	Lys	Thr	Trp	Thr	Val	Asn	Gln	Thr	Leu	Ile	Ala	Phe	
			435			440						445				
atc	ggc	ttt	gcc	ttg	tcc	gca	ctg	ttt	gcc	atc	gtc	tga				1386
Ile	Gly	Phe	Ala	Leu	Ser	Ala	Leu	Leu	Phe	Ala	Ile	Val				
	450					455				460						

<210> 10177

<211> 461

<212> PRT

<213> Neisseria gonorrhoeae FA 1090

<400> 10177

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

PF59083SeqList PF59083.txt

Val Met His Val Phe Leu Pro Pro His Pro Gly Pro Ile Ala Ser
 165 170 175
 Glu Phe Tyr Gly Ala Asn Ile Gly Gln Val Leu Ile Leu Gly Leu Pro
 180 185 190
 Thr Ala Phe Ile Thr Trp Tyr Phe Ser Gly Tyr Met Leu Gly Lys Val
 195 200 205
 Leu Gly Arg Ala Ile His Val Pro Val Pro Glu Leu Leu Ser Gly Gly
 210 215 220
 Thr Gln Asp Ser Asp Pro Pro Lys Glu Pro Ala Lys Ala Gly Thr Val
 225 230 235 240
 Val Ala Val Met Leu Ile Pro Met Leu Leu Ile Phe Leu Asn Thr Gly
 245 250 255
 Val Ser Ala Leu Ile Ser Glu Lys Leu Val Ser Ala Asp Glu Thr Trp
 260 265 270
 Val Gln Thr Ala Lys Met Ile Gly Ser Thr Pro Val Ala Leu Leu Ile
 275 280 285
 Ser Val Leu Ala Ala Leu Leu Val Leu Gly Arg Lys Arg Gly Glu Ser
 290 295 300
 Gly Ser Thr Leu Glu Lys Thr Val Asp Gly Ala Leu Ala Pro Ala Cys
 305 310 315 320
 Ser Val Ile Leu Ile Thr Gly Ala Gly Gly Met Phe Gly Gly Val Leu
 325 330 335
 Arg Ala Ser Gly Ile Gly Lys Ala Leu Ala Asp Ser Met Ala Asp Leu
 340 345 350
 Gly Ile Pro Val Leu Leu Gly Cys Phe Leu Val Ala Leu Ala Leu Arg
 355 360 365
 Ile Ala Gln Gly Ser Ala Thr Val Ala Leu Thr Thr Ala Ala Ala Leu
 370 375 380
 Met Ala Pro Ala Val Ala Ala Gly Phe Thr Asp Trp Gln Leu Ala
 385 390 395 400
 Cys Ile Val Leu Ala Thr Ala Ala Gly Ser Val Gly Cys Ser His Phe
 405 410 415
 Asn Asp Ser Gly Phe Trp Leu Val Gly Arg Leu Leu Asp Met Asp Val
 420 425 430
 Pro Thr Thr Leu Lys Thr Trp Thr Val Asn Gln Thr Leu Ile Ala Phe
 435 440 445 450
 Ile Gly Phe Ala Leu Ser Ala Leu Leu Phe Ala Ile Val
 455 460

<210> 10178

<211> 1353

<212> DNA

<213> Pseudomonas syringae pv. syringae B728a

<220>

<221> CDS

<222> (1)..(1353)

<223> transl_table=11

<400> 10178

atg ttc ggt atg acc cat gag acg ttc ctg ctc gtc gat gcg ttg gtg	48
Met Phe Gly Met Thr His Glu Thr Phe Leu Leu Val Asp Ala Leu Val	
1 5 10 15	
acc atc gtc ggc ctg gtg ctg ctg atc acc acc ttc aag gtg cac cct	96
Thr Ile Val Gly Leu Val Leu Leu Ile Thr Thr Phe Lys Val His Pro	
20 25 30	
ttc gtc gcg ttg acc ctg gcg gca ggc ttt ctt ggc ctg acc tcg gga	144
Phe Val Ala Leu Thr Leu Ala Ala Gly Phe Leu Gly Leu Thr Ser Gly	
35 40 45	
atg ccg gtg gaa aaa gtc atg aaa tcc ttc cag gac ggc ttc ggc ggc	192
Met Pro Val Glu Lys Val Met Lys Ser Phe Gln Asp Gly Phe Gly Gly	
50 55 60	
gta ctg ggc ttc gtt ggt atc atc ctc ggc ctg ggc acc atg ctc ggc	240
Val Leu Gly Phe Val Gly Ile Ile Leu Gly Leu Gly Thr Met Leu Gly	
65 70 75 80	
aag ctg atg gcc gac tcg ggc ggc gcg gac cag att gcg caa acg ctg	288
Lys Leu Met Ala Asp Ser Gly Gly Ala Asp Gln Ile Ala Gln Thr Leu	
85 90 95	
ata cgc acc ttc ggc aaa cag aaa gtg cac tgg gca atg atg ttc tct	336
100 105 110	

PF59083SeqList PF59083.txt

Ile	Arg	Thr	Phe	Gly	Lys	Gln	Lys	Val	His	Trp	Ala	Met	Met	Phe	Ser		
gcc	ttt	ctg	gtg	ggc	atc	ccg	ctg	ttc	ttc	gag	atc	ggc	ttt	gtc	ctg	384	
Ala	Phe	Leu	Val	Gly	Ile	Pro	Leu	Phe	Phe	Glu	Ile	Gly	Phe	Val	Leu		
	115						120					125					
ctg	atc	ccg	ctg	gtg	ttc	atc	gtc	gcg	cgg	cgc	acc	ggc	gtg	ccc	atc	432	
Leu	Ile	Pro	Leu	Val	Phe	Ile	Val	Ala	Arg	Arg	Thr	Gly	Val	Pro	Ile		
	130					135					140						
gtc	aag	atc	ggc	att	ccg	ctg	ctg	gca	ggc	ctg	tcg	gcc	gta	cac	ggc	480	
Val	Lys	Ile	Gly	Ile	Pro	Leu	Leu	Ala	Gly	Leu	Ser	Ala	Val	His	Gly		
	145				150					155					160		
ctg	gtt	cct	ccg	cat	cca	ggc	ccg	ttg	ctg	gcc	atc	ggc	atc	ttc	ggg	528	
Leu	Val	Pro	Pro	His	Pro	Gly	Pro	Leu	Leu	Ala	Ile	Gly	Ile	Phe	Gly		
				165				170						175			
gct	gac	atc	ggc	aaa	acc	att	ttc	tac	gga	ctg	atc	gtt	gcg	ctg	ccg	576	
Ala	Asp	Ile	Gly	Lys	Thr	Ile	Phe	Tyr	Gly	Leu	Ile	Val	Ala	Leu	Pro		
			180					185					190				
acg	gcc	atc	atc	gct	ggc	ccg	atc	ttc	ggc	aac	tgg	att	tcc	aaa	agc	624	
Thr	Ala	Ile	Ile	Ala	Gly	Pro	Ile	Phe	Gly	Asn	Trp	Ile	Ser	Lys	Ser		
	195					200						205					
atc	ccc	ggc	aca	ccg	tcc	aag	gaa	ctg	atg	gat	cag	atc	gcc	aag	gag	672	
Ile	Pro	Gly	Thr	Pro	Ser	Lys	Glu	Leu	Met	Asp	Gln	Ile	Ala	Lys	Glu		
	210					215					220						
tcg	agc	act	gaa	aac	ctg	cca	ggc	ttc	ggc	atc	acg	ctg	gtg	acc	atc	720	
Ser	Ser	Thr	Glu	Asn	Leu	Pro	Gly	Phe	Gly	Ile	Thr	Leu	Val	Thr	Ile		
	225				230					235				240			
ctg	ctg	ccg	gtc	ttc	ctg	atg	ctg	ctc	aag	acc	ttt	gcc	gac	gtg	gtg	768	
Leu	Leu	Pro	Val	Phe	Leu	Met	Leu	Leu	Lys	Thr	Phe	Ala	Asp	Val	Val		
			245					250					255				
ttg	ccg	gaa	aac	atg	ttc	cgc	atc	trg	atg	gac	ctg	atc	ggc	cac		816	
Leu	Pro	Glu	Asn	Asn	Met	Phe	Arg	Ile	Trp	Met	Asp	Leu	Ile	Gly	His		
		260					265					270					
ccg	atc	acc	gcc	ctg	ctt	gcc	gcg	ctg	ttg	ctg	gcg	ttc	tac	acc	ttt	864	
Pro	Ile	Thr	Ala	Leu	Leu	Ala	Ala	Leu	Leu	Leu	Ala	Phe	Tyr	Thr	Phe		
	275						280					285					
ggc	gcc	gcg	cgt	ggc	ttc	gac	cgc	agc	aag	atc	atg	aag	ctg	ctg	gac	912	
Gly	Ala	Ala	Arg	Gly	Phe	Asp	Arg	Ser	Lys	Ile	Met	Lys	Leu	Leu	Asp		
	290					295				300							
cag	agt	ctg	gcc	ccg	gtg	gcg	gca	atc	gtg	ctg	att	gtc	ggc	gca	ggc	960	
Gln	Ser	Leu	Ala	Pro	Val	Ala	Ala	Ile	Val	Leu	Ile	Val	Gly	Ala	Gly		
	305				310				315					320			
ggc	ggc	ttc	aag	cag	atg	ctg	gtc	gcc	agt	ggc	gta	ggc	gac	gtg	atc	1008	
Gly	Gly	Phe	Lys	Gln	Met	Leu	Val	Ala	Ser	Gly	Val	Gly	Asp	Val	Ile		
			325					330					335				
ggg	cac	atg	gcc	gtg	cag	gcg	cag	atc	aac	ccg	atc	atg	ctg	gcc	ttg	1056	
Gly	His	Met	Ala	Val	Gln	Ala	Gln	Ile	Asn	Pro	Ile	Met	Leu	Ala	Trp		
		340					345					350					
ctg	gtt	gcg	gcg	gtc	atc	cgc	gtc	gca	aca	ggc	tcg	gcg	acg	gtg	gca	1104	
Leu	Val	Ala	Ala	Val	Ile	Arg	Val	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala		
	355						360					365					
acc	att	acc	ggc	gct	ggc	atc	gta	gcg	ccg	gtg	gtc	ggc	ctg	att	cca	1152	
Thr	Ile	Thr	Gly	Ala	Gly	Ile	Val	Ala	Pro	Val	Val	Gly	Leu	Ile	Pro		
	370				375						380						
ggg	gtc	aat	cgc	gag	ctg	ctg	gtg	ctg	gca	acc	ggc	ggc	ggc	tcg	ttg	1200	
Gly	Val	Asn	Arg	Glu	Leu	Leu	Val	Leu	Ala	Thr	Gly	Ala	Gly	Ser	Leu		
	385				390				395					400			
atc	ctg	tcg	cac	gtc	aat	gac	gcc	ggg	ttc	trg	ctg	gtg	aag	cag	tac	1248	
Ile	Leu	Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Leu	Val	Lys	Gln	Tyr		
			405					410					415				
ttc	aac	atg	acc	gtt	gcc	gag	acc	ttc	aag	acc	tgg	acg	gtg	atg	gag	1296	
Phe	Asn	Met	Thr	Val	Ala	Glu	Thr	Phe	Lys	Thr	Trp	Thr	Val	Met	Glu		
			420				425					430					
acc	atc	ctc	tcg	gtc	gtc	ggc	ctg	atc	ttc	atc	atg	ctg	ttg	tca	atg	1344	
Thr	Ile	Leu	Ser	Val	Val	Gly	Leu	Ile	Phe	Ile	Met	Leu	Leu	Ser	Met		
		435					440					445					
gcg	gtg	taa														1353	
Ala	Val																
	450																

PF59083SeqList PF59083.txt

<210> 10179

<211> 450

<212> PRT

<213> Pseudomonas syringae pv. syringae B728a

<400> 10179

```

Met Phe Gly Met Thr His Glu Thr Phe Leu Leu Val Asp Ala Leu Val
1      5      10      15
Thr Ile Val Gly Leu Val Leu Leu Ile Thr Thr Phe Lys Val His Pro
20      25      30
Phe Val Ala Leu Thr Leu Ala Ala Gly Phe Leu Gly Leu Thr Ser Gly
35      40      45
Met Pro Val Glu Lys Val Met Lys Ser Phe Gln Asp Gly Phe Gly Gly
50      55      60
Val Leu Gly Phe Val Gly Ile Ile Leu Gly Leu Gly Thr Met Leu Gly
65      70      75      80
Lys Leu Met Ala Asp Ser Gly Gly Ala Asp Gln Ile Ala Gln Thr Leu
85      90      95
Ile Arg Thr Phe Gly Lys Gln Lys Val His Trp Ala Met Met Phe Ser
100     105     110
Ala Phe Leu Val Gly Ile Pro Leu Phe Phe Glu Ile Gly Phe Val Leu
115     120     125
Leu Ile Pro Leu Val Phe Ile Val Ala Arg Arg Thr Gly Val Pro Ile
130     135     140
Val Lys Ile Gly Ile Pro Leu Leu Ala Gly Leu Ser Ala Val His Gly
145     150     155     160
Leu Val Pro Pro His Pro Gly Pro Leu Leu Ala Ile Gly Ile Phe Gly
165     170     175
Ala Asp Ile Gly Lys Thr Ile Phe Tyr Gly Leu Ile Val Ala Leu Pro
180     185     190
Thr Ala Ile Ile Ala Gly Pro Ile Phe Gly Asn Trp Ile Ser Lys Ser
195     200     205
Ile Pro Gly Thr Pro Ser Lys Glu Leu Met Asp Gln Ile Ala Lys Glu
210     215     220
Ser Ser Thr Glu Asn Leu Pro Gly Phe Gly Ile Thr Leu Val Thr Ile
225     230     235     240
Leu Leu Pro Val Phe Leu Met Leu Leu Lys Thr Phe Ala Asp Val Val
245     250     255
Leu Pro Glu Asn Met Phe Arg Ile Trp Met Asp Leu Ile Gly His
260     265     270
Pro Ile Thr Ala Leu Leu Ala Ala Leu Leu Leu Ala Phe Tyr Thr Phe
275     280     285
Gly Ala Ala Arg Gly Phe Asp Arg Ser Lys Ile Met Lys Leu Leu Asp
290     295     300
Gln Ser Leu Ala Pro Val Ala Ala Ile Val Leu Ile Val Gly Ala Gly
305     310     315     320
Gly Gly Phe Lys Gln Met Leu Val Ala Ser Gly Val Gly Asp Val Ile
325     330     335
Gly His Met Ala Val Gln Ala Gln Ile Asn Pro Ile Met Leu Ala Trp
340     345     350
Leu Val Ala Ala Val Ile Arg Val Ala Thr Gly Ser Ala Thr Val Ala
355     360     365
Thr Ile Thr Gly Ala Gly Ile Val Ala Pro Val Val Gly Leu Ile Pro
370     375     380
Gly Val Asn Arg Glu Leu Leu Val Leu Ala Thr Gly Ala Gly Ser Leu
385     390     395     400
Ile Leu Ser His Val Asn Asp Ala Gly Phe Trp Leu Val Lys Gln Tyr
405     410     415
Phe Asn Met Thr Val Ala Glu Thr Phe Lys Thr Trp Thr Val Met Glu
420     425     430
Thr Ile Leu Ser Val Val Gly Leu Ile Phe Ile Met Leu Leu Ser Met
435     440     445
Ala Val
450

```

<210> 10180

<211> 1353

<212> DNA

<213> Pseudomonas fluorescens Pf0-1

PF59083SeqList PF59083.txt

<220>
 <221> CDS
 <222> (1)..(1353)
 <223> transl_table=11

<400> 10180

atg ttt ggc atg tcc cat gac gcc tac ctg ctg ctc gat gca gtg gtt	48
Met Phe Gly Met Ser His Asp Ala Tyr Leu Leu Leu Asp Ala Val Val	
1 5 10 15	
acg gtg atc gga ctc atc gtc ctg atc acc aag ttc aag att cac ccc	96
Thr Val Ile Gly Leu Ile Val Leu Ile Thr Lys Phe Lys Ile His Pro	
20 25 30	
ttc att gcc ctg acc atc gcc gcc gcg ttc ctt ggc ctg acg tcc ggc	144
Phe Ile Ala Leu Thr Ile Ala Ala Phe Leu Gly Thr Ser Gly	
35 40 45	
atg ccg atc ggc acg atc atc aag gcg ttc cag gac ggc ttc ggt ggc	192
Met Pro Ile Gly Thr Ile Ile Lys Ala Phe Gln Asp Gly Phe Gly Gly	
50 55 60	
gtg ctc ggt ttt gtc ggc atc atc ctc gcc ctg ggc acg atg ctc ggc	240
Val Leu Gly Phe Val Gly Ile Ile Leu Ala Leu Gly Thr Met Leu Gly	
65 70 75 80	
aag atg atg gcc gaa tcc ggt ggt gcc gat cag atc gcc cag acc ctg	288
Lys Met Met Ala Glu Ser Gly Gly Ala Asp Gln Ile Ala Gln Thr Leu	
85 90 95	
atc cgc gcc ttc ggc aag gac aag gtg cag tgg gcg atg atg ttc gcc	336
Ile Arg Ala Phe Gly Lys Asp Lys Val Gln Trp Ala Met Met Phe Ala	
100 105 110	
gcg ttc ctg gtg ggc att ccg ctg ttc ttc gaa atc ggc ttc gtg ttg	384
Ala Phe Leu Val Gly Ile Pro Leu Phe Phe Glu Ile Gly Phe Val Leu	
115 120 125	
ctg att ccg ctg gtg ttc atc gtg gct cgc cgc act ggt gtg tcg atc	432
Leu Ile Pro Leu Val Phe Ile Val Ala Arg Arg Thr Gly Val Ser Ile	
130 135 140	
atc aag atc ggt atc ccg ctg ctc gcc ggt ctg tcc gcc gtg cac ggc	480
Ile Lys Ile Gly Ile Pro Leu Leu Ala Gly Leu Ser Ala Val His Gly	
145 150 155 160	
ttg gtg ccg ccg cac ccg ggc ccg ctg ctg gcc atc ggc gtg ttc ggt	528
Leu Val Pro Pro His Pro Gly Pro Leu Leu Ala Ile Gly Val Phe Gly	
165 170 175	
gcc gac atc ggc aag acc att ctg tac ggt ctg atc gtc gcg ctg ccg	576
Ala Asp Ile Gly Lys Thr Ile Leu Tyr Gly Leu Ile Val Ala Leu Pro	
180 185 190	
acc gcc atc atc gcc ggc ccg atc ttc ggt acg ttc atc gcc aag cac	624
Thr Ala Ile Ala Gly Pro Ile Phe Gly Thr Phe Ile Ala Lys His	
195 200 205	
att ccc ggt acg ccg aac cag gaa ctg gtc gat caa ctg gcc cgt gaa	672
Ile Pro Gly Thr Pro Asn Gln Glu Leu Val Asp Gln Leu Ala Arg Glu	
210 215 220	
aac gat tcg gcc aac ctg agc ttc agc atc acc ctg gtc acc gtg	720
Asn Asp Ser Ala Asn Leu Pro Ser Phe Ser Ile Thr Leu Val Thr Val	
225 230 235 240	
ctg ctg ccg gtg ttc ctg atg ctg ctg aaa acc ttc gct gac gtg gcc	768
Leu Leu Pro Val Phe Leu Met Leu Leu Lys Thr Phe Ala Asp Val Ala	
245 250 255	
ctg ccg gac ggt cat ttc ttc cgc acc tgg atg gac atg atc ggt cac	816
Leu Pro Asp Gly His Phe Phe Arg Thr Trp Met Asp Met Ile Gly His	
260 265 270	
ccg atc tcg gca ctg ctg ctg gca ttg ctg ctg tcg ctg tac acc ttc	864
Pro Ile Ser Ala Leu Leu Leu Ala Leu Leu Leu Ser Leu Tyr Thr Phe	
275 280 285	
ggt cac aag cag ggc atc ggt tct cag cag atg ctc aaa tgg ctg gac	912
Gly His Lys Gln Gly Ile Gly Ser Gln Gln Met Leu Lys Trp Leu Asp	
290 295 300	
gcg agc ctg gcg ccg acc ggc gca atc att ctg atc ggc gcc ggc	960
Ala Ser Leu Ala Pro Thr Ala Ala Ile Ile Leu Ile Ile Gly Ala Gly	
305 310 315 320	
ggt ggc ttc aag cag atg ctg gtg acc agc ggc gtg ggc gac gtg atc	1008
Gly Gly Phe Lys Gln Met Leu Val Thr Ser Gly Val Gly Asp Val Ile	

PF59083SeqList PF59083.txt

ggc	cac	atg	gcg	gtc	agc	gcg	cag	atc	tcg	ccg	atc	ctg	ctg	gcg	tgg	1056
Gly	His	Met	Ala	Val	Ser	Ala	Gln	Ile	Ser	Pro	Ile	Leu	Leu	Ala	Trp	
			340				345						350			
ctg	gtg	gcg	gcg	gtg	atc	cgc	atc	gcg	acc	ggc	tcg	gcc	acc	gtg	gcg	1104
Leu	Val	Ala	Ala	Val	Ile	Arg	Ile	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	
			355				360						365			
acc	atc	act	ggc	gcg	ggc	atc	gtg	gtg	ccg	gtg	gtg	ggg	atg	atc	ccg	1152
Thr	Ile	Thr	Gly	Ala	Gly	Ile	Val	Val	Pro	Val	Val	Gly	Met	Ile	Pro	
			370				375					380				
ggc	gtg	aac	cgt	gag	ctg	ctg	gtg	ctg	gcc	acc	ggc	ggc	ggc	tcg	ctg	1200
Gly	Val	Asn	Arg	Glu	Leu	Leu	Val	Leu	Ala	Thr	Gly	Ala	Gly	Ser	Leu	
					390					395					400	
atc	ctg	tcc	cac	gtc	aac	gac	gcc	ggc	ttc	tgg	ctg	gtg	aag	cag	tac	1248
Ile	Leu	Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Leu	Val	Lys	Gln	Tyr	
				405					410					415		
ttc	aac	atg	acc	gtg	gcc	gag	acc	ttc	aag	acc	tgg	acg	gcg	atg	gaa	1296
Phe	Asn	Met	Thr	Val	Ala	Glu	Thr	Phe	Lys	Thr	Trp	Thr	Ala	Met	Glu	
			420					425					430			
acc	atc	ctg	tcg	gtg	gtg	ggg	ctg	ggc	ttt	att	ctg	ttg	ttg	tcg	ctg	1344
Thr	Ile	Leu	Ser	Val	Val	Gly	Leu	Gly	Phe	Ile	Leu	Leu	Leu	Ser	Leu	
			435				440					445				
ttc	gtt	taa														1353
Phe	Val															
	450															

<210> 10181

<211> 450

<212> PRT

<213> Pseudomonas fluorescens Pf0-1

<400> 10181

Met	Phe	Gly	Met	Ser	His	Asp	Ala	Tyr	Leu	Leu	Leu	Asp	Ala	Val	Val	
1				5					10					15		
Thr	Val	Ile	Gly	Leu	Ile	Val	Leu	Ile	Thr	Lys	Phe	Lys	Ile	His	Pro	
			20					25					30			
Phe	Ile	Ala	Leu	Thr	Ile	Ala	Ala	Ala	Phe	Leu	Gly	Leu	Thr	Ser	Gly	
		35				40						45				
Met	Pro	Ile	Gly	Thr	Ile	Ile	Lys	Ala	Phe	Gln	Asp	Gly	Phe	Gly	Gly	
	50					55					60					
Val	Leu	Gly	Phe	Val	Gly	Ile	Ile	Leu	Ala	Leu	Gly	Thr	Met	Leu	Gly	
65					70					75					80	
Lys	Met	Met	Ala	Glu	Ser	Gly	Gly	Ala	Asp	Gln	Ile	Ala	Gln	Thr	Leu	
			85					90					95			
Ile	Arg	Ala	Phe	Gly	Lys	Asp	Lys	Val	Gln	Trp	Ala	Met	Met	Phe	Ala	
		100						105					110			
Ala	Phe	Leu	Val	Gly	Ile	Pro	Leu	Phe	Phe	Glu	Ile	Gly	Phe	Val	Leu	
	115						120					125				
Leu	Ile	Pro	Leu	Val	Phe	Ile	Val	Ala	Arg	Arg	Thr	Gly	Val	Ser	Ile	
	130					135					140					
Ile	Lys	Ile	Gly	Ile	Pro	Leu	Leu	Ala	Gly	Leu	Ser	Ala	Val	His	Gly	
145					150					155					160	
Leu	Val	Pro	Pro	His	Pro	Gly	Pro	Leu	Leu	Ala	Ile	Gly	Val	Phe	Gly	
			165						170					175		
Ala	Asp	Ile	Gly	Lys	Thr	Ile	Leu	Tyr	Gly	Leu	Ile	Val	Ala	Leu	Pro	
		180						185					190			
Thr	Ala	Ile	Ile	Ala	Gly	Pro	Ile	Phe	Gly	Thr	Phe	Ile	Ala	Lys	His	
	195						200					205				
Ile	Pro	Gly	Thr	Pro	Asn	Gln	Glu	Leu	Val	Asp	Gln	Leu	Ala	Arg	Glu	
	210					215						220				
Asn	Asp	Ser	Ala	Asn	Leu	Pro	Ser	Phe	Ser	Ile	Thr	Leu	Val	Thr	Val	
225					230					235					240	
Leu	Leu	Pro	Val	Phe	Leu	Met	Leu	Leu	Lys	Thr	Phe	Ala	Asp	Val	Ala	
			245						250					255		
Leu	Pro	Asp	Gly	His	Phe	Phe	Arg	Thr	Trp	Met	Asp	Met	Ile	Gly	His	
		260						265					270			
Pro	Ile	Ser	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ser	Leu	Tyr	Thr	Phe	
	275						280					285				
Gly	His	Lys	Gln	Gly	Ile	Gly	Ser	Gln	Gln	Met	Leu	Lys	Trp	Leu	Asp	

PF59083SeqList PF59083.txt

```

290          295          300
Ala Ser Leu Ala Pro Thr Ala Ala Ile Ile Leu Ile Ile Gly Ala Gly
305 Gly Gly Phe Lys Gln Met Leu Val Thr Ser Gly Val Gly Asp Val Ile
Gly His Met Ala Val Ser Ala Gln Ile Ser Pro Ile Leu Leu Ala Trp
Leu Val Ala Ala Val Ile Arg Ile Ala Thr Gly Ser Ala Thr Val Ala
Thr Ile Thr Gly Ala Gly Ile Val Val Pro Val Val Gly Met Ile Pro
370 Gly Val Asn Arg Glu Leu Leu Val Leu Ala Thr Gly Ala Gly Ser Leu
385 Ile Leu Ser His Val Asn Asp Ala Gly Phe Trp Leu Val Lys Gln Tyr
Phe Asn Met Thr Val Ala Glu Thr Phe Lys Thr Trp Thr Ala Met Glu
Thr Ile Leu Ser Val Val Gly Leu Gly Phe Ile Leu Leu Leu Ser Leu
Phe Val
450

```

<210> 10182

<211> 1359

<212> DNA

<213> Rhodospirillum rubrum ATCC 11170

<220>

<221> CDS

<222> (1)..(1359)

<223> transl_table=11

<400> 10182

```

atg cac ccc gat aca acg ctg atc ctt atc gca gcc gcc tcg atc gtt      48
Met His Pro Asp Thr Leu Ile Leu Ile Ala Ala Ala Ser Ile Val
1          5          10          15
ctt ctg gtg ctg ctg gtt acc cgc ctg aag ctt cac ccc ttt ttg gcc      96
Leu Leu Val Leu Leu Val Thr Arg Leu Lys Leu His Pro Phe Leu Ala
20          25          30
ctg atg gtc gcc gcc ttt ctt ggg ctg gcc agc ggc ctc gcg ccg      144
Leu Met Val Ala Ala Ala Phe Leu Gly Leu Ala Ser Gly Leu Ala Pro
35          40          45
acc gat gcg gtc aag acc ttc cag aag ggc ttt ggc aat atc ctg ggc      192
Thr Asp Ala Val Lys Thr Phe Gln Lys Gly Phe Gly Asn Ile Leu Gly
50          55          60
tcg gtc ggc ctg gtc gtc ggc ctt ggc agc atg ttg ggc ggc ctg ttg      240
Ser Val Gly Leu Val Val Gly Leu Gly Ser Met Leu Gly Gly Leu Leu
65          70          75          80
ctc aac acc ggg ggt gcc gat cgc atc gcc aac gcc ttc gtc ggt cgc      288
Leu Asn Thr Gly Gly Ala Asp Arg Ile Ala Asn Ala Phe Val Gly Arg
85          90          95
ggg tcg acg gtg tgg ctg ccc aca tcg atc tgc gcg gcg gcc ttg ctg      336
Gly Ser Thr Val Trp Leu Pro Thr Ser Ile Cys Ala Ala Ala Leu Leu
100          105          110
atc ggc atg ccc cat ctg ttt gat gtc agc ttc gtc atg ctg gtg ccg      384
Ile Gly Met Pro His Leu Phe Asp Val Ser Phe Val Met Leu Val Pro
115          120          125
ctg gtc ttc gcc atc gcc aag cgc acc ggc agc cat ctg atg cgt gtc      432
Leu Val Phe Ala Ile Ala Lys Arg Thr Gly Ser His Leu Met Arg Val
130          135          140
ggc ctg ccg atg gcg gcg ggg ctt tac gtc tcg cac ggc ttc ttg ctg      480
Gly Leu Pro Met Ala Ala Gly Leu Tyr Val Ser His Gly Phe Leu Leu
145          150          155          160
ccc cat ccc tcg ccg acc ttg gct ttg gcc atc tat cat ggc gac gcc      528
Pro His Pro Ser Thr Leu Ala Leu Ala Ile Tyr His Gly Asp Ala
165          170          175
ggg cgg gcg atc ctc ttt ggt ttc ctg ctg gcg atc ccg acg gcc atc      576
Gly Arg Ala Ile Leu Phe Gly Phe Leu Leu Ala Ile Pro Thr Ala Ile
180          185          190

```

PF59083SeqList PF59083.txt

ctc	tcg	ggc	ccg	ctg	ctc	acc	tcc	ttt	gcc	atg	cgt	tgg	ttc	aag	gat	624
Leu	Ser	Gly	Pro	Leu	Leu	Thr	Ser	Phe	Ala	Met	Arg	Trp	Phe	Lys	Asp	
		195					200					205				
ccg	atc	gac	atc	acc	cat	agc	ccg	atc	atg	acg	gcg	gcc	gga	cgg	agc	672
Pro	Ile	Asp	Ile	Thr	His	Ser	Pro	Ile	Met	Thr	Ala	Ala	Gly	Arg	Ser	
		210					215					220				
gat	gtc	acc	acg	ctt	gat	aac	gcc	ccc	cga	ctg	ccg	gtg	gtt	ctg	ctg	720
Asp	Val	Thr	Thr	Leu	Asp	Asn	Ala	Pro	Arg	Leu	Pro	Val	Val	Leu	Leu	
		225					230				235				240	
acc	gtc	ctg	ctg	ccg	ccc	ggt	ttg	atg	ctg	ttg	cgc	acc	ctg	ttg	gcc	768
Thr	Val	Leu	Leu	Pro	Pro	Gly	Leu	Met	Leu	Leu	Arg	Thr	Leu	Leu	Ala	
				245					250						255	
gac	cat	gtt	ccc	gaa	ggc	gcc	gcc	cgg	gcc	ttt	ctc	gat	ggc	atc	ggc	816
Asp	His	Val	Pro	Glu	Gly	Ala	Ala	Arg	Ala	Phe	Leu	Asp	Gly	Ile	Gly	
			260					265					270			
aat	ccc	atc	gtc	tcg	ctg	gcc	atc	gcc	gtg	ttg	ttt	gcc	atc	tgg	gcc	864
Asn	Pro	Ile	Val	Ser	Leu	Ala	Ile	Ala	Val	Leu	Phe	Ala	Ile	Trp	Ala	
			275				280					285				
ctt	ggg	gtg	cgc	tcg	ggc	cgt	tcg	ctg	ggc	gag	atc	cag	aag	ctg	ctc	912
Leu	Gly	Val	Arg	Ser	Gly	Arg	Ser	Leu	Gly	Glu	Ile	Gln	Lys	Leu	Leu	
		290					295				300					
ggc	aaa	agc	ctg	gcc	ccg	gcc	gcc	ggg	gtg	atc	ctg	atc	gtc	ggc	gcc	960
Gly	Lys	Ser	Leu	Ala	Pro	Ala	Ala	Gly	Val	Ile	Leu	Ile	Val	Gly	Ala	
		305				310				315					320	
ggt	ggc	ggt	ctc	aag	gaa	atg	ctg	ctc	ggc	acc	cat	atc	ggc	gac	atg	1008
Gly	Gly	Gly	Leu	Lys	Glu	Met	Leu	Leu	Gly	Thr	His	Ile	Gly	Asp	Met	
				325					330					335		
atc	gcc	agc	ggc	gcg	gcg	caa	tgg	gcg	atc	tcg	ccc	ctg	gtg	ctg	gcc	1056
Ile	Ala	Ser	Gly	Ala	Ala	Gln	Trp	Ala	Ile	Ser	Pro	Leu	Val	Leu	Ala	
			340					345					350			
tgg	gtg	atc	gcc	gcc	ctg	atg	cgc	atc	gcc	gtc	ggc	tcg	gcc	acc	gtc	1104
Trp	Val	Ile	Ala	Ala	Leu	Met	Arg	Ile	Ala	Val	Gly	Ser	Ala	Thr	Val	
			355				360					365				
gcc	acg	gtc	acc	gcc	gcc	ggg	ttg	atg	gcg	ccg	gtg	cag	gcg	ctc	cac	1152
Ala	Thr	Val	Thr	Ala	Ala	Gly	Leu	Met	Ala	Pro	Val	Gln	Ala	Leu	His	
		370				375					380					
ccc	gaa	atc	agc	ccc	gaa	ttg	atg	acc	atc	tcg	gtc	gcc	acc	ggc	ggg	1200
Pro	Glu	Ile	Ser	Pro	Glu	Leu	Met	Thr	Ile	Ser	Val	Ala	Thr	Gly	Gly	
		385				390				395					400	
ctg	atg	ctc	tcc	cac	ctc	aac	gac	agc	ggc	ttc	tgg	ctg	ttc	aag	gaa	1248
Leu	Met	Leu	Ser	His	Leu	Asn	Asp	Ser	Gly	Phe	Trp	Leu	Phe	Lys	Glu	
				405					410					415		
tac	ttc	caa	ctc	acc	gtc	gcc	cag	acg	ctg	aaa	agc	tgg	acg	ttg	atg	1296
Tyr	Phe	Gln	Leu	Thr	Val	Ala	Gln	Thr	Leu	Lys	Ser	Trp	Thr	Leu	Met	
			420					425					430			
gtc	tcg	gtc	cag	tcg	gcg	ctt	ggt	ctg	gcc	ggt	gtt	ctg	ctg	atc	gac	1344
Val	Ser	Val	Gln	Ser	Ala	Leu	Gly	Leu	Ala	Gly	Val	Leu	Leu	Ile	Asp	
			435				440					445				
gcg	gtg	atc	cgc	taa												1359
Ala	Val	Ile	Arg													
		450														

<210> 10183

<211> 452

<212> PRT

<213> Rhodospirillum rubrum ATCC 11170

<400> 10183

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

PF59083SeqList PF59083.txt

```

      85      90      95
Gly Ser Thr Val Trp Leu Pro Thr Ser Ile Cys Ala Ala Ala Leu Leu
      100      105      110
Ile Gly Met Pro His Leu Phe Asp Val Ser Phe Val Met Leu Val Pro
      115      120      125
Leu Val Phe Ala Ile Ala Lys Arg Thr Gly Ser His Leu Met Arg Val
      130      135      140
Gly Leu Pro Met Ala Ala Gly Leu Tyr Val Ser His Gly Phe Leu Leu
      145      150      155
Pro His Pro Ser Pro Thr Leu Ala Leu Ala Ile Tyr His Gly Asp Ala
      160      165      170
Gly Arg Ala Ile Leu Phe Gly Phe Leu Leu Ala Ile Pro Thr Ala Ile
      175      180      185
Leu Ser Gly Pro Leu Leu Thr Ser Phe Ala Met Arg Trp Phe Lys Asp
      190      195      200
Pro Ile Asp Ile Thr His Ser Pro Ile Met Thr Ala Ala Gly Arg Ser
      205      210      215
Asp Val Thr Thr Leu Asp Asn Ala Pro Arg Leu Pro Val Val Leu Leu
      220      225      230
Thr Val Leu Leu Pro Gly Leu Met Leu Leu Arg Thr Leu Leu Ala
      235      240      245
Asp His Val Pro Glu Gly Ala Ala Arg Ala Phe Leu Asp Gly Ile Gly
      250      255      260
Asn Pro Ile Val Ser Leu Ala Ile Ala Val Leu Phe Ala Ile Trp Ala
      265      270      275
Leu Gly Val Arg Ser Gly Arg Ser Leu Gly Glu Ile Gln Lys Leu Leu
      280      285      290
Gly Lys Ser Leu Ala Pro Ala Ala Gly Val Ile Leu Ile Val Gly Ala
      295      300      305
Gly Gly Gly Leu Lys Glu Met Leu Leu Gly Thr His Ile Gly Asp Met
      310      315      320
Ile Ala Ser Gly Ala Ala Gln Trp Ala Ile Ser Pro Leu Val Leu Ala
      325      330      335
Trp Val Ile Ala Ala Leu Met Arg Ile Ala Val Gly Ser Ala Thr Val
      340      345      350
Ala Thr Val Thr Ala Ala Gly Leu Met Ala Pro Val Gln Ala Leu His
      355      360      365
Pro Glu Ile Ser Pro Glu Leu Met Thr Ile Ser Val Ala Thr Gly Gly
      370      375      380
Leu Met Leu Ser His Leu Asn Asp Ser Gly Phe Trp Leu Phe Lys Glu
      385      390      395
Tyr Phe Gln Leu Thr Val Ala Gln Thr Leu Lys Ser Trp Thr Leu Met
      400      405      410
Val Ser Val Gln Ser Ala Leu Gly Leu Ala Gly Val Leu Leu Ile Asp
      415      420      425
Ala Val Ile Arg
      430      435      440
      445      450

```

<210> 10184

<211> 1386

<212> DNA

<213> Moorella thermoacetica ATCC 39073

<220>

<221> CDS

<222> (1)..(1386)

<223> transl_table=11

<400> 10184

```

atg gga ggc att tcc gga att cag ata att att ggt ctg att gtt ggt      48
Met Gly Gly Ile Ser Gly Ile Gln Ile Ile Ile Gly Leu Ile Val Gly
      1      5      10      15
atc ttt gtg ctt gta tat tta ata ctg agg acc aaa att cat gct ttt      96
Ile Phe Val Leu Val Tyr Leu Ile Leu Arg Thr Lys Ile His Ala Phe
      20      25      30
cct gct ctt atc att gcg gct tcc gta atc ggg tta att ggt ggt atg      144
Pro Ala Leu Ile Ile Ala Ala Ser Val Ile Gly Leu Ile Gly Gly Met
      35      40      45
tca cca tct aca ggt gat att aac ctt gct aaa tca atc act act ggc      192

```

PF59083SeqList PF59083.txt															
Ser	Pro	Ser	Thr	Gly	Asp	Ile	Asn	Leu	Ala	Lys	Ser	Ile	Thr	Thr	Gly
50	55	60													
ttt	ggt	aat	act	tta	gca	agt	atc	ggt	ctc	gta	att	ggt	ttt	ggc	gta
Phe	Gly	Asn	Thr	Leu	Ala	Ser	Ile	Gly	Leu	Val	Ile	Gly	Phe	Gly	Val
65	70	75													
atg	atg	gga	cga	ttg	ctg	gag	gta	tcc	ggg	gct	gcc	gaa	cgt	atg	gct
Met	Met	Gly	Arg	Leu	Leu	Glu	Val	Ser	Gly	Ala	Ala	Glu	Arg	Met	Ala
tat	act	ttc	tta	aag	tat	cta	gga	cgt	gga	aaa	gaa	gaa	tgg	gcg	ctg
Tyr	Thr	Phe	Leu	Lys	Tyr	Leu	Gly	Arg	Gly	Lys	Glu	Glu	Trp	Ala	Leu
gcc	gca	acg	gga	tat	gtc	att	tct	att	cct	att	ttc	tgc	gat	tcg	ggt
Ala	Ala	Thr	Gly	Tyr	Val	Ile	Ser	Ile	Pro	Ile	Phe	Cys	Asp	Ser	Gly
ttt	gtt	att	tta	aca	ccc	ctg	gtt	aaa	gcg	tta	tca	cgt	aga	acc	aaa
Phe	Val	Ile	Leu	Thr	Pro	Leu	Val	Lys	Ala	Leu	Ser	Arg	Arg	Thr	Lys
aaa	tcc	gta	ctt	gct	ctt	ggt	gtc	gct	ctg	gca	gcc	ggt	cta	gtg	gct
Lys	Ser	Val	Leu	Ala	Leu	Gly	Val	Ala	Leu	Ala	Ala	Gly	Leu	Val	Ala
145	150	155													
acc	cat	agt	gca	gta	cca	cca	aca	ccg	gga	cct	ctg	gca	gta	gca	ggc
Thr	His	Ser	Ala	Val	Pro	Pro	Thr	Pro	Gly	Pro	Leu	Ala	Val	Ala	Gly
att	ttt	aaa	gtt	gat	gta	ggt	atg	gta	att	att	tcc	ggg	ctt	ata	ttt
Ile	Phe	Lys	Val	Asp	Val	Gly	Met	Val	Ile	Ile	Ser	Gly	Leu	Ile	Phe
acc	ata	cca	ata	act	ata	gct	ggg	gtt	ttg	tac	ggc	aaa	tgg	ttg	ggt
Thr	Ile	Pro	Ile	Thr	Ile	Ala	Gly	Val	Leu	Tyr	Gly	Lys	Trp	Leu	Gly
aaa	aaa	ata	tat	caa	tta	ccc	agt	gaa	gat	ggt	cag	agc	tgg	ata	cga
Lys	Lys	Ile	Tyr	Gln	Leu	Pro	Ser	Glu	Asp	Gly	Gln	Ser	Trp	Ile	Arg
cca	cct	tac	caa	tct	tct	cag	att	gcc	gaa	gaa	gca	ttg	cct	gaa	aat
Pro	Pro	Tyr	Gln	Ser	Ser	Gln	Ile	Ala	Glu	Glu	Ala	Leu	Pro	Glu	Asn
225	230	235													
ggc	aac	ctg	cct	tcc	gct	ttt	ata	tcc	ttt	gcc	cct	gtt	gtt	att	cct
Gly	Asn	Leu	Pro	Ser	Ala	Phe	Ile	Ser	Phe	Ala	Pro	Val	Val	Ile	Pro
tta	att	tta	atc	ttt	gtc	aat	acg	ttg	ctg	aca	gct	atg	aaa	ata	aac
Leu	Ile	Leu	Ile	Phe	Val	Asn	Thr	Leu	Leu	Thr	Ala	Met	Lys	Ile	Asn
caa	cta	tgg	gcg	cgc	tac	cta	gtt	ttc	ctg	ggt	aat	ccg	gta	ata	gcg
Gln	Leu	Trp	Ala	Arg	Tyr	Leu	Val	Phe	Leu	Gly	Asn	Pro	Val	Ile	Ala
gtt	ggt	att	ggt	ctt	att	att	gct	att	tat	ggt	ctg	gct	ccg	aaa	ctt
Val	Gly	Ile	Gly	Leu	Ile	Ile	Ala	Ile	Tyr	Gly	Leu	Ala	Pro	Lys	Leu
tct	cgg	tct	gaa	gta	cta	aaa	aag	atg	gaa	gaa	ggg	gtt	tct	tca	gct
Ser	Arg	Ser	Glu	Val	Leu	Lys	Lys	Met	Glu	Glu	Gly	Val	Ser	Ser	Ala
305	310	315													
ggt	ata	att	atc	tta	att	aca	ggt	gct	ggt	ggc	gca	tta	ggc	cag	gtg
Gly	Ile	Ile	Ile	Leu	Ile	Thr	Gly	Ala	Gly	Gly	Ala	Leu	Gly	Gln	Val
tta	agg	gac	agt	ggt	gtc	ggt	aat	tat	gta	gct	caa	ctt	att	gct	tct
Leu	Arg	Asp	Ser	Gly	Val	Gly	Asn	Tyr	Val	Ala	Gln	Leu	Ile	Ala	Ser
agc	cct	ctg	cct	cca	ttt	ttg	tta	ccc	ttt	ttt	ggt	gct	act	ttt	gta
Ser	Pro	Leu	Pro	Pro	Phe	Leu	Leu	Pro	Phe	Phe	Val	Ala	Thr	Phe	Val
cga	tta	gtc	cag	gga	agc	ggt	aca	gta	gcc	atg	att	acc	tct	gct	tcc
Arg	Leu	Val	Gln	Gly	Ser	Gly	Thr	Val	Ala	Met	Ile	Thr	Ser	Ala	Ser
att	act	gca	cca	att	ttg	gcc	aat	ctt	tcc	gtt	aat	cca	atc	att	gct
Ile	Thr	Ala	Pro	Ile	Leu	Ala	Asn	Leu	Ser	Val	Asn	Pro	Ile	Ile	Ala
385	390	395													
gtt	caa	gca	gcc	aat	tta	ggt	tca	ttg	ata	tat	tct	tat	ttc	aat	gac
Val	Gln	Ala	Ala	Asn	Leu	Gly	Ser	Leu	Ile	Tyr	Ser	Tyr	Phe	Asn	Asp
agt	ttt	ttc	tgg	gta	gtc	aat	aga	ttt	tta	ggt	gtc	gat	gac	att	aag

PF59083SeqList PF59083.txt

Ser	Phe	Phe	Trp	Val	Val	Asn	Arg	Phe	Leu	Gly	Val	Asp	Asp	Ile	Lys	
			420					425				430				
gaa	caa	aca	ctg	acg	tgg	tcg	gtt	ccg	act	aca	att	gct	tgg	ggc	gtt	1344
Glu	Gln	Thr	Leu	Thr	Trp	Ser	Val	Pro	Thr	Thr	Ile	Ala	Trp	Gly	Val	
		435					440					445				
tct	ttg	att	atg	tta	tac	att	gcc	aac	gcc	att	tta	agc	taa			1386
Ser	Leu	Ile	Met	Leu	Tyr	Ile	Ala	Asn	Ala	Ile	Leu	Ser				
	450					455					460					

<210> 10185
 <211> 461
 <212> PRT
 <213> Moorella thermoacetica ATCC 39073

<400> 10185
 Met Gly Gly Ile Ser Gly Ile Gln Ile Ile Ile Gly Leu Ile Val Gly
 1 5 10 15
 Ile Phe Val Leu Val Tyr Leu Ile Leu Arg Thr Lys Ile His Ala Phe
 20 25 30
 Pro Ala Leu Ile Ile Ala Ala Ser Val Ile Gly Leu Ile Gly Gly Met
 35 40 45
 Ser Pro Ser Thr Gly Asp Ile Asn Leu Ala Lys Ser Ile Thr Thr Gly
 50 55 60
 Phe Gly Asn Thr Leu Ala Ser Ile Gly Leu Val Ile Gly Phe Gly Val
 65 70 75 80
 Met Met Gly Arg Leu Leu Glu Val Ser Gly Ala Ala Glu Arg Met Ala
 85 90 95
 Tyr Thr Phe Leu Lys Tyr Leu Gly Arg Gly Lys Glu Glu Trp Ala Leu
 100 105 110
 Ala Ala Thr Gly Tyr Val Ile Ser Ile Pro Ile Phe Cys Asp Ser Gly
 115 120 125
 Phe Val Ile Leu Thr Pro Leu Val Lys Ala Leu Ser Arg Arg Thr Lys
 130 135 140
 Lys Ser Val Leu Ala Leu Gly Val Ala Leu Ala Gly Leu Val Ala
 145 150 155 160
 Thr His Ser Ala Val Pro Pro Thr Pro Gly Pro Leu Ala Val Ala Gly
 165 170 175
 Ile Phe Lys Val Asp Val Gly Met Val Ile Ile Ser Gly Leu Ile Phe
 180 185 190
 Thr Ile Pro Ile Thr Ile Ala Gly Val Leu Tyr Gly Lys Trp Leu Gly
 195 200 205
 Lys Lys Ile Tyr Gln Leu Pro Ser Glu Asp Gly Gln Ser Trp Ile Arg
 210 215 220
 Pro Pro Tyr Gln Ser Ser Gln Ile Ala Glu Glu Ala Leu Pro Glu Asn
 225 230 235 240
 Gly Asn Leu Pro Ser Ala Phe Ile Ser Phe Ala Pro Val Val Ile Pro
 245 250 255
 Leu Ile Leu Ile Phe Val Asn Thr Leu Leu Thr Ala Met Lys Ile Asn
 260 265 270
 Gln Leu Trp Ala Arg Tyr Leu Val Phe Leu Gly Asn Pro Val Ile Ala
 275 280 285
 Val Gly Ile Gly Leu Ile Ile Ala Ile Tyr Gly Leu Ala Pro Lys Leu
 290 295 300
 Ser Arg Ser Glu Val Leu Lys Lys Met Glu Glu Gly Val Ser Ser Ala
 305 310 315 320
 Gly Ile Ile Ile Leu Ile Thr Gly Ala Gly Gly Ala Leu Gly Gln Val
 325 330 335
 Leu Arg Asp Ser Gly Val Gly Asn Tyr Val Ala Gln Leu Ile Ala Ser
 340 345 350
 Ser Pro Leu Pro Pro Phe Leu Leu Pro Phe Phe Val Ala Thr Phe Val
 355 360 365
 Arg Leu Val Gln Gly Ser Gly Thr Val Ala Met Ile Thr Ser Ala Ser
 370 375 380
 Ile Thr Ala Pro Ile Leu Ala Asn Leu Ser Val Asn Pro Ile Ile Ala
 385 390 395 400
 Val Gln Ala Ala Asn Leu Gly Ser Leu Ile Tyr Ser Tyr Phe Asn Asp
 405 410 415
 Ser Phe Phe Trp Val Val Asn Arg Phe Leu Gly Val Asp Asp Ile Lys
 420 425 430

PF59083SeqList PF59083.txt

Glu Gln Thr Leu Thr Trp Ser Val Pro Thr Thr Ile Ala Trp Gly Val
 435 440 445
 Ser Leu Ile Met Leu Tyr Ile Ala Asn Ala Ile Leu Ser
 450 455 460

<210> 10186
 <211> 1314
 <212> DNA
 <213> Saccharophagus degradans 2-40

<220>
 <221> CDS
 <222> (1)..(1314)
 <223> transl_table=11

<400> 10186
 atg gaa att ttc ggt gtt tta gcg tca atc gta ctg ctt gtg ggc cta 48
 Met Glu Ile Phe Gly Val Leu Ala Ser Ile Val Leu Leu Val Gly Leu
 1 5 10 15
 att gtt tgg cta aaa att cac ccc ttt tta gca ttt ttg gcc acc tct 96
 Ile Val Trp Leu Lys Ile His Pro Phe Leu Ala Phe Leu Ala Thr Ser
 20 25 30
 ata ttc gca ggt att att ctt aat att cca ctg caa gat att ccg cag 144
 Ile Phe Ala Gly Ile Ile Leu Asn Ile Pro Leu Gln Asp Ile Pro Gln
 35 40 45
 gcg att gaa aca ggc ata ggt tca acg ctt agc ggt tta gta ata gtt 192
 Ala Ile Glu Thr Gly Ile Gly Ser Thr Leu Ser Gly Leu Val Ile Val
 50 55 60
 att tgc gta ggc gcc atg ttt ggc aag ctg gta tca gaa agt ggt gca 240
 Ile Cys Val Gly Ala Met Phe Gly Lys Leu Val Ser Glu Ser Gly Ala
 65 70 75 80
 gca caa aaa ata gca cag gta ttg ata ggc gca ttc ggc ccc aag cgc 288
 Ala Gln Lys Ile Ala Gln Val Leu Ile Gly Ala Phe Gly Pro Lys Arg
 85 90 95
 atc act tgg gcg ctt atg ctc aca ggc ggt att gtc ggt atc cca ctg 336
 Ile Thr Trp Ala Leu Met Leu Thr Gly Phe Ile Val Gly Ile Pro Leu
 100 105 110
 ttt tac aac gtg ggt ttt gta ctg tta gtg cca ctc gta ttt tct gtt 384
 Phe Tyr Asn Val Gly Phe Val Leu Leu Val Pro Leu Val Phe Ser Val
 115 120 125
 gtt tac caa tct aag ctg cca gcc gtt tat ttg ggt atc cca tta ctt 432
 Val Tyr Gln Ser Lys Leu Pro Ala Val Tyr Leu Gly Ile Pro Leu Leu
 130 135 140
 gct gcc ttg tct gtt acg cat ggc ttt cta ccg ccg cat cca tcg cct 480
 Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Ser Pro
 145 150 155 160
 aca gcc atg gtg ccc atg ttc aac gct gaa tta agc aca acg ctt att 528
 Thr Ala Met Val Pro Met Phe Asn Ala Glu Leu Ser Thr Thr Leu Ile
 165 170 175
 tac ggt tta att gtg gca ata ccc acc atg att ctt gcg gga ccg gtg 576
 Tyr Gly Leu Ile Val Ala Ile Pro Thr Met Ile Leu Ala Gly Pro Val
 180 185 190
 ttt gcc aat gct tta aaa aat att aaa tcg aca ccg cta gcc aca ttt 624
 Phe Ala Asn Ala Leu Lys Asn Ile Lys Ser Thr Pro Leu Ala Thr Phe
 195 200 205
 act ccc aaa gac cta cct gat aac cag cta cct agc gcc acc aat gca 672
 Thr Pro Lys Asp Leu Pro Asp Asn Gln Leu Pro Ser Ala Thr Asn Ala
 210 215 220
 ttc gct aca gcc ctg cta ccc gtt gtt ctt att gct gga cta tcg ttt 720
 Phe Ala Thr Ala Leu Leu Pro Val Val Leu Ile Ala Gly Leu Ser Phe
 225 230 235 240
 ttg ccg tcg cag gca gca act ggc tcg cag cta cac aac cta ttc aca 768
 Leu Pro Ser Gln Ala Ala Thr Gly Ser Gln Leu His Asn Leu Phe Thr
 245 250 255
 ttc tta gcc aat cct tca ctc ata atg ctt gca gca ctt gcg gtt gct 816
 Phe Leu Ala Asn Pro Ser Leu Ile Met Leu Ala Ala Leu Ala Val Ala
 260 265 270
 act tac acg ctg ggc att cgc caa aac gtg aaa ata caa aca ctt atg 864
 Thr Tyr Thr Leu Gly Ile Arg Gln Asn Val Lys Ile Gln Thr Leu Met

PF59083SeqList PF59083.txt

275	280	285	
gaa agg tat gcc gat gcg ata aaa gac atc tcc ata att atg tta att	290	295	300
Glu Arg Tyr Ala Asp Ala Ile Lys Asp Ile Ser Ile Ile Met Leu Ile			
gtg gct gga gcg ggt gcg cta aag cag gtt ttt ttg agt ggc gta	305	310	315
Val Ala Gly Ala Gly Ala Leu Lys Gln Val Phe Val Leu Ser Gly Val			
agt tca gat att ggc gca ctg atg cag aac tta gcc att aac cct ctg	325	330	335
Ser Ser Asp Ile Gly Ala Leu Met Gln Asn Leu Ala Ile Asn Pro Leu			
tta ctg ggt tgg ttt att gcc aca gtg ata cga att tgc ctg ggg tct	340	345	350
Leu Leu Gly Trp Phe Ile Ala Thr Val Ile Arg Ile Cys Leu Gly Ser			
gca acg gtg gca ggc cta acc gct gcc ggc ata atg gcg cca gtt ctg	355	360	365
Ala Thr Val Ala Gly Leu Thr Ala Ala Gly Ile Met Ala Pro Val Leu			
ccc ttg acc ggc gcc gac ccg aac tta atg att ctt gct att ggc gcg	370	375	380
Pro Leu Thr Gly Ala Asp Pro Asn Leu Met Ile Leu Ala Ile Gly Ala			
ggg agc ttg atg tgc agt cac gtt aac gac tca ggc ttt tgg atg ttt	385	390	395
Gly Ser Leu Met Cys Ser His Val Asn Asp Ser Gly Phe Trp Met Phe			
aag gag tac ttc aat tta agc gta aaa gac acc ctt aaa tcc tgg aca	405	410	415
Lys Glu Tyr Phe Asn Leu Ser Val Lys Asp Thr Leu Lys Ser Trp Thr			
tta atg gaa acc atc gta ggt att ggt gga att aca gcg gta ctc att	420	425	430
Leu Met Glu Thr Ile Val Gly Ile Gly Gly Ile Thr Ala Val Leu Ile			
ctt gac gtt ttt gtg taa			
Leu Asp Val Phe Val			

<210> 10187

<211> 437

<212> PRT

<213> Saccharophagus degradans 2-40

<400> 10187

Met Glu Ile Phe Gly Val Leu Ala Ser Ile Val Leu Leu Val Gly Leu	1	5	10	15
Ile Val Trp Leu Lys Ile His Pro Phe Leu Ala Phe Leu Ala Thr Ser		20	25	30
Ile Phe Ala Gly Ile Ile Leu Asn Ile Pro Leu Gln Asp Ile Pro Gln		35	40	45
Ala Ile Glu Thr Gly Ile Gly Ser Thr Leu Ser Gly Leu Val Ile Val		50	55	60
Ile Cys Val Gly Ala Met Phe Gly Lys Leu Val Ser Glu Ser Gly Ala		65	70	75
Ala Gln Lys Ile Ala Gln Val Leu Ile Gly Ala Phe Gly Pro Lys Arg		80	85	90
Ile Thr Trp Ala Leu Met Leu Thr Gly Phe Ile Val Gly Ile Pro Leu		95	100	105
Phe Tyr Asn Val Gly Phe Val Leu Leu Val Pro Leu Val Phe Ser Val		110	115	120
Val Tyr Gln Ser Lys Leu Pro Ala Val Tyr Leu Gly Ile Pro Leu Leu		125	130	135
Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Ser Pro		140	145	150
Thr Ala Met Val Pro Met Phe Asn Ala Glu Leu Ser Thr Thr Leu Ile		155	160	165
Tyr Gly Leu Ile Val Ala Ile Pro Thr Met Ile Leu Ala Gly Pro Val		170	175	180
Phe Ala Asn Ala Leu Lys Asn Ile Lys Ser Thr Pro Leu Ala Thr Phe		185	190	195
Thr Pro Lys Asp Leu Pro Asp Asn Gln Leu Pro Ser Ala Thr Asn Ala		200	205	210
Phe Ala Thr Ala Leu Leu Pro Val Val Leu Ile Ala Gly Leu Ser Phe		215	220	225
Leu Pro Ser Gln Ala Ala Thr Gly Ser Gln Leu His Asn Leu Phe Thr		230	235	240

PF59083SeqList PF59083.txt

245 250 255
 Phe Leu Ala Asn Pro Ser Leu Ile Met Leu Ala Ala Leu Ala Val Ala
 260 265 270
 Thr Tyr Thr Leu Gly Ile Arg Gln Asn Val Lys Ile Gln Thr Leu Met
 275 280 285
 Glu Arg Tyr Ala Asp Ala Ile Lys Asp Ile Ser Ile Ile Met Leu Ile
 290 295 300
 Val Ala Gly Ala Gly Ala Leu Lys Gln Val Phe Val Leu Ser Gly Val
 305 310 315 320
 Ser Ser Asp Ile Gly Ala Leu Met Gln Asn Leu Ala Ile Asn Pro Leu
 325 330 335
 Leu Leu Gly Trp Phe Ile Ala Thr Val Ile Arg Ile Cys Leu Gly Ser
 340 345 350
 Ala Thr Val Ala Gly Leu Thr Ala Ala Gly Ile Met Ala Pro Val Leu
 355 360 365
 Pro Leu Thr Gly Ala Asp Pro Asn Leu Met Ile Leu Ala Ile Gly Ala
 370 375 380
 Gly Ser Leu Met Cys Ser His Val Asn Asp Ser Gly Phe Trp Met Phe
 385 390 395 400
 Lys Glu Tyr Phe Asn Leu Ser Val Lys Asp Thr Leu Lys Ser Trp Thr
 405 410 415
 Leu Met Glu Thr Ile Val Gly Ile Gly Gly Ile Thr Ala Val Leu Ile
 420 425 430
 Leu Asp Val Phe Val
 435

<210> 10188

<211> 1398

<212> DNA

<213> Burkholderia xenovorans LB400

<220>

<221> CDS

<222> (1)..(1398)

<223> transl_table=11

<400> 10188

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

PF59083SeqList PF59083.txt

				165				170					175				
gat	atc	ggc	agg	acc	atc	gcc	tat	ggc	ctg	att	gtc	ggc	gtg	ccg	acc		576
Asp	Ile	Gly	Arg	Thr	Ile	Ala	Tyr	Gly	Leu	Ile	Val	Gly	Val	Pro	Thr		
			180					185					190				
gcg	atc	gtc	gcg	ggg	ccg	ttg	ttt	gcg	ttg	atg	atc	agc	cgc	tat	atc		624
Ala	Ile	Val	Ala	Gly	Pro	Leu	Phe	Ala	Leu	Met	Ile	Ser	Arg	Tyr	Ile		
			195				200					205					
aag	ctg	ccg	aaa	gac	aac	gcg	ctc	gcc	tcg	caa	ttt	ctc	ggc	gcc	gat		672
Lys	Leu	Pro	Lys	Asp	Asn	Ala	Leu	Ala	Ser	Gln	Phe	Leu	Gly	Ala	Asp		
			210			215					220						
gaa	acc	ggg	gcg	gcg	aac	aac	ggc	aac	ggc	gag	caa	aag	acc	gcg	ccc		720
Glu	Thr	Gly	Ala	Ala	Asn	Asn	Gly	Asn	Gly	Glu	Gln	Lys	Thr	Ala	Pro		
225					230				235						240		
agg	cgc	gaa	ctg	ccg	agc	ttc	ggc	gtg	acg	ctg	ttc	acg	atc	ctg	ttg		768
Arg	Arg	Glu	Leu	Pro	Ser	Phe	Gly	Val	Thr	Leu	Phe	Thr	Ile	Leu	Leu		
				245				250						255			
ccg	gtt	atc	ctg	atg	ctg	gtg	ggc	agt	tgg	gcc	gac	ctc	gtg	ttc	acg		816
Pro	Val	Ile	Leu	Met	Leu	Val	Gly	Ser	Trp	Ala	Asp	Leu	Val	Phe	Thr		
			260				265						270				
ccg	aag	acc	ctc	gcg	aac	gat	ctg	ctg	cgt	ttc	gtc	ggc	aat	tcg	gat		864
Pro	Lys	Thr	Leu	Ala	Asn	Asp	Leu	Leu	Arg	Phe	Val	Gly	Asn	Ser	Asp		
			275			280						285					
gtg	gcg	ctg	ctg	gtc	gcg	gtg	ctg	gtc	agt	ttc	tgg	acc	ttt	ggg	gcg		912
Val	Ala	Leu	Leu	Val	Ala	Val	Leu	Val	Ser	Phe	Trp	Thr	Phe	Gly	Ala		
			290			295					300						
agc	cgt	ggc	ttc	gat	cgc	gag	cag	atc	cag	aaa	ttc	tgc	ggc	gaa	tgt		960
Ser	Arg	Gly	Phe	Asp	Arg	Glu	Gln	Ile	Gln	Lys	Phe	Cys	Gly	Glu	Cys		
305				310				315							320		
ctc	gcg	ccg	atc	gcg	ggc	att	acg	ctg	att	gtc	ggc	gcg	ggc	ggc	ggc		1008
Leu	Ala	Pro	Ile	Ala	Gly	Ile	Thr	Leu	Ile	Val	Gly	Ala	Gly	Gly	Gly		
				325				330						335			
ttt	ggg	cgc	gtg	ctg	atg	gat	agc	ggc	att	tcg	aag	gag	atc	gtc	aac		1056
Phe	Gly	Arg	Val	Leu	Met	Asp	Ser	Gly	Ile	Ser	Lys	Glu	Ile	Val	Asn		
			340				345						350				
gcg	gcg	acg	tcg	gcg	cat	ctg	tcg	ccg	ctg	ctg	ttc	ggc	tgg	ctg	gtc		1104
Ala	Ala	Thr	Ser	Ala	His	Leu	Ser	Pro	Leu	Leu	Phe	Gly	Trp	Leu	Val		
			355			360						365					
gcg	gcg	ctg	att	cgc	ctg	gcc	acc	ggc	tcg	gcg	acg	gtc	gcg	atg	acc		1152
Ala	Ala	Leu	Ile	Arg	Leu	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	Met	Thr		
			370			375						380					
acc	gct	tgc	ggc	atc	gtc	gcg	ccg	atc	gcg	gcg	gcg	ggc	gcg	gtg	cag		1200
Thr	Ala	Cys	Gly	Ile	Val	Ala	Pro	Ile	Ala	Ala	Ala	Gly	Ala	Val	Gln		
385				390				395						400			
gtg	aag	ccg	gaa	ctg	ctg	gtg	ctg	gcc	acg	ggg	tcg	ggc	tcg	ctg	atc		1248
Val	Lys	Pro	Glu	Leu	Val	Leu	Ala	Thr	Gly	Ser	Gly	Ser	Ser	Leu	Ile		
				405				410						415			
ttt	tcg	cac	gtg	aac	gac	ggc	ggg	ttc	tgg	ctg	atc	aag	gaa	tac	ttc		1296
Phe	Ser	His	Val	Asn	Asp	Gly	Gly	Phe	Trp	Leu	Ile	Lys	Glu	Tyr	Phe		
			420				425						430				
ggg	atg	acg	gtg	ggg	cag	acc	ttc	aag	aca	tgg	tcg	ctc	ctc	gaa	acc		1344
Gly	Met	Thr	Val	Gly	Gln	Thr	Phe	Lys	Thr	Trp	Ser	Leu	Leu	Glu	Thr		
			435			440						445					
atc	atc	tcg	ctg	atg	ggg	ctg	ggg	ttg	acc	ttc	gca	ctc	gcg	acg	gtc		1392
Ile	Ile	Ser	Leu	Met	Gly	Leu	Gly	Leu	Thr	Phe	Ala	Leu	Ala	Thr	Val		
						455					460						
gtg	taa																1398
Val																	
465																	

<210> 10189
 <211> 465
 <212> PRT
 <213> Burkholderia xenovorans LB400

<400> 10189
 Met Glu Ala Val His Gly Ser Met Leu Leu Val Phe Ala Ala Ile Ala
 1 5 10 15
 Ile Ala Leu Leu Ile Leu Leu Ile Thr Arg Tyr Lys Val Tyr Pro Phe
 20 25 30

PF59083SeqList PF59083.txt

```

Leu Val Leu Ile Ile Val Ser Leu Leu Leu Gly Leu Ala Ser Gly Met
    35      40      45
Pro Ile Gly Thr Ile Val Lys Ser Phe Glu Thr Gly Asn Gly Asn Thr
    50      55      60
Leu Gly His Ile Ala Ile Val Val Gly Leu Gly Thr Met Leu Gly Lys
    65      70      75      80
Met Met Ala Glu Ser Gly Gly Ala Glu Arg Ile Ala Thr Thr Leu Ile
    85      90      95
Asp Phe Phe Gly Glu Lys Asn Ile His Trp Ala Met Met Ile Val Ala
    100      105      110
Ile Ile Val Gly Leu Pro Val Phe Phe Glu Val Gly Phe Val Leu Leu
    115      120      125
Ile Pro Ile Ala Phe Asn Val Ala Lys Arg Thr Asn Lys Ser Leu Leu
    130      135      140
Leu Val Gly Leu Pro Met Val Ala Gly Leu Ser Val Val His Gly Leu
    145      150      155      160
Leu Pro Pro His Pro Ala Ala Met Leu Ala Val Gln Ala Tyr His Ala
    165      170      175
Asp Ile Gly Arg Thr Ile Ala Tyr Gly Leu Ile Val Gly Val Pro Thr
    180      185      190
Ala Ile Val Ala Gly Pro Leu Phe Ala Leu Met Ile Ser Arg Tyr Ile
    195      200      205
Lys Leu Pro Lys Asp Asn Ala Leu Ala Ser Gln Phe Leu Gly Ala Asp
    210      215      220
Glu Thr Gly Ala Ala Asn Asn Gly Asn Gly Glu Gln Lys Thr Ala Pro
    225      230      235      240
Arg Arg Glu Leu Pro Ser Phe Gly Val Thr Leu Phe Thr Ile Leu Leu
    245      250      255
Pro Val Ile Leu Met Leu Val Gly Ser Trp Ala Asp Leu Val Phe Thr
    260      265      270
Pro Lys Thr Leu Ala Asn Asp Leu Leu Arg Phe Val Gly Asn Ser Asp
    275      280      285
Val Ala Leu Leu Val Ala Val Leu Val Ser Phe Trp Thr Phe Gly Ala
    290      295      300
Ser Arg Gly Phe Asp Arg Glu Gln Ile Gln Lys Phe Cys Gly Glu Cys
    305      310      315      320
Leu Ala Pro Ile Ala Gly Ile Thr Leu Ile Val Gly Ala Gly Gly Gly
    325      330      335
Phe Gly Arg Val Leu Met Asp Ser Gly Ile Ser Lys Glu Ile Val Asn
    340      345      350
Ala Ala Thr Ser Ala His Leu Ser Pro Leu Leu Phe Gly Trp Leu Val
    355      360      365
Ala Ala Leu Ile Arg Leu Ala Thr Gly Ser Ala Thr Val Ala Met Thr
    370      375      380
Thr Ala Cys Gly Ile Val Ala Pro Ile Ala Ala Gly Ala Val Gln
    385      390      395      400
Val Lys Pro Glu Leu Leu Val Leu Ala Thr Gly Ser Gly Ser Leu Ile
    405      410      415
Phe Ser His Val Asn Asp Gly Gly Phe Trp Leu Ile Lys Glu Tyr Phe
    420      425      430
Gly Met Thr Val Gly Gln Thr Phe Lys Thr Trp Ser Leu Leu Glu Thr
    435      440      445
Ile Ile Ser Leu Met Gly Leu Gly Leu Thr Phe Ala Leu Ala Thr Val
    450      455      460
Val
465

```

<210> 10190

<211> 1362

<212> DNA

<213> Ralstonia metallidurans CH34

<220>

<221> CDS

<222> (1)..(1362)

<223> transl_table=11

<400> 10190

atg ggt gcc gtt aca gga acc acg ctc ttg gtc tat gcg ctg atc gcc
Seite 10786

PF59083SeqList PF59083.txt

Met	Gly	Ala	Val	Thr	Gly	Thr	Thr	Leu	Leu	Val	Tyr	Ala	Leu	Ile	Ala	
1				5				10					15			
gtg	atc	gcg	ctg	gtg	atc	ctg	atc	gcc	aaa	ttc	aaa	ctg	aac	cca	ttc	96
Val	Ile	Ala	Leu	Val	Ile	Leu	Ile	Ala	Lys	Phe	Lys	Leu	Asn	Pro	Phe	
			20					25					30			
atc	acg	ctc	gtg	gtg	gtc	tcg	gtg	gcg	ctg	ggc	ttc	gcc	gtg	ggg	atg	144
Ile	Thr	Leu	Val	Val	Val	Ser	Val	Ala	Leu	Gly	Phe	Ala	Val	Gly	Met	
		35				40						45				
ccg	atg	ggc	gac	atc	atc	aag	tcg	ttc	gaa	gcg	ggt	gtc	ggc	ggc	acg	192
Pro	Met	Gly	Asp	Ile	Ile	Lys	Ser	Phe	Glu	Ala	Gly	Val	Gly	Gly	Thr	
		50				55					60					
ctc	ggg	cat	atc	gcg	ctc	gtg	atc	ggg	ctc	ggc	acg	atg	ctt	ggc	aag	240
Leu	Gly	His	Ile	Ala	Leu	Val	Ile	Gly	Leu	Gly	Thr	Met	Leu	Gly	Lys	
65					70			75							80	
atg	atg	gcc	gaa	tcg	ggc	ggc	gcc	gag	cgc	atc	gcg	ctg	acg	ctg	gtc	288
Met	Met	Ala	Glu	Ser	Gly	Gly	Ala	Glu	Arg	Ile	Ala	Leu	Thr	Leu	Val	
				85				90						95		
gac	ttc	ttc	ggc	gag	aag	aac	gtg	cac	tgg	gcg	atg	gtg	gtc	atc	gcc	336
Asp	Phe	Phe	Gly	Glu	Lys	Asn	Val	His	Trp	Ala	Met	Val	Val	Ile	Ala	
			100					105					110			
ttc	atc	gtc	ggc	ctg	ccg	gtg	ttc	ttc	gag	gta	ggc	ttc	gtg	ctg	ctc	384
Phe	Ile	Val	Gly	Leu	Pro	Val	Phe	Phe	Glu	Val	Gly	Phe	Val	Leu	Leu	
		115					120					125				
gtc	ccg	atc	gcc	ttc	aac	gtc	gcc	aag	cgc	acc	aat	acc	tcg	atg	gtg	432
Val	Pro	Ile	Ala	Phe	Asn	Val	Ala	Lys	Arg	Thr	Asn	Thr	Ser	Met	Val	
		130				135					140					
ctg	gtt	ggc	atc	ccg	atg	gtc	gcc	ggc	ctc	tcg	gtg	gtg	cac	ggg	ctg	480
Leu	Val	Gly	Ile	Pro	Met	Val	Ala	Gly	Leu	Ser	Val	Val	His	Gly	Leu	
145					150			155							160	
att	ccg	ccg	cac	cct	gcc	gcg	ctg	ctg	gct	gtg	cag	gcc	tac	ggc	gct	528
Ile	Pro	Pro	His	Pro	Ala	Ala	Leu	Leu	Ala	Val	Gln	Ala	Tyr	Gly	Ala	
				165				170						175		
gac	atg	ggc	aag	acg	atc	atg	tac	gcg	ctg	atc	gtc	ggt	gtc	ccg	aca	576
Asp	Met	Gly	Lys	Thr	Ile	Met	Tyr	Ala	Leu	Ile	Val	Gly	Val	Pro	Thr	
			180					185					190			
gcc	gcc	atc	gct	ggc	ccg	ctg	ttc	gcc	aag	ctg	atc	gac	cgc	cac	gtg	624
Ala	Ala	Ile	Ala	Gly	Pro	Leu	Phe	Ala	Lys	Leu	Ile	Asp	Arg	His	Val	
		195					200					205				
aag	ctg	ccc	gag	gtc	aac	ccg	ctg	gcc	gcg	cag	ttc	acc	gaa	gaa	gcc	672
Lys	Leu	Pro	Glu	Val	Asn	Pro	Leu	Ala	Ala	Gln	Phe	Thr	Glu	Glu	Ala	
		210				215					220					
gag	aac	atc	aag	gcc	acg	cgc	caa	ttg	cca	ggc	ttc	ggc	atc	act	gtc	720
Glu	Asn	Ile	Lys	Ala	Thr	Arg	Gln	Leu	Pro	Gly	Phe	Gly	Ile	Thr	Val	
225					230			235							240	
ttc	acg	atc	ctg	ctg	ccg	gtg	att	ctg	atg	ctg	att	ggt	agc	tgg	gcg	768
Phe	Thr	Ile	Leu	Leu	Pro	Val	Ile	Leu	Met	Leu	Ile	Gly	Ser	Trp	Ala	
				245				250						255		
gac	ctg	att	gcc	acg	ccg	aag	acc	ttc	gcc	aac	gac	ttc	ctc	aag	ctg	816
Asp	Leu	Ile	Ala	Thr	Pro	Lys	Thr	Phe	Ala	Asn	Asp	Phe	Leu	Lys	Leu	
			260					265					270			
atc	ggt	aac	tcg	gtc	atg	gca	ctg	ctg	atc	gcc	gcg	ctg	gtc	agc	ttc	864
Ile	Gly	Asn	Ser	Val	Met	Ala	Leu	Leu	Ile	Ala	Ala	Leu	Val	Ser	Phe	
		275					280					285				
tat	acc	ttc	ggc	aag	gcc	cgc	ggc	ttc	ggt	cgc	gat	gcg	atc	ctg	aag	912
Tyr	Thr	Phe	Gly	Lys	Ala	Arg	Gly	Phe	Gly	Arg	Asp	Ala	Ile	Leu	Lys	
		290				295					300					
ttc	acc	aac	gag	tgc	gtg	gcg	ccg	acc	gcc	atc	atc	acc	ctc	gtg	gtg	960
Phe	Thr	Asn	Glu	Cys	Val	Ala	Pro	Thr	Ala	Ile	Ile	Thr	Leu	Val	Val	
305					310					315					320	
ggt	gcc	ggc	ggt	ggc	ttc	ggc	cgc	atc	ctg	cgc	gac	tcc	ggc	atc	tcc	1008
Gly	Ala	Gly	Gly	Gly	Phe	Gly	Arg	Ile	Leu	Arg	Asp	Ser	Gly	Ile	Ser	
				325				330					335			
acc	gcc	atc	gtc	gac	gtg	gca	acc	cac	gca	aac	gtc	tcg	gtg	ctg	gta	1056
Thr	Ala	Ile	Val	Asp	Val	Ala	Thr	His	Ala	Asn	Val	Ser	Val	Leu	Val	
			340					345					350			
ttg	ggc	tgg	ctg	gtg	gcc	gtg	atg	atc	cgc	atc	gcc	acc	ggc	tcg	gcc	1104
Leu	Gly	Trp	Leu	Val	Ala	Val	Met	Ile	Arg	Ile	Ala	Thr	Gly	Ser	Ala	
		355					360					365				
acc	gtg	gcc	atg	acc	acc	gcc	gcc	ggc	atc	gtc	gcc	ccg	atc	gcc	gcc	1152

PF59083SeqList PF59083.txt

Thr	Val	Ala	Met	Thr	Thr	Ala	Ala	Gly	Ile	Val	Ala	Pro	Ile	Ala	Ala	
	370					375					380					
agc	gtg	ccg	ggc	acg	cg	ccc	gaa	ctg	ctg	gtg	ctg	acg	acc	ggc	gcc	1200
Ser	Val	Pro	Gly	Thr	Arg	Pro	Glu	Leu	Leu	Val	Leu	Thr	Thr	Gly	Ala	
	385				390					395					400	
ggg	tcg	ctg	atc	ctg	tcg	cac	gtc	aac	gac	ggc	ggc	ttc	tgg	ctg	gtc	1248
Gly	Ser	Leu	Ile	Leu	Ser	His	Val	Asn	Asp	Gly	Gly	Phe	Trp	Leu	Val	
				405					410					415		
aag	gag	tac	ttc	aac	atg	acc	gtg	acc	cag	acc	ttc	aag	acc	tgg	tcg	1296
Lys	Glu	Tyr		Asn	Met	Thr	Val		Gln	Thr	Phe	Lys		Trp	Ser	
				420				425					430			
gtc	gcc	gaa	acg	atc	att	tcg	gtc	gtg	gcg	ttg	cta	ctg	acg	ctg	gga	1344
Val	Ala	Glu	Thr	Ile	Ile	Ser	Val	Val	Ala	Leu	Leu	Leu	Thr	Leu	Gly	
		435					440					445				
ctg	gcg	acg	gtg	acc	tga											1362
Leu	Ala	Thr	Val	Thr												
	450															

<210> 10191

<211> 453

<212> PRT

<213> Ralstonia metallidurans CH34

<400> 10191

Met	Gly	Ala	Val	Thr	Gly	Thr	Thr	Leu	Leu	Val	Tyr	Ala	Leu	Ile	Ala	
1				5					10					15		
Val	Ile	Ala	Leu	Val	Ile	Leu	Ile	Ala	Lys	Phe	Lys	Leu	Asn	Pro	Phe	
			20					25					30			
Ile	Thr	Leu	Val	Val	Val	Ser	Val	Ala	Leu	Gly	Phe	Ala	Val	Gly	Met	
			35				40					45				
Pro	Met	Gly	Asp	Ile	Ile	Lys	Ser	Phe	Glu	Ala	Gly	Val	Gly	Gly	Thr	
	50					55					60					
Leu	Gly	His	Ile	Ala	Leu	Val	Ile	Gly	Leu	Gly	Thr	Met	Leu	Gly	Lys	
65					70					75				80		
Met	Met	Ala	Glu	Ser	Gly	Gly	Ala	Glu	Arg	Ile	Ala	Leu	Thr	Leu	Val	
				85					90					95		
Asp	Phe	Phe	Gly	Glu	Lys	Asn	Val	His	Trp	Ala	Met	Val	Val	Ile	Ala	
			100					105					110			
Phe	Ile	Val	Gly	Leu	Pro	Val	Phe	Glu	Val	Gly	Phe	Val	Val	Leu	Leu	
			115					120				125				
Val	Pro	Ile	Ala	Phe	Asn	Val	Ala	Lys	Arg	Thr	Asn	Thr	Ser	Met	Val	
	130					135					140					
Leu	Val	Gly	Ile	Pro	Met	Val	Ala	Gly	Leu	Ser	Val	Val	His	Gly	Leu	
145					150					155				160		
Ile	Pro	Pro	His	Pro	Ala	Ala	Leu	Leu	Ala	Val	Gln	Ala	Tyr	Gly	Ala	
				165					170					175		
Asp	Met	Gly	Lys	Thr	Ile	Met	Tyr	Ala	Leu	Ile	Val	Gly	Val	Pro	Thr	
			180					185					190			
Ala	Ala	Ile	Ala	Gly	Pro	Leu	Phe	Ala	Lys	Leu	Ile	Asp	Arg	His	Val	
			195					200				205				
Lys	Leu	Pro	Glu	Val	Asn	Pro	Leu	Ala	Ala	Gln	Phe	Thr	Glu	Glu	Ala	
	210					215					220					
Glu	Asn	Ile	Lys	Ala	Thr	Arg	Gln	Leu	Pro	Gly	Phe	Gly	Ile	Thr	Val	
225					230					235				240		
Phe	Thr	Ile	Leu	Leu	Pro	Val	Ile	Leu	Met	Leu	Ile	Gly	Ser	Trp	Ala	
				245					250					255		
Asp	Leu	Ile	Ala	Thr	Pro	Lys	Thr	Phe	Ala	Asn	Asp	Phe	Leu	Lys	Leu	
			260					265					270			
Ile	Gly	Asn	Ser	Val	Met	Ala	Leu	Ile	Ala	Ala	Leu	Val	Ser	Phe		
			275				280					285				
Tyr	Thr	Phe	Gly	Lys	Ala	Arg	Gly	Phe	Gly	Arg	Asp	Ala	Ile	Leu	Lys	
	290					295					300					
Phe	Thr	Asn	Glu	Cys	Val	Ala	Pro	Thr	Ala	Ile	Ile	Thr	Leu	Val	Val	
305					310					315				320		
Gly	Ala	Gly	Gly	Gly	Phe	Gly	Arg	Ile	Leu	Arg	Asp	Ser	Gly	Ile	Ser	
				325					330					335		
Thr	Ala	Ile	Val	Asp	Val	Ala	Thr	His	Ala	Asn	Val	Ser	Val	Leu	Val	
			340					345					350			
Leu	Gly	Trp	Leu	Val	Ala	Val	Met	Ile	Arg	Ile	Ala	Thr	Gly	Ser	Ala	

PF59083SeqList PF59083.txt

```

      355      360      365
Thr Val Ala Met Thr Thr Ala Ala Gly Ile Val Ala Pro Ile Ala Ala
370      375      380
Ser Val Pro Gly Thr Arg Pro Glu Leu Leu Val Leu Thr Thr Gly Ala
385      390      395
Gly Ser Leu Ile Leu Ser His Val Asn Asp Gly Gly Phe Trp Leu Val
400      405      410
Lys Glu Tyr Phe Asn Met Thr Val Thr Gln Thr Phe Lys Thr Trp Ser
420      425      430
Val Ala Glu Thr Ile Ile Ser Val Val Ala Leu Leu Leu Thr Leu Gly
435      440      445
Leu Ala Thr Val Thr
450

```

<210> 10192
 <211> 1314
 <212> DNA
 <213> *Cytophaga hutchinsonii* ATCC 33406

<220>
 <221> CDS
 <222> (1)..(1314)
 <223> transl_table=11

```

<400> 10192
atg tcc tta ctt ttt att tta cta aca atc atc aca acg tta att ttt      48
Met Ser Leu Leu Phe Ile Leu Leu Thr Ile Ile Thr Thr Leu Ile Phe
1      5      10
tta acg gct gtt ctt aaa ata tcc cca ttc ata tcg ttt atc ctt gtt      96
Leu Thr Ala Val Leu Lys Ile Ser Pro Phe Ile Ser Phe Ile Leu Val
20      25      30
acc att ctt gcc ggt ata cta ctt ggt atg cca ttg ggt aat atc gta      144
Thr Ile Leu Ala Gly Ile Leu Leu Gly Met Pro Leu Gly Asn Ile Val
35      40      45
cag tct ttt cag aaa ggt atc ggc gat atg ctc gga agt att ctg gtt      192
Gln Ser Phe Gln Lys Gly Ile Gly Asp Met Leu Gly Ser Ile Leu Val
50      55      60
aca tta act gcc ggc gcc atg ctc ggt aag ctg gtg gct gaa agc ggt      240
Thr Leu Thr Ala Gly Ala Met Leu Gly Lys Leu Val Ala Glu Ser Gly
65      70      75
gcg gca acg gtt atc gca gat aag atc att gct gtg tgc ggt aaa aaa      288
Ala Ala Thr Val Ile Ala Asp Lys Ile Ile Ala Val Cys Gly Lys Lys
85      90      95
tac ctg cag tgg ggc tta ctg tta aca ggt ttg att att ggt att cca      336
Tyr Leu Gln Trp Gly Leu Leu Leu Thr Gly Leu Ile Ile Gly Ile Pro
100      105      110
ttg ttt tat aat gta ggc ttt gta ttg atc ata ccg att gtt ttt acc      384
Leu Phe Tyr Asn Val Gly Phe Val Leu Ile Ile Pro Ile Val Phe Thr
115      120      125
ttg tct tac cgg tat aaa ttg cct gcc gtg tat gtg ggc att ccg atg      432
Leu Ser Tyr Arg Tyr Lys Leu Pro Ala Val Tyr Val Gly Ile Pro Met
130      135      140
ctt gca gcc ttg tct gtg gcg cat agt ctg ttg ccg ccg cat cct tct      480
Leu Ala Ala Leu Ser Val Ala His Ser Leu Leu Pro Pro His Pro Ser
145      150      155
ccg gca tca ctg gta ggt acc ttt cag gca agt atg atc aaa aca ttc      528
Pro Ala Ser Leu Val Gly Thr Phe Gln Ala Ser Met Ile Lys Thr Phe
165      170      175
tta tac ggt att gcc gtt gca gtg ccg gca att att ctg gcc gga cct      576
Leu Tyr Gly Ile Ala Val Ala Val Pro Ala Ile Ile Leu Ala Gly Pro
180      185      190
gtt ttt gca cgc aca tta agg cat att caa ccg cag gga gaa ctt cct      624
Val Phe Ala Arg Thr Leu Arg His Ile Gln Pro Gln Gly Glu Leu Pro
195      200      205
ctg gtt gag cac acg gtt gct gcc cat tcc tta ccg ggt gtg ttt aac      672
Leu Val Glu His Thr Val Ala Ala His Ser Leu Pro Gly Val Phe Asn
210      215      220
agc att ttc tct gcg ttg ttg ccg gta ttt cta tta ctg acg acc ttt      720
Ser Ile Phe Ser Ala Leu Leu Pro Val Phe Leu Leu Leu Thr Thr Phe

```

PF59083SeqList PF59083.txt

225	230	235	240	
ctg ctt tcg ttt atc ata gaa aac aaa caa gta att cag gta ctt tca				768
Leu Leu Ser Phe Ile Ile Glu Asn Lys Gln Val Ile Gln Val Leu Ser				
245	250	255		
ttc ata aaa gag ccg tct gtg ctt atg ctg ctt tcg ttg tta gtt gta			816	
Phe Ile Lys Glu Pro Ser Val Leu Met Leu Leu Ser Leu Val Val				
260	265	270		
agc att aca tta ggt acg cag caa cgg act agc atg aag cac atc atg			864	
Ser Ile Thr Leu Gly Thr Gln Gln Arg Thr Ser Met Lys His Ile Met				
275	280	285		
cgt aca tat gaa gca gga ata aaa gat atc gcc atg atc ctg ctg atc			912	
Arg Thr Tyr Glu Ala Gly Ile Lys Asp Ile Ala Met Ile Leu Leu Ile				
290	295	300		
atc gga gca tcc ggc ggg tta aaa caa gta ctc att gat agt gaa gca			960	
Ile Gly Ala Ser Gly Gly Leu Lys Gln Val Leu Ile Asp Ser Glu Ala				
305	310	315		
agc atc gtc ctt gcc gga tat ttc caa tcg ctt cag ata aac ccg ctg			1008	
Ser Ile Val Leu Ala Gly Tyr Phe Gln Ser Leu Gln Ile Asn Pro Leu				
325	330	335		
ata tta ggc tgg ctc att gcc gct atc atc cgt ctg tgc ctg ggt tca			1056	
Ile Leu Gly Trp Leu Ile Ala Ala Ile Ile Arg Leu Cys Leu Gly Ser				
340	345	350		
gcc acc gta gcc ggt tta aca gct gcc ggt att att gct ccg ctc atg			1104	
Ala Thr Val Ala Gly Leu Thr Ala Ala Gly Ile Ile Ala Pro Leu Met				
355	360	365		
ccg cat ata agt gca gat ccc aac ctg atg att ctt gcc ata ggc gca			1152	
Pro His Ile Ser Ala Asp Pro Asn Leu Met Ile Leu Ala Ile Gly Ala				
370	375	380		
ggc agt att ttc tgt tcg cat gta aac gat acg ggt ttc tgg atg ttt			1200	
Gly Ser Ile Phe Cys Ser His Val Asn Asp Thr Gly Phe Trp Met Phe				
385	390	395		
aaa gaa tac ttt aac gta tct ata aaa gat acg ttt tta tcc tgg aca			1248	
Lys Glu Tyr Phe Asn Val Ser Ile Lys Asp Thr Phe Leu Ser Trp Thr				
405	410	415		
atc atg gaa agc att gtg tct gtt gcg ggc ctg gcc ggc gta ctg ctt			1296	
Ile Met Glu Ser Ile Val Ser Val Ala Gly Leu Ala Gly Val Leu Leu				
420	425	430		
tta agc ata tgg ctt taa			1314	
Leu Ser Ile Trp Leu				
435				

<210> 10193

<211> 437

<212> PRT

<213> Cytophaga hutchinsonii ATCC 33406

<400> 10193

Met Ser Leu Leu Phe Ile Leu Leu Thr Ile Ile Thr Thr Leu Ile Phe	
1 5 10 15	
Leu Thr Ala Val Leu Lys Ile Ser Pro Phe Ile Ser Phe Ile Leu Val	
20 25 30	
Thr Ile Leu Ala Gly Ile Leu Leu Gly Met Pro Leu Gly Asn Ile Val	
35 40 45	
Gln Ser Phe Gln Lys Gly Ile Gly Asp Met Leu Gly Ser Ile Leu Val	
50 55 60	
Thr Leu Thr Ala Gly Ala Met Leu Gly Lys Leu Val Ala Glu Ser Gly	
65 70 75 80	
Ala Ala Thr Val Ile Ala Asp Lys Ile Ile Ala Val Cys Gly Lys Lys	
85 90 95	
Tyr Leu Gln Trp Gly Leu Leu Leu Thr Gly Leu Ile Ile Gly Ile Pro	
100 105 110	
Leu Phe Tyr Asn Val Gly Phe Val Leu Ile Ile Pro Ile Val Phe Thr	
115 120 125	
Leu Ser Tyr Arg Tyr Lys Leu Pro Ala Val Tyr Val Gly Ile Pro Met	
130 135 140	
Leu Ala Ala Leu Ser Val Ala His Ser Leu Leu Pro Pro His Pro Ser	
145 150 155 160	
Pro Ala Ser Leu Val Gly Thr Phe Gln Ala Ser Met Ile Lys Thr Phe	
165 170 175	

PF59083SeqList PF59083.txt

Leu Tyr Gly Ile Ala Val Ala Val Pro Ala Ile Ile Leu Ala Gly Pro
 180 185 190
 Val Phe Ala Arg Thr Leu Arg His Ile Gln Pro Gln Gly Glu Leu Pro
 195 200 205
 Leu Val Glu His Thr Val Ala His Ser Leu Pro Gly Val Phe Asn
 210 215 220
 Ser Ile Phe Ser Ala Leu Leu Pro Val Phe Leu Leu Leu Thr Thr Phe
 225 230 235 240
 Leu Leu Ser Phe Ile Ile Glu Asn Lys Gln Val Ile Gln Val Leu Ser
 245 250 255
 Phe Ile Lys Glu Pro Ser Val Leu Met Leu Leu Ser Leu Leu Val Val
 260 265 270
 Ser Ile Thr Leu Gly Thr Gln Gln Arg Thr Ser Met Lys His Ile Met
 275 280 285
 Arg Thr Tyr Glu Ala Gly Ile Lys Asp Ile Ala Met Ile Leu Leu Ile
 290 295 300
 Ile Gly Ala Ser Gly Gly Leu Lys Gln Val Leu Ile Asp Ser Glu Ala
 305 310 315 320
 Ser Ile Val Leu Ala Gly Tyr Phe Gln Ser Leu Gln Ile Asn Pro Leu
 325 330 335
 Ile Leu Gly Trp Leu Ile Ala Ala Ile Ile Arg Leu Cys Leu Gly Ser
 340 345 350
 Ala Thr Val Ala Gly Leu Thr Ala Ala Gly Ile Ile Ala Pro Leu Met
 355 360 365
 Pro His Ile Ser Ala Asp Pro Asn Leu Met Ile Leu Ala Ile Gly Ala
 370 375 380
 Gly Ser Ile Phe Cys Ser His Val Asn Asp Thr Gly Phe Trp Met Phe
 385 390 395 400
 Lys Glu Tyr Phe Asn Val Ser Ile Lys Asp Thr Phe Leu Ser Trp Thr
 405 410 415
 Ile Met Glu Ser Ile Val Ser Val Ala Gly Leu Ala Gly Val Leu Leu
 420 425 430
 Leu Ser Ile Trp Leu
 435

<210> 10194
 <211> 1395
 <212> DNA
 <213> Rhodococcus sp. RHA1

<220>
 <221> CDS
 <222> (1)..(1395)
 <223> transl_table=11

<400> 10194
 atg agt acc gcg tca cta ctc gca gcg gcc gac agt gcc ggc cac gac 48
 Met Ser Thr Ala Ser Leu Leu Ala Ala Ala Asp Ser Ala Gly His Asp
 1 5 10 15
 gcg cgg ctg atc acg gct gcc gtc gtc ggc gtc gcc gtc atc atc gcg 96
 Ala Arg Leu Ile Thr Ala Ala Val Val Gly Val Ala Val Ile Ile Ala
 20 25 30
 ctg atc acc tgg ctc aaa ctc cac ccg ttc ctc gcg ctg tcg atc ggc 144
 Leu Ile Thr Trp Leu Lys Leu His Pro Phe Leu Ala Leu Ser Ile Gly
 35 40 45
 gcc gtc ggc gtc ggt atc gcc gca ggt ctg ggc ggg caa gac tcg gtg 192
 Ala Val Gly Val Gly Ile Ala Ala Gly Leu Gly Gly Gln Asp Ser Val
 50 55 60
 aag tct ttc gtc gag ggc ttc ggg gcc acg atg ggc agc gtc gga atc 240
 Lys Ser Phe Val Glu Gly Phe Gly Ala Thr Met Gly Ser Val Gly Ile
 65 70 75 80
 ctc atc gga ttc ggt gcc atg ttc ggc aag ctg ctc gcc gat tcc ggt 288
 Leu Ile Gly Phe Gly Ala Met Phe Gly Lys Leu Leu Ala Asp Ser Gly
 85 90 95
 ggc gcc gac cgc gtc gtc gac acc ctc gtc gga cgg gca ggt ccg cgg 336
 Gly Ala Asp Arg Val Val Asp Thr Leu Val Gly Arg Ala Gly Pro Arg
 100 105 110
 acg ctg ccg tgg atg atg gcg ctg gtc ggc gca gtg atc ggc ctg ccg 384
 Thr Leu Pro Trp Met Met Ala Leu Val Gly Ala Val Ile Gly Leu Pro

PF59083SeqList PF59083.txt																
	115					120					125					
atg	ttc	ttc	gag	atc	ggc	ctc	gtg	ctg	ctg	atg	ccc	gtc	atc	atc	ctg	432
Met	Phe	Phe	Glu	Ile	Gly	Leu	Val	Leu	Leu	Met	Pro	Val	Ile	Ile	Leu	
	130					135					140					480
gtc	gcg	cgg	cgt	tcg	gga	ctg	tcg	ctg	atg	cgg	atc	gcg	att	ccc	acg	
Val	Ala	Arg	Arg	Ser	Gly	Leu	Ser	Leu	Met	Arg	Ile	Ala	Ile	Pro	Thr	
145					150					155					160	528
ctg	gca	ggt	ctg	tcg	gcc	atg	cac	ggt	ctc	gtt	ccg	ccg	cac	ccc	ggg	
Leu	Ala	Gly	Leu	Ser	Ala	Met	His	Gly	Leu	Val	Pro	Pro	His	Pro	Gly	
				165					170					175		576
ccc	ctg	gtc	gcg	gtg	gcg	gcc	ctg	aac	gcc	aac	ctc	gga	ctc	acc	ctc	
Pro	Leu	Val	Ala	Val	Ala	Ala	Leu	Asn	Ala	Asn	Leu	Gly	Leu	Thr	Leu	
			180					185					190			624
gcg	ctc	ggc	gtc	ctc	gtc	gcg	atc	ccc	acc	gtc	gtc	atc	gcc	gga	ccg	
Ala	Leu	Gly	Val	Leu	Val	Ala	Ile	Pro	Thr	Val	Val	Ile	Ala	Gly	Pro	
		195					200					205				672
ctg	ttc	agc	aag	ctg	gcg	gca	cgc	tgg	gtg	gac	gtc	ccc	gtc	ccc	gag	
Leu	Phe	Ser	Lys	Leu	Ala	Ala	Arg	Trp	Val	Asp	Val	Pro	Val	Pro	Glu	
		210				215					220					720
ctc	tac	gtg	acc	gtc	gaa	gac	cgg	gaa	ggc	gcc	gag	gct	gcc	gcc	gag	
Leu	Tyr	Val	Thr	Val	Glu	Asp	Arg	Glu	Gly	Ala	Glu	Ala	Ala	Ala	Glu	
225					230				235						240	768
cg	gcg	cgg	ccc	agc	ttc	gcg	gcc	acc	ctg	tcc	gcg	atc	ctg	ctg	cct	
Arg	Arg	Arg	Pro	Ser	Phe	Ala	Ala	Thr	Leu	Ser	Ala	Ile	Leu	Leu	Pro	
				245					250				255			816
gtc	gtc	ctg	atg	ctg	ggc	aag	gcg	atc	gcc	gac	gtc	atc	gcc	gcc	gac	
Val	Val	Leu	Met	Leu	Gly	Lys	Ala	Ile	Ala	Asp	Val	Ile	Ala	Ala	Asp	
			260					265					270			864
tcg	gag	tcg	ccc	gcg	aag	gcg	ctg	ctc	gac	ttc	ctc	ggt	aca	ccg	gtc	
Ser	Glu	Ser	Pro	Ala	Lys	Ala	Leu	Leu	Asp	Phe	Leu	Gly	Thr	Pro	Val	
		275					280					285				912
gtg	gcc	ctc	ggg	ctc	gcg	gtg	ctc	gcc	ggg	atg	gcg	ctt	ctc	ggc	cg	
Val	Ala	Leu	Gly	Leu	Ala	Val	Leu	Ala	Gly	Met	Ala	Leu	Leu	Gly	Arg	
		290				295					300					960
ggt	ggc	ggc	atg	gac	cg	aag	gcc	atc	gcc	gtc	tcg	ctg	gag	agt	tcg	
Gly	Gly	Gly	Met	Asp	Arg	Lys	Ala	Ile	Ala	Val	Ser	Leu	Glu	Ser	Ser	
305					310				315						320	1008
ctg	ccc	ccg	atc	gcc	gga	atc	ctc	ctc	atc	gtc	ggc	gcc	ggc	ggc	gga	
Leu	Pro	Pro	Ile	Ala	Gly	Ile	Leu	Leu	Ile	Val	Gly	Ala	Gly	Gly	Gly	
				325				330					335			1056
ttc	aag	cag	gtc	ctg	atc	gac	acc	ggc	atc	gcc	gat	gtg	atc	gcc	gac	
Phe	Lys	Gln	Val	Leu	Ile	Asp	Thr	Gly	Ile	Ala	Asp	Val	Ile	Ala	Asp	
			340					345					350			1104
gcg	atc	aag	gac	agc	gcc	ctg	ccc	gtt	ctg	ttc	ctc	gcc	tgg	ctc	gtg	
Ala	Ile	Lys	Asp	Ser	Ala	Leu	Pro	Val	Leu	Phe	Leu	Ala	Trp	Leu	Val	
		355					360					365				1152
gcc	gtg	ctc	atc	cg	gtc	gcc	acc	gga	tcg	gcc	acc	gtc	gcg	acg	gtc	
Ala	Val	Leu	Ile	Arg	Val	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala	Thr	Val	
		370				375					380					1200
acc	gcg	tcc	ggc	atc	ctc	gcg	ccc	gtc	gcc	gcc	gaa	ctg	acc	tcg	acg	
Thr	Ala	Ser	Gly	Ile	Leu	Ala	Pro	Val	Ala	Ala	Glu	Leu	Thr	Ser	Thr	
				390						395					400	1248
cac	gtg	tcg	ctg	atg	gtg	ctg	gcg	atc	ggc	tcc	ggc	tcg	ctg	ttc	ctg	
His	Val	Ser	Leu	Met	Val	Leu	Ala	Ile	Gly	Ser	Gly	Ser	Leu	Phe	Leu	
				405					410					415		1296
tcg	cac	gtc	aac	gac	gcg	gga	ttc	tgg	ctg	gtg	aag	gaa	tac	ctc	ggc	
Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Leu	Val	Lys	Glu	Tyr	Leu	Gly	
			420					425					430			1344
gtc	acg	gtg	gta	cag	aac	ctg	aag	acg	tgg	acg	gtg	atg	gaa	tgc	atc	
Val	Thr	Val	Val	Gln	Asn	Leu	Lys	Thr	Trp	Thr	Val	Met	Glu	Cys	Ile	
		435					440					445				1392
atc	tcc	gtc	acc	ggt	ctc	gcc	ggg	gtc	ctc	gca	ctg	agc	gta	ttc	atc	
Ile	Ser	Val	Thr	Gly	Leu	Ala	Gly	Val	Leu	Ala	Leu	Ser	Val	Phe	Ile	
		450				455					460					1395
taa																

PF59083SeqList PF59083.txt

<211> 464

<212> PRT

<213> Rhodococcus sp. RHA1

<400> 10195

```

Met Ser Thr Ala Ser Leu Leu Ala Ala Ala Asp Ser Ala Gly His Asp
1      5      10
Ala Arg Leu Ile Thr Ala Ala Val Val Gly Val Ala Val Ile Ile Ala
      20      25      30
Leu Ile Thr Trp Leu Lys Leu His Pro Phe Leu Ala Leu Ser Ile Gly
      35      40      45
Ala Val Gly Val Gly Ile Ala Ala Gly Leu Gly Gly Gln Asp Ser Val
      50      55      60
Lys Ser Phe Val Glu Gly Phe Gly Ala Thr Met Gly Ser Val Gly Ile
65      70      75      80
Leu Ile Gly Phe Gly Ala Met Phe Gly Lys Leu Leu Ala Asp Ser Gly
      85      90      95
Gly Ala Asp Arg Val Val Asp Thr Leu Val Gly Arg Ala Gly Pro Arg
      100      105      110
Thr Leu Pro Trp Met Met Ala Leu Val Gly Ala Val Ile Gly Leu Pro
      115      120      125
Met Phe Phe Glu Ile Gly Leu Val Leu Leu Met Pro Val Ile Ile Leu
      130      135      140
Val Ala Arg Arg Ser Gly Leu Ser Leu Met Arg Ile Ala Ile Pro Thr
145      150      155      160
Leu Ala Gly Leu Ser Ala Met His Gly Leu Val Pro Pro His Pro Gly
      165      170      175
Pro Leu Val Ala Val Ala Ala Leu Asn Ala Asn Leu Gly Leu Thr Leu
      180      185      190
Ala Leu Gly Val Leu Val Ala Ile Pro Thr Val Val Ile Ala Gly Pro
      195      200      205
Leu Phe Ser Lys Leu Ala Ala Arg Trp Val Asp Val Pro Val Pro Glu
      210      215      220
Leu Tyr Val Thr Val Glu Asp Arg Glu Gly Ala Glu Ala Ala Ala Glu
225      230      235      240
Arg Arg Arg Pro Ser Phe Ala Ala Thr Leu Ser Ala Ile Leu Leu Pro
      245      250      255
Val Val Leu Met Leu Gly Lys Ala Ile Ala Asp Val Ile Ala Ala Asp
      260      265      270
Ser Glu Ser Pro Ala Lys Ala Leu Asp Phe Leu Gly Thr Pro Val
      275      280      285
Val Ala Leu Gly Leu Ala Val Leu Ala Gly Met Ala Leu Leu Gly Arg
      290      295      300
Gly Gly Gly Met Asp Arg Lys Ala Ile Ala Val Ser Leu Glu Ser Ser
305      310      315      320
Leu Pro Pro Ile Ala Gly Ile Leu Leu Ile Val Gly Ala Gly Gly Gly
      325      330      335
Phe Lys Gln Val Leu Ile Asp Thr Gly Ile Ala Asp Val Ile Ala Asp
      340      345      350
Ala Ile Lys Asp Ser Ala Leu Pro Val Leu Phe Leu Ala Trp Leu Val
      355      360      365
Ala Val Leu Ile Arg Val Ala Thr Gly Ser Ala Thr Val Ala Thr Val
      370      375      380
Thr Ala Ser Gly Ile Leu Ala Pro Val Ala Ala Glu Leu Thr Ser Thr
385      390      395      400
His Val Ser Leu Met Val Leu Ala Ile Gly Ser Gly Ser Leu Phe Leu
      405      410      415
Ser His Val Asn Asp Ala Gly Phe Trp Leu Val Lys Glu Tyr Leu Gly
      420      425      430
Val Thr Val Val Gln Asn Leu Lys Thr Trp Thr Val Met Glu Cys Ile
      435      440      445
Ile Ser Val Thr Gly Leu Ala Gly Val Leu Ala Leu Ser Val Phe Ile
450      455      460

```

<210> 10196

<211> 1338

<212> DNA

<213> Haemophilus somnus 129PT

PF59083SeqList PF59083.txt

<220>
 <221> CDS
 <222> (1)..(1338)
 <223> transl_table=11

<400> 10196

atg aat act caa ctt tac ctt gtc gca gtt tta ata tca ggt ttg gca	48
Met Asn Thr Gln Leu Tyr Leu Val Ala Val Leu Ile Ser Gly Leu Ala	
1 5 10 15	
ctt att att ttt tct att ttg aag tta aag ctt cat cct ttt tta gca	96
Leu Ile Ile Phe Ser Ile Leu Lys Leu Lys Leu His Pro Phe Leu Ala	
20 25 30	
ttg tta ctg tca ggt ttt tat gtt gga att ttg atg gga atg aaa cca	144
Leu Leu Leu Ser Gly Phe Tyr Val Gly Ile Leu Met Gly Met Lys Pro	
35 40 45	
tta gaa atg ctg gat gct ata gaa aac ggt ata ggc gga aca ttg ggg	192
Leu Glu Met Leu Asp Ala Ile Glu Asn Gly Ile Gly Gly Thr Leu Gly	
50 55 60	
ttc ctt gct gct gtt ata gga ctg gga aca att tta gga aaa atg att	240
Phe Leu Ala Ala Val Ile Gly Leu Gly Thr Ile Leu Gly Lys Met Ile	
65 70 75 80	
gag gta tct ggc gga gct gaa cgg att gga ttg aca ctt caa aaa att	288
Glu Val Ser Gly Gly Ala Glu Arg Ile Gly Leu Thr Leu Gln Lys Ile	
85 90 95	
aga tgg ctt tca cct gat gtg ata atg gtt ttg atc gga ttg att tgt	336
Arg Trp Leu Ser Pro Asp Val Ile Met Val Leu Ile Gly Leu Ile Cys	
100 105 110	
ggg att aca ctt ttt gtt gaa gtc ggc gtg gtt tta ttg att cct tta	384
Gly Ile Thr Leu Phe Val Glu Val Gly Val Val Leu Leu Ile Pro Leu	
115 120 125	
gca ttt tcg att gcc aaa cgt act aaa gta tca tta tta act tta gct	432
Ala Phe Ser Ile Ala Lys Arg Thr Lys Val Ser Leu Leu Thr Leu Ala	
130 135 140	
att ccg tta tgt acc gct ctt atg gct gtt cat tgt att gtt ccc cct	480
Ile Pro Leu Cys Thr Ala Leu Met Ala Val His Cys Ile Val Pro Pro	
145 150 155 160	
cat cct gct gct ctt tat gta acc aat gcg tta ggt gca gat atg gga	528
His Pro Ala Ala Leu Tyr Val Thr Asn Ala Leu Gly Ala Asp Met Gly	
165 170 175	
aaa gtc att att tat gga tta ctt att ggg tta ttt aca tca cta ttc	576
Lys Val Ile Ile Tyr Gly Leu Leu Ile Gly Leu Phe Thr Ser Leu Phe	
180 185 190	
gct ggt ccc gtg ttt tta cgt atg atg aaa cgt caa gtt ccg ttt aag	624
Ala Gly Pro Val Phe Leu Arg Met Met Lys Arg Gln Val Pro Phe Lys	
195 200 205	
aaa gtc cca gag gaa ttt tct tct tta acg gta cgt caa gaa cat gaa	672
Lys Val Pro Glu Glu Phe Ser Ser Leu Thr Val Arg Gln Glu His Glu	
210 215 220	
ctt ccg tct tta ttt gct aca tta ttt aca att ttg tta ccg ata gta	720
Leu Pro Ser Leu Phe Ala Thr Leu Phe Thr Ile Leu Leu Pro Ile Val	
225 230 235 240	
tta atg ctg ttt aaa acg ctt gct gaa ttg acc ata gaa aaa aag act	768
Leu Met Leu Phe Lys Thr Leu Ala Glu Leu Thr Ile Glu Lys Lys Thr	
245 250 255	
gtt ttt tat acc gca ctt gaa gtg att ggc aat cct att act gct atg	816
Val Phe Tyr Thr Ala Leu Glu Val Ile Gly Asn Pro Ile Thr Ala Met	
260 265 270	
ctt att ggg gca ttt gtt gcg tat tat ttg ctt ggt ata aaa cat cac	864
Leu Ile Gly Ala Phe Val Ala Tyr Tyr Leu Leu Gly Ile Lys His His	
275 280 285	
caa agt atg gaa tcc tta tta aaa aat act gaa aat gga ttt atg gct	912
Gln Ser Met Glu Ser Leu Leu Lys Asn Thr Glu Asn Gly Phe Met Ala	
290 295 300	
att ggt aat att tta ctg att ata ggt gcc gga ggg gca ttt aac agt	960
Ile Gly Asn Ile Leu Leu Ile Ile Gly Ala Gly Gly Ala Phe Asn Ser	
305 310 315 320	
att tta aag gcg agc gga tta agt gat gga ttg gct gag att tta gca	1008
Ile Leu Lys Ala Ser Gly Leu Ser Asp Gly Leu Ala Glu Ile Leu Ala	
325 330 335	

PF59083SeqList PF59083.txt

aat	ttt	aat	aca	cat	cct	att	cta	ttg	gca	tg	ctt	ggt	gct	att	gtt	1056
Asn	Phe	Asn	Thr	His	Pro	Ile	Leu	Leu	Ala	Trp	Leu	Val	Ala	Ile	Val	
			340					345					350			
tta	cat	gcc	gca	gtg	gg	tct	gca	acg	gta	gca	atg	atg	gga	gca	acg	1104
Leu	His	Ala	Ala	Val	Gly	Ser	Ala	Thr	Val	Ala	Met	Met	Gly	Ala	Thr	
		355					360					365				
gca	atc	gtg	tcg	cca	tta	ctt	gtt	act	tac	cct	gat	att	agc	ccc	gaa	1152
Ala	Ile	Val	Ser	Pro	Leu	Leu	Val	Thr	Tyr	Pro	Asp	Ile	Ser	Pro	Glu	
	370					375					380					
att	att	gtc	ctt	gct	att	gg	tct	gg	gcg	ata	gga	tgc	act	att	gta	1200
Ile	Ile	Val	Leu	Ala	Ile	Gly	Ser	Gly	Ala	Ile	Gly	Cys	Thr	Ile	Val	
	385				390					395					400	
acg	gat	tct	ctc	ttt	tgg	ttg	gtc	aag	caa	tat	tgt	gg	gca	acc	ttg	1248
Thr	Asp	Ser	Leu	Phe	Trp	Leu	Val	Lys	Gln	Tyr	Cys	Gly	Ala	Thr	Leu	
			405					410					415			
aat	gac	att	ttt	aaa	tat	tat	acc	gg	gca	act	ttc	atc	gct	tcc	gta	1296
Asn	Asp	Ile	Phe	Lys	Tyr	Tyr	Thr	Gly	Ala	Thr	Phe	Ile	Ala	Ser	Val	
			420				425					430				
tta	gca	ctc	ggg	ttt	aca	ttt	tta	tta	tca	aca	gtg	att	tag			1338
Leu	Ala	Leu	Gly	Phe	Thr	Phe	Leu	Leu	Ser	Thr	Val	Ile				
		435					440					445				

<210> 10197

<211> 445

<212> PRT

<213> Haemophilus somnus 129PT

<400> 10197

Met	Asn	Thr	Gln	Leu	Tyr	Leu	Val	Ala	Val	Leu	Ile	Ser	Gly	Leu	Ala	
1				5					10					15		
Leu	Ile	Ile	Phe	Ser	Ile	Leu	Lys	Leu	Lys	Leu	His	Pro	Phe	Leu	Ala	
			20					25					30			
Leu	Leu	Leu	Ser	Gly	Phe	Tyr	Val	Gly	Ile	Leu	Met	Gly	Met	Lys	Pro	
		35					40					45				
Leu	Glu	Met	Leu	Asp	Ala	Ile	Glu	Asn	Gly	Ile	Gly	Gly	Thr	Leu	Gly	
	50					55					60					
Phe	Leu	Ala	Ala	Val	Ile	Gly	Leu	Gly	Thr	Ile	Leu	Gly	Lys	Met	Ile	
65					70					75					80	
Glu	Val	Ser	Gly	Gly	Ala	Glu	Arg	Ile	Gly	Leu	Thr	Leu	Gln	Lys	Ile	
			85					90					95			
Arg	Trp	Leu	Ser	Pro	Asp	Val	Ile	Met	Val	Leu	Ile	Gly	Leu	Ile	Cys	
			100					105					110			
Gly	Ile	Thr	Leu	Phe	Val	Glu	Val	Gly	Val	Val	Leu	Leu	Ile	Pro	Leu	
		115				120						125				
Ala	Phe	Ser	Ile	Ala	Lys	Arg	Thr	Lys	Val	Ser	Leu	Leu	Thr	Leu	Ala	
	130					135					140					
Ile	Pro	Leu	Cys	Thr	Ala	Leu	Met	Ala	Val	His	Cys	Ile	Val	Pro	Pro	
145					150					155					160	
His	Pro	Ala	Ala	Leu	Tyr	Val	Thr	Asn	Ala	Leu	Gly	Ala	Asp	Met	Gly	
			165					170					175			
Lys	Val	Ile	Ile	Tyr	Gly	Leu	Leu	Ile	Gly	Leu	Phe	Thr	Ser	Leu	Phe	
			180					185					190			
Ala	Gly	Pro	Val	Phe	Leu	Arg	Met	Met	Lys	Arg	Gln	Val	Pro	Phe	Lys	
		195					200					205				
Lys	Val	Pro	Glu	Glu	Phe	Ser	Leu	Thr	Val	Arg	Gln	Glu	His	Glu		
	210					215					220					
Leu	Pro	Ser	Leu	Phe	Ala	Thr	Leu	Phe	Thr	Ile	Leu	Leu	Pro	Ile	Val	
225					230					235					240	
Leu	Met	Leu	Phe	Lys	Thr	Leu	Ala	Glu	Leu	Thr	Ile	Glu	Lys	Lys	Thr	
			245					250					255			
Val	Phe	Tyr	Thr	Ala	Leu	Glu	Val	Ile	Gly	Asn	Pro	Ile	Thr	Ala	Met	
			260					265					270			
Leu	Ile	Gly	Ala	Phe	Val	Ala	Tyr	Tyr	Leu	Leu	Gly	Ile	Lys	His	His	
		275					280					285				
Gln	Ser	Met	Glu	Ser	Leu	Leu	Lys	Asn	Thr	Glu	Asn	Gly	Phe	Met	Ala	
	290					295					300					
Ile	Gly	Asn	Ile	Leu	Leu	Ile	Ile	Gly	Ala	Gly	Gly	Ala	Phe	Asn	Ser	
305					310					315					320	
Ile	Leu	Lys	Ala	Ser	Gly	Leu	Ser	Asp	Gly	Leu	Ala	Glu	Ile	Leu	Ala	

PF59083SeqList PF59083.txt

```

          325          330          335
Asn Phe Asn Thr His Pro Ile Leu Leu Ala Trp Leu Val Ala Ile Val
          340          345          350
Leu His Ala Ala Val Gly Ser Ala Thr Val Ala Met Met Gly Ala Thr
          355          360          365
Ala Ile Val Ser Pro Leu Leu Val Thr Tyr Pro Asp Ile Ser Pro Glu
          370          375          380
Ile Ile Val Leu Ala Ile Gly Ser Gly Ala Ile Gly Cys Thr Ile Val
          385          390          395
Thr Asp Ser Leu Phe Trp Leu Val Lys Gln Tyr Cys Gly Ala Thr Leu
          405          410          415
Asn Asp Ile Phe Lys Tyr Tyr Thr Gly Ala Thr Phe Ile Ala Ser Val
          420          425          430
Leu Ala Leu Gly Phe Thr Phe Leu Leu Ser Thr Val Ile
          435          440          445

```

<210> 10198

<211> 1353

<212> DNA

<213> Pediococcus pentosaceus ATCC 25745

<220>

<221> CDS

<222> (1)..(1353)

<223> transl_table=11

<400> 10198

```

atg gaa att atg gtc tta gtt att gga ata att tta ttg tta act tta      48
Met Glu Ile Met Val Leu Val Ile Gly Ile Ile Leu Leu Leu Thr Leu
 1          5          10          15
att ata aaa ttt aag atg aat act tat gtt tca ttg att att act gcg      96
Ile Ile Lys Phe Lys Met Asn Thr Tyr Val Ser Leu Ile Ile Thr Ala
          20          25          30
gtg gtt gtt gga tta ggt tta ggg atg ccg gct agc cag att gcc acc      144
Val Val Val Gly Leu Gly Leu Gly Met Pro Ala Ser Gln Ile Ala Thr
          35          40          45
acg att caa aat gga att ggg agt caa ttg ggt gaa cta gcg ttg gta      192
Thr Ile Gln Asn Gly Ile Gly Ser Gln Leu Gly Glu Leu Ala Leu Val
          50          55          60
ttt ggc ttt gga gct atg ttg ggt cgc ttg gtt gcc gac gca ggg gga      240
Phe Gly Phe Gly Ala Met Leu Gly Arg Leu Val Ala Asp Ala Gly Gly
          65          70          75          80
gcc tat cgg att gct aat acc tta atc gat aaa ttc gga cgc cgc ttc      288
Ala Tyr Arg Ile Ala Asn Thr Leu Ile Asp Lys Phe Gly Arg Arg Phe
          85          90          95
tta caa att gct gtt gta gtt gct tcg ttt att att ggg att gca ctt      336
Leu Gln Ile Ala Val Val Val Ala Ser Phe Ile Ile Gly Ile Ala Leu
          100          105          110
ttc ttt gaa gta gga atc gtg tta tta gta cca att gta ttc gca att      384
Phe Phe Glu Val Gly Ile Val Leu Val Pro Ile Val Phe Ala Ile
          115          120          125
gcg atc gaa gca ggg gtt cca gtt ctt tcc tta gga att cca atg gca      432
Ala Ile Glu Ala Gly Val Pro Val Leu Ser Leu Gly Ile Pro Met Ala
          130          135          140
gca gcc tta tca gtt act cac gga ttt ttg cca cca cat cca gct cct      480
Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Ala Pro
          145          150          155          160
act gca att gct gca gtc ctg aat gct aat gct gga aag gtt tta ctt      528
Thr Ala Ile Ala Val Leu Asn Ala Asn Ala Gly Lys Val Leu Leu
          165          170          175
tac gga gtg att att gca att cca act gtt tat att gca ggt gta tta      576
Tyr Gly Val Ile Ile Ala Ile Pro Thr Val Tyr Ile Ala Gly Val Leu
          180          185          190
ttt tca aaa att gct aaa aaa tat ctt cca gaa gcg ttt aaa aga aat      624
Phe Ser Lys Ile Ala Lys Lys Tyr Leu Pro Glu Ala Phe Lys Arg Asn
          195          200          205          210
ggg aat tta aaa gct tta gga cct caa aaa caa ttt aaa tta gag gaa      672
Gly Asn Leu Lys Ala Leu Gly Pro Gln Lys Gln Phe Lys Leu Glu Glu
          210          215          220

```

PF59083SeqList PF59083.txt

act	ccg	gga	ttc	ggg	att	tcg	ggt	tta	act	gct	ctt	ttc	cca	gtc	atc	720
Thr	Pro	Gly	Phe	Gly	Ile	Ser	Val	Leu	Thr	Ala	Leu	Phe	Pro	Val	Ile	
225					230					235					240	
tta	atg	gct	atc	aca	acg	ata	tat	gaa	ttg	att	gtc	cac	gac	ggg	gtt	768
Leu	Met	Ala	Ile	Thr	Ile	Tyr	Glu	Leu	Ile	Val	His	Asp	Gly	Val		
				245				250						255		
acg	cct	aaa	aat	cct	aat	gcg	ggt	gac	aat	ttt	ttt	gga	ttt	atc	ggg	816
Thr	Pro	Lys	Asn	Pro	Asn	Ala	Val	Asp	Asn	Phe	Phe	Gly	Phe	Ile	Gly	
			260					265					270			
tct	cct	agt	ata	gct	atg	tta	att	tca	tta	ttg	ttt	gca	atg	tgg	ttg	864
Ser	Pro	Ser	Ile	Ala	Met	Leu	Ile	Ser	Leu	Leu	Phe	Ala	Met	Trp	Leu	
			275				280					285				
atg	ggg	tat	cac	cgt	aag	att	gct	agt	aaa	gat	att	atg	gct	act	tta	912
Met	Gly	Tyr	His	Arg	Lys	Ile	Ala	Ser	Lys	Asp	Ile	Met	Ala	Thr	Leu	
			290			295				300						
gaa	gat	gcg	gtg	aaa	tca	att	gca	atg	ctc	ctt	ctg	gta	att	ggg	ggg	960
Glu	Asp	Ala	Val	Lys	Ser	Ile	Ala	Met	Leu	Leu	Leu	Val	Ile	Gly	Gly	
305					310					315					320	
gga	ggg	gcg	ttt	aaa	caa	ggt	tta	att	gat	ggg	ggg	ggt	gga	gat	gcg	1008
Gly	Gly	Ala	Phe	Lys	Gln	Val	Leu	Ile	Asp	Gly	Gly	Val	Gly	Asp	Ala	
				325					330					335		
gtc	aaa	aat	atc	ttt	gca	tca	tct	agt	atc	tct	cct	cta	att	tta	gga	1056
Val	Lys	Asn	Ile	Phe	Ala	Ser	Ser	Ser	Ile	Ser	Pro	Leu	Ile	Leu	Gly	
			340					345					350			
tgg	ttg	ata	gcg	gta	gtc	ctt	cga	gtg	tta	gga	tcc	gca	acg	gtg		1104
Trp	Leu	Ile	Ala	Val	Val	Leu	Arg	Val	Ala	Leu	Gly	Ser	Ala	Thr	Val	
			355				360					365				
gca	tct	cta	act	gct	gcc	ggg	tta	gta	tta	ccc	tta	atg	caa	ggg	gcg	1152
Ala	Ser	Leu	Thr	Ala	Ala	Gly	Leu	Val	Leu	Pro	Leu	Met	Gln	Gly	Ala	
			370			375				380						
gga	att	gat	cct	gca	tta	atg	gtg	tta	tca	ggt	gga	gca	gga	agt	tta	1200
Gly	Ile	Asp	Pro	Ala	Leu	Met	Val	Leu	Ser	Val	Gly	Ala	Gly	Ser	Leu	
385					390					395					400	
gct	gcg	agt	cac	ggt	aat	gat	gca	ggc	ttc	ttg	atg	ttc	aaa	gaa	tac	1248
Ala	Ala	Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Met	Phe	Lys	Glu	Tyr	
				405				410						415		
ttt	gat	tta	tcc	ggt	aaa	gaa	acc	tta	cta	aca	tgg	aca	gta	cta	gaa	1296
Phe	Asp	Leu	Ser	Val	Lys	Glu	Thr	Leu	Leu	Thr	Trp	Thr	Val	Leu	Glu	
			420					425					430			
aca	gtc	att	tcg	att	ggt	gga	tta	att	ggc	gtg	tta	tta	tta	agt	ttg	1344
Thr	Val	Ile	Ser	Ile	Val	Gly	Leu	Ile	Gly	Val	Leu	Leu	Leu	Ser	Leu	
			435				440					445				
att	gtt	taa														1353
Ile	Val															
	450															

<210> 10199

<211> 450

<212> PRT

<213> *Pediococcus pentosaceus* ATCC 25745

<400> 10199

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

PF59083SeqList PF59083.txt

130 135 140
Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Ala Pro
145 150 155 160
Thr Ala Ile Ala Ala Val Leu Asn Ala Asn Ala Gly Lys Val Leu Leu
165 170 175
Tyr Gly Val Ile Ala Ile Pro Thr Val Tyr Ile Ala Gly Val Leu
180 185 190
Phe Ser Lys Ile Ala Lys Lys Tyr Leu Pro Glu Ala Phe Lys Arg Asn
195 200 205
Gly Asn Leu Lys Ala Leu Gly Pro Gln Lys Gln Phe Lys Leu Glu Glu
210 215 220
Thr Pro Gly Phe Gly Ile Ser Val Leu Thr Ala Leu Phe Pro Val Ile
225 230 235 240
Leu Met Ala Ile Thr Thr Ile Tyr Glu Leu Ile Val His Asp Gly Val
245 250 255
Thr Pro Lys Asn Pro Asn Ala Val Asp Asn Phe Phe Gly Phe Ile Gly
260 265 270
Ser Pro Ser Ile Ala Met Leu Ile Ser Leu Leu Phe Ala Met Trp Leu
275 280 285
Met Gly Tyr His Arg Lys Ile Ala Ser Lys Asp Ile Met Ala Thr Leu
290 295 300
Glu Asp Ala Val Lys Ser Ile Ala Met Leu Leu Leu Val Ile Gly Gly
305 310 315 320
Gly Gly Ala Phe Lys Gln Val Leu Ile Asp Gly Gly Val Gly Asp Ala
325 330 335
Val Lys Asn Ile Phe Ala Ser Ser Ser Ile Ser Pro Leu Ile Leu Gly
340 345 350
Trp Leu Ile Ala Val Val Leu Arg Val Ala Leu Gly Ser Ala Thr Val
355 360 365
Ala Ser Leu Thr Ala Ala Gly Leu Val Leu Pro Leu Met Gln Gly Ala
370 375 380
Gly Ile Asp Pro Ala Leu Met Val Leu Ser Val Gly Ala Gly Ser Leu
385 390 395 400
Ala Ala Ser His Val Asn Asp Ala Gly Phe Trp Met Phe Lys Glu Tyr
405 410 415
Phe Asp Leu Ser Val Lys Glu Thr Leu Leu Thr Trp Thr Val Leu Glu
420 425 430
Thr Val Ile Ser Ile Val Gly Leu Ile Gly Val Leu Leu Leu Ser Leu
435 440 445
Ile Val
450

<210> 10200
<211> 1500
<212> DNA
<213> Oenococcus oeni PSU-1

<220>
<221> CDS
<222> (1)..(1500)
<223> transl_table=11

<400> 10200
atg tcg tca ctt gca gct att act gtc gat ccg aaa acc ggc ttt ttt 48
Met Ser Ser Leu Ala Ala Ile Thr Val Asp Pro Lys Thr Gly Phe Phe
1 5 10 15
tct tgg ctg gtt aac ggg ttt aat att tgg cct ttc ctg att tta gtt 96
Ser Trp Leu Val Asn Gly Phe Asn Ile Trp Pro Phe Leu Ile Leu Val
20 25 30
tta gga atc gct tta ctt tta act ttg att tta aaa ttt aaa atc aat 144
Leu Gly Ile Ala Leu Leu Leu Thr Leu Ile Leu Lys Phe Lys Ile Asn
35 40 45
act ttt gtt act ttg atc ctt gtt tca att att gtt gct ttc gct ttg 192
Thr Phe Val Thr Leu Ile Leu Val Ser Ile Ile Val Ala Phe Ala Leu
50 55 60
gga atg aat ccg gcc ggg att gct gcg gca ata caa aac gga att ggt 240
Gly Met Asn Pro Ala Gly Ile Ala Ala Ala Ile Gln Asn Gly Ile Gly
65 70 75 80
gga acc ttg ggc gaa ttg gtt gtt gtc ttc gga ttt ggt tct atg atc 288

PF59083SeqList PF59083.txt

Gly	Thr	Leu	Gly	Glu	Leu	Val	Val	Val	Phe	Gly	Phe	Gly	Ser	Met	Ile	
ggc	cgc	ttg	ggt	tcc	gat	tcc	ggt	ggt	tct	tat	cga	att	gcc	aaa	act	336
Gly	Arg	Leu	Val	Ser	Asp	Ser	Gly	Gly	Ser	Tyr	Arg	Ile	Ala	Lys	Thr	
		100					105						110			
ttg	att	gct	aaa	ttc	gga	cgg	aaa	agg	ctc	caa	tgg	gcg	ggt	gct	ttt	384
Leu	Ile	Ala	Lys	Phe	Gly	Arg	Lys	Arg	Leu	Gln	Trp	Ala	Val	Ala	Phe	
		115					120					125				
gct	tcg	ttt	att	att	gga	att	tcc	ctg	ctg	ttt	gaa	ggt	gga	tta	ggt	432
Ala	Ser	Phe	Ile	Ile	Gly	Ile	Ser	Leu	Leu	Phe	Glu	Val	Gly	Leu	Val	
	130					135					140					
ggt	ttg	att	cca	atc	gtc	ttt	gcg	atc	gcc	ttg	gaa	gcc	gat	ggt	cct	480
Val	Leu	Ile	Pro	Ile	Val	Phe	Ala	Ile	Ala	Leu	Glu	Ala	Asp	Val	Pro	
145					150				155						160	
ttg	ctc	tat	ttg	ggt	att	cca	atg	gcg	acc	gcc	ttg	tcg	gcg	gcc	caa	528
Leu	Leu	Tyr	Leu	Gly	Ile	Pro	Met	Ala	Thr	Ala	Leu	Ser	Ala	Ala	Gln	
			165					170						175		
ggc	ttt	ctg	cct	cct	caa	cca	tca	ccg	acg	gcg	gtc	agc	aat	ctt	ctt	576
Gly	Phe	Leu	Pro	Pro	Gln	Pro	Ser	Pro	Thr	Ala	Val	Ser	Asn	Leu	Leu	
		180					185						190			
ggt	gcc	aac	atg	gga	atg	gtc	ttg	att	tat	gga	att	atc	gtg	gca	att	624
Gly	Ala	Asn	Met	Gly	Met	Val	Leu	Ile	Tyr	Gly	Ile	Ile	Val	Ala	Ile	
		195				200					205					
ccg	gcg	atg	att	atc	gct	ggt	cct	gtg	ttt	acg	aga	ata	gcc	caa	aaa	672
Pro	Ala	Met	Ile	Ile	Ala	Gly	Pro	Val	Phe	Thr	Arg	Ile	Ala	Gln	Lys	
	210					215					220					
tat	gta	cca	aaa	gct	ttt	aaa	att	acc	aag	cat	cta	gac	gct	ttg	gga	720
Tyr	Val	Pro	Lys	Ala	Phe	Lys	Ile	Thr	Lys	His	Leu	Asp	Ala	Leu	Gly	
225				230					235						240	
aca	ggt	aag	gaa	ttt	aaa	tta	gag	gat	acc	ccg	tca	ttt	gga	att	tct	768
Thr	Val	Lys	Glu	Phe	Lys	Leu	Glu	Asp	Thr	Pro	Ser	Phe	Gly	Ile	Ser	
			245					250					255			
att	ttg	act	tcc	ttg	atg	gca	ggt	atc	ttt	atg	ggt	att	aca	aca	att	816
Ile	Leu	Thr	Ser	Leu	Met	Ala	Val	Ile	Phe	Met	Val	Ile	Thr	Thr	Ile	
		260					265						270			
att	acg	atg	ggt	ggt	aat	ggt	gga	aaa	cag	ggt	tac	acc	ggt	acg	atc	864
Ile	Thr	Met	Val	Val	Asn	Gly	Gly	Lys	Gln	Val	Tyr	Thr	Gly	Thr	Ile	
		275				280					285					
ggt	gat	gct	gca	tgg	aag	gca	atg	aga	act	gcg	gac	caa	aaa	ggt	tat	912
Gly	Asp	Ala	Ala	Trp	Lys	Ala	Met	Arg	Thr	Ala	Asp	Gln	Lys	Gly	Tyr	
	290					295					300					
ctg	ctt	cat	cca	aca	act	ttt	cag	aaa	atc	att	gct	ttt	ctt	ggc	aat	960
Leu	Leu	His	Pro	Thr	Thr	Phe	Gln	Lys	Ile	Ile	Ala	Phe	Leu	Gly	Asn	
305				310					315						320	
cct	tta	att	gcg	atg	gta	att	gct	tta	ttg	ttt	gct	ctt	tgg	tca	atg	1008
Pro	Leu	Ile	Ala	Met	Val	Ile	Ala	Leu	Leu	Phe	Ala	Leu	Trp	Ser	Met	
			325					330					335			
gga	ccg	ctt	cag	ggg	cgt	tcg	att	aaa	gat	ggt	aat	aat	aca	tta	acc	1056
Gly	Pro	Leu	Gln	Gly	Arg	Ser	Ile	Lys	Asp	Val	Asn	Asn	Thr	Leu	Thr	
		340						345					350			
gat	gct	atc	aaa	tcg	att	gcg	aat	ttg	ctg	atg	ggt	att	ggt	ggt	gga	1104
Asp	Ala	Ile	Lys	Ser	Ile	Ala	Asn	Leu	Leu	Met	Val	Ile	Gly	Gly	Gly	
		355				360					365					
gct	gcc	ttt	aaa	ggt	gtc	ctg	act	tcc	ggt	gga	att	tca	acc	gca	att	1152
Ala	Ala	Phe	Lys	Gly	Val	Leu	Thr	Ser	Gly	Gly	Ile	Ser	Thr	Ala	Ile	
	370					375					380					
gct	cag	gcc	ttt	gct	cac	tcg	tca	atg	tcg	ccg	att	ctg	ttt	gcc	tgg	1200
Ala	Gln	Ala	Phe	Ala	His	Ser	Ser	Met	Ser	Pro	Ile	Leu	Phe	Ala	Trp	
385				390					395						400	
ttg	ggt	gct	gta	ata	att	cgt	ggt	tca	ggt	tcg	gcg	act	ggt	gcc	1248	
Leu	Val	Ala	Val	Ile	Ile	Arg	Val	Ser	Val	Gly	Ser	Ala	Thr	Val	Ala	
			405					410					415			
gga	atg	act	tca	gct	ggt	att	ggt	gct	ccg	att	gta	gct	tcg	caa	aca	1296
Gly	Met	Thr	Ser	Ala	Gly	Ile	Val	Ala	Pro	Ile	Val	Ala	Ser	Gln	Thr	
		420				425						430				
gct	att	aac	ccg	gca	ttt	ggt	ggt	ttg	gct	atc	ggt	gcc	ggt	tcg	cta	1344
Ala	Ile	Asn	Pro	Ala	Phe	Val	Val	Leu	Ala	Ile	Gly	Ala	Gly	Ser	Leu	
		435				440					445					
gct	gcc	agc	cat	ggt	aac	gat	gct	ggt	ttc	tgg	atg	ttc	aag	gaa	ttc	1392

PF59083SeqList PF59083.txt

Ala	Ala	Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Met	Phe	Lys	Glu	Phe	
450						455					460					
ttt	gat	ttg	gat	gtt	aaa	gaa	act	ttg	aaa	acc	tgg	act	gta	ttg	gag	1440
Phe	Asp	Leu	Asp	Val	Lys	Glu	Thr	Leu	Lys	Thr	Trp	Thr	Val	Leu	Glu	
465					470					475					480	
act	ttg	att	tcc	gta	gtt	gga	tta	tta	atg	gtt	ctt	ttg	ttg	tcg	acg	1488
Thr	Leu	Ile	Ser	Val	Val	Gly	Leu	Leu	Met	Val	Leu	Leu	Leu	Ser	Thr	
				485					490					495		
att	ttc	cac	tga													1500
Ile	Phe	His														

<210> 10201

<211> 499

<212> PRT

<213> Oenococcus oeni PSU-1

<400> 10201

Met	Ser	Ser	Leu	Ala	Ala	Ile	Thr	Val	Asp	Pro	Lys	Thr	Gly	Phe	Phe	
1				5					10					15		
Ser	Trp	Leu	Val	Asn	Gly	Phe	Asn	Ile	Trp	Pro	Phe	Leu	Ile	Leu	Val	
			20					25					30			
Leu	Gly	Ile	Ala	Leu	Leu	Leu	Thr	Leu	Ile	Leu	Lys	Phe	Lys	Ile	Asn	
		35					40					45				
Thr	Phe	Val	Thr	Leu	Ile	Leu	Val	Ser	Ile	Ile	Val	Ala	Phe	Ala	Leu	
	50					55					60					
Gly	Met	Asn	Pro	Ala	Gly	Ile	Ala	Ala	Ala	Ile	Gln	Asn	Gly	Ile	Gly	
65					70					75					80	
Gly	Thr	Leu	Gly	Glu	Leu	Val	Val	Val	Phe	Gly	Phe	Gly	Ser	Met	Ile	
				85					90					95		
Gly	Arg	Leu	Val	Ser	Asp	Ser	Gly	Gly	Ser	Tyr	Arg	Ile	Ala	Lys	Thr	
			100					105					110			
Leu	Ile	Ala	Lys	Phe	Gly	Arg	Lys	Arg	Leu	Gln	Trp	Ala	Val	Ala	Phe	
		115					120					125				
Ala	Ser	Phe	Ile	Ile	Gly	Ile	Ser	Leu	Leu	Phe	Glu	Val	Gly	Leu	Val	
	130					135					140					
Val	Leu	Ile	Pro	Ile	Val	Phe	Ala	Ile	Ala	Leu	Glu	Ala	Asp	Val	Pro	
145					150					155					160	
Leu	Leu	Tyr	Leu	Gly	Ile	Pro	Met	Ala	Thr	Ala	Leu	Ser	Ala	Ala	Gln	
				165					170					175		
Gly	Phe	Leu	Pro	Pro	Gln	Pro	Ser	Pro	Thr	Ala	Val	Ser	Asn	Leu	Leu	
			180					185					190			
Gly	Ala	Asn	Met	Gly	Met	Val	Leu	Ile	Tyr	Gly	Ile	Ile	Val	Ala	Ile	
		195					200					205				
Pro	Ala	Met	Ile	Ile	Ala	Gly	Pro	Val	Phe	Thr	Arg	Ile	Ala	Gln	Lys	
	210					215					220					
Tyr	Val	Pro	Lys	Ala	Phe	Lys	Ile	Thr	Lys	His	Leu	Asp	Ala	Leu	Gly	
225					230					235					240	
Thr	Val	Lys	Glu	Phe	Lys	Leu	Glu	Asp	Thr	Pro	Ser	Phe	Gly	Ile	Ser	
				245					250					255		
Ile	Leu	Thr	Ser	Leu	Met	Ala	Val	Ile	Phe	Met	Val	Ile	Thr	Thr	Ile	
			260					265					270			
Ile	Thr	Met	Val	Val	Asn	Gly	Gly	Lys	Gln	Val	Tyr	Thr	Gly	Thr	Ile	
		275					280						285			
Gly	Asp	Ala	Ala	Trp	Lys	Ala	Met	Arg	Thr	Ala	Asp	Gln	Lys	Gly	Tyr	
	290					295					300					
Leu	Leu	His	Pro	Thr	Thr	Phe	Gln	Lys	Ile	Ile	Ala	Phe	Leu	Gly	Asn	
					310					315					320	
Pro	Leu	Ile	Ala	Met	Val	Ile	Ala	Leu	Leu	Phe	Ala	Leu	Trp	Ser	Met	
				325					330					335		
Gly	Pro	Leu	Gln	Gly	Arg	Ser	Ile	Lys	Asp	Val	Asn	Asn	Thr	Leu	Thr	
			340					345					350			
Asp	Ala	Ile	Lys	Ser	Ile	Ala	Asn	Leu	Leu	Met	Val	Ile	Gly	Gly	Gly	
		355					360					365				
Ala	Ala	Phe	Lys	Gly	Val	Leu	Thr	Ser	Gly	Gly	Ile	Ser	Thr	Ala	Ile	
	370					375					380					
Ala	Gln	Ala	Phe	Ala	His	Ser	Ser	Met	Ser	Pro	Ile	Leu	Phe	Ala	Trp	
	385				390					395					400	
Leu	Val	Ala	Val	Ile	Ile	Arg	Val	Ser	Val	Gly	Ser	Ala	Thr	Val	Ala	

PF59083SeqList PF59083.txt

405 410 415
 Gly Met Thr Ser Ala Gly Ile Val Ala Pro Ile Val Ala Ser Gln Thr
 420 425 430
 Ala Ile Asn Pro Ala Phe Val Val Leu Ala Ile Gly Ala Gly Ser Leu
 435 440 445
 Ala Ala Ser His Val Asn Asp Ala Gly Phe Trp Met Phe Lys Glu Phe
 450 455 460
 Phe Asp Leu Asp Val Lys Glu Thr Leu Lys Thr Trp Thr Val Leu Glu
 465 470 475 480
 Thr Leu Ile Ser Val Gly Leu Leu Met Val Leu Leu Leu Ser Thr
 485 490 495
 Ile Phe His

<210> 10202

<211> 1335

<212> DNA

<213> Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293

<220>

<221> CDS

<222> (1)..(1335)

<223> transl_table=11

<400> 10202

atg cca ttg tta aca gtt ttg att ggt gtc att tta ctc gta ttc ttg	48
Met Pro Leu Leu Thr Val Leu Ile Gly Val Ile Leu Leu Val Phe Leu	
1 5 10 15	
att act aaa ttt aag ttg aac act ttt tta tcg tta gtc att aca gcg	96
Ile Thr Lys Phe Lys Leu Asn Thr Phe Leu Ser Leu Val Ile Thr Ala	
20 25 30	
ttt gtt gtc ggc tta att tta ggt att cca gtt tct gat att tca aca	144
Phe Val Val Gly Leu Ile Leu Gly Ile Pro Val Ser Asp Ile Ser Thr	
35 40 45	
agt att gag aca gga ata ggt ggt cag tta ggc cac tta gcg att ata	192
Ser Ile Glu Thr Gly Ile Gly Gly Gln Leu Gly His Leu Ala Ile Ile	
50 55 60	
ttt gga ttt gga tcg atg ctt gga aag tta att tcc gac gca ggt ggt	240
Phe Gly Phe Gly Ser Met Leu Gly Lys Leu Ile Ser Asp Ala Gly Gly	
65 70 75 80	
ggc ttt cga att gcg cac cag ctc att gcg act ttt gga aaa aaa cgc	288
Gly Phe Arg Ile Ala His Gln Leu Ile Ala Thr Phe Gly Lys Lys Arg	
85 90 95	
att caa att gct gtt att att acg tcg ttt att att ggt tta gct ttg	336
Ile Gln Ile Ala Val Ile Ile Thr Ser Phe Ile Ile Gly Leu Ala Leu	
100 105 110	
ttt ttt gaa gtt gga tta gtc gtg tta ttg cca att atc ttc gtc att	384
Phe Phe Glu Val Gly Leu Val Val Leu Leu Pro Ile Ile Phe Val Ile	
115 120 125	
gca cgt gaa gta aat atg cct ctt ttg tac ctt ggt att cca atg gct	432
Ala Arg Glu Val Asn Met Pro Leu Leu Tyr Leu Gly Ile Pro Met Ala	
130 135 140	
gcg aca tta aat gtt gca cac ggt ttc tta cca ccg cat cct gca ccg	480
Ala Thr Leu Asn Val Ala His Gly Phe Leu Pro Pro His Pro Ala Pro	
145 150 155 160	
act gct gta tca cag gtg ttg aat gcg cct ttg ggg cac gtt tta ctg	528
Thr Ala Val Ser Gln Val Leu Asn Ala Pro Leu Gly His Val Leu Leu	
165 170 175	
att ggt att tta gtg tca att ccc acg atc att att tct ggt ccg gtg	576
Ile Gly Ile Leu Val Ser Ile Pro Thr Ile Ile Ile Ser Gly Pro Val	
180 185 190	
ttc aac tat ttt ttg cat cga gta tat ccg caa gtt tat aaa aaa gat	624
Phe Asn Tyr Phe Leu His Arg Val Tyr Pro Gln Val Tyr Lys Lys Asp	
195 200 205	
att aat att tct gtt tta ggt gag tac aaa gaa ttc gag ttg aaa gat	672
Ile Asn Ile Ser Val Leu Gly Glu Tyr Lys Glu Phe Glu Leu Lys Asp	
210 215 220	
aca cca aag ttt ggt att agt gtt ttg aca gca tta tta cca gta ata	720
Thr Pro Lys Phe Gly Ile Ser Val Leu Thr Ala Leu Leu Pro Val Ile	

PF59083SeqList PF59083.txt

225					230					235					240	
ttg att agt att gca acc atc tta tca ttt gtt ttg cca gct aag tca																768
Leu Ile Ser Ile Ala Thr Ile Leu Ser Phe Val Leu Pro Ala Lys Ser																
				245					250					255		
gtt att tat caa atc gtc aca ttt atc ggt gca cct gat gta gct atg																816
Val Ile Tyr Gln Ile Val Thr Phe Ile Gly Ala Pro Asp Val Ala Met																
			260						265					270		
ctc ata tca tta att gtt gcg att ttc acc atg ggt att ttc cgt gga																864
Leu Ile Ser Leu Ile Val Ala Ile Phe Thr Met Gly Ile Phe Arg Gly																
		275					280						285			
ttg aat atc aaa gaa att ggt gac gca atg tct gaa tcg gtt aaa caa																912
Leu Asn Ile Lys Glu Ile Gly Asp Ala Met Ser Glu Ser Val Lys Gln																
		290				295						300				
att gct atg atg ttg tta atc att ggt ggt ggt ggt gcc ttc aaa caa																960
Ile Ala Met Met Leu Ile Ile Gly Gly Gly Gly Ala Phe Lys Gln																
		305			310					315					320	
gta tta gtt gat ggt ggt gtt tct aag tat att ggc gat tta ttc gga																1008
Val Leu Val Asp Gly Gly Val Ser Lys Tyr Ile Gly Asp Leu Phe Gly																
			325						330					335		
caa act aat ttg tcc cca att ctt gtt gct tgg tta atc gct gct tta																1056
Gln Thr Asn Leu Ser Pro Ile Leu Val Ala Trp Leu Ile Ala Ala Leu																
		340					345						350			
ctt cgc gtc agc cta gga tca tct act gtt gct tcg ata aca gca gcc																1104
Leu Arg Val Ser Leu Gly Ser Ser Thr Val Ala Ser Ile Thr Ala Ala																
		355				360						365				
agt tta gtt act tca gtt gtg tcc aac tca agt gtg agt cct gta tta																1152
Ser Leu Val Thr Ser Val Val Ser Asn Ser Ser Val Ser Pro Val Leu																
		370			375							380				
gta gtt ttg gca att ggt gct gga agt ata ttt gct gat cat gtt aat																1200
Val Val Leu Ala Ile Gly Ala Gly Ser Ile Phe Ala Asp His Val Asn																
		385			390					395					400	
gat gct gga ttc tgg atg ata aaa gaa tat ttt ggt tta aca ttg aaa																1248
Asp Ala Gly Phe Trp Met Ile Lys Glu Tyr Phe Gly Leu Thr Leu Lys																
			405						410					415		
gaa acg ttc tta tct tgg acg aca tta acc agt gtc atc tcc gtt tcg																1296
Glu Thr Phe Leu Ser Trp Thr Thr Leu Thr Ser Val Ile Ser Val Ser																
		420					425						430			
ggt ctg tta tcg att cta ctc gtg tca tgt ttt atg tag																1335
Gly Leu Leu Ser Ile Leu Leu Val Ser Cys Phe Met																
		435				440										

<210> 10203

<211> 444

<212> PRT

<213> Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293

<400> 10203

Met Pro Leu Leu Thr Val Leu Ile Gly Val Ile Leu Leu Val Phe Leu																
1 5 10 15																
Ile Thr Lys Phe Lys Leu Asn Thr Phe Leu Ser Leu Val Ile Thr Ala																
	20						25					30				
Phe Val Val Gly Leu Ile Leu Gly Ile Pro Val Ser Asp Ile Ser Thr																
	35					40					45					
Ser Ile Glu Thr Gly Ile Gly Gln Leu Gly His Leu Ala Ile Ile																
	50				55				60							
Phe Gly Phe Gly Ser Met Leu Gly Lys Leu Ile Ser Asp Ala Gly Gly																80
65 70 75																
Gly Phe Arg Ile Ala His Gln Leu Ile Ala Thr Phe Gly Lys Lys Arg																
	85						90					95				
Ile Gln Ile Ala Val Ile Ile Thr Ser Phe Ile Ile Gly Leu Ala Leu																
	100					105					110					
Phe Phe Glu Val Gly Leu Val Val Leu Leu Pro Ile Ile Phe Val Ile																
	115					120				125						
Ala Arg Glu Val Asn Met Pro Leu Leu Tyr Leu Gly Ile Pro Met Ala																
	130				135				140							
Ala Thr Leu Asn Val Ala His Gly Phe Leu Pro Pro His Pro Ala Pro																160
145 150 155																
Thr Ala Val Ser Gln Val Leu Asn Ala Pro Leu Gly His Val Leu Leu																
	165						170					175				

PF59083SeqList PF59083.txt

Ile Gly Ile Leu Val Ser Ile Pro Thr Ile Ile Ile Ser Gly Pro Val
 180 185 190
 Phe Asn Tyr Phe Leu His Arg Val Tyr Pro Gln Val Tyr Lys Lys Asp
 195 200 205
 Ile Asn Ile Ser Val Leu Gly Glu Tyr Lys Glu Phe Glu Leu Lys Asp
 210 215 220
 Thr Pro Lys Phe Gly Ile Ser Val Leu Thr Ala Leu Leu Pro Val Ile
 225 230 235 240
 Leu Ile Ser Ile Ala Thr Ile Leu Ser Phe Val Leu Pro Ala Lys Ser
 245 250 255
 Val Ile Tyr Gln Ile Val Thr Phe Ile Gly Ala Pro Asp Val Ala Met
 260 265 270
 Leu Ile Ser Leu Ile Val Ala Ile Phe Thr Met Gly Ile Phe Arg Gly
 275 280 285
 Leu Asn Ile Lys Glu Ile Gly Asp Ala Met Ser Glu Ser Val Lys Gln
 290 295 300
 Ile Ala Met Met Leu Leu Ile Ile Gly Gly Gly Gly Ala Phe Lys Gln
 305 310 315 320
 Val Leu Val Asp Gly Gly Val Ser Lys Tyr Ile Gly Asp Leu Phe Gly
 325 330 335
 Gln Thr Asn Leu Ser Pro Ile Leu Val Ala Trp Leu Ile Ala Ala Leu
 340 345 350
 Leu Arg Val Ser Leu Gly Ser Ser Thr Val Ala Ser Ile Thr Ala Ala
 355 360 365
 Ser Leu Val Thr Ser Val Val Ser Asn Ser Ser Val Ser Pro Val Leu
 370 375 380
 Val Val Leu Ala Ile Gly Ala Gly Ser Ile Phe Ala Asp His Val Asn
 385 390 395 400
 Asp Ala Gly Phe Trp Met Ile Lys Glu Tyr Phe Gly Leu Thr Leu Lys
 405 410 415
 Glu Thr Phe Leu Ser Trp Thr Thr Leu Thr Ser Val Ile Ser Val Ser
 420 425 430
 Gly Leu Leu Ser Ile Leu Leu Val Ser Cys Phe Met
 435 440

<210> 10204
 <211> 1344
 <212> DNA
 <213> Solibacter usitatus Ellin6076

<220>
 <221> CDS
 <222> (1)..(1344)
 <223> transl_table=11

<400> 10204
 atg ccc gcc aat ggg act tac cta atc tgc att acc gta gcg acc ctg 48
 Met Pro Ala Asn Gly Thr Tyr Leu Ile Cys Ile Thr Val Ala Thr Leu
 1 5 10 15
 gcc tgc ctt ctt ctc ctc atc ctg gtc gga aaa ctg cac gcc ttt ctg 96
 Ala Cys Leu Leu Leu Ile Leu Val Gly Lys Leu His Ala Phe Leu
 20 25 30
 gct ctc ctg att tcg tcg atg ttc atg ggc ctc gcc gcc gga atg gcc 144
 Ala Leu Leu Ile Ser Ser Met Phe Met Gly Leu Ala Ala Gly Met Ala
 35 40 45
 ccg gaa aag gtt ctc aag tcc atc cag acc ggc ttc ggc gat gct ctc 192
 Pro Glu Lys Val Leu Lys Ser Ile Gln Thr Gly Phe Gly Asp Ala Leu
 50 55 60
 gga ttc atc gcg gtg gtg atc ggc ctc ggc gcc atg atc ggc cgt ttc 240
 Gly Phe Ile Ala Val Val Ile Gly Leu Gly Ala Met Ile Gly Arg Phe
 65 70 75 80
 ctc gag tac tcc ggc ggc ggc cgc gcg ctc gcc gac tgg ctg ctc gtc 288
 Leu Glu Tyr Ser Gly Gly Gly Arg Ala Leu Ala Asp Trp Leu Leu Val
 85 90 95
 aag ttc ggc aag aac cac gcc gca tgg gcc gtg ctc att gcc tct ttc 336
 Lys Phe Gly Lys Asn His Ala Ala Trp Ala Val Leu Ile Ala Ser Phe
 100 105 110
 ctc gtc gga ctc ccg atc ttc ttc gag gtc gga ttc atc atc ctc atc 384
 Leu Val Gly Leu Pro Ile Phe Phe Glu Val Gly Phe Ile Ile Leu Ile

PF59083SeqList PF59083.txt																
ccc	atc	gtc	tgg	agc	ctc	acc	cgc	gag	acc	aag	cgc	tcc	ctg	ctt	ttc	432
Pro	Ile	Val	Trp	Ser	Leu	Thr	Arg	Glu	Thr	Lys	Arg	Ser	Leu	Leu	Phe	
130	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	
tac	ggg	ctg	ccg	atg	gcc	gcc	gcg	ctc	acc	atg	acg	cat	tcc	ctg	gtg	480
Tyr	Gly	Leu	Pro	Met	Ala	Ala	Ala	Leu	Thr	Met	Thr	His	Ser	Leu	Val	
145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	
ccg	ccc	cac	ccc	gct	ccc	gcg	gcc	gcc	gcg	cag	ttg	atg	ggg	ggc	gat	528
Pro	Pro	His	Pro	Ala	Pro	Ala	Ala	Ala	Ala	Gln	Leu	Met	Gly	Gly	Asp	
ctc	gcc	cac	acc	atc	atc	tac	ggc	gtg	ctg	atg	tcg	atc	ccg	atg	acc	576
Leu	Ala	His	Thr	Ile	Ile	Tyr	Gly	Val	Leu	Met	Ser	Ile	Pro	Met	Thr	
ctg	att	gcc	ggc	atc	gtg	tat	gcc	acc	tgg	gtg	gcg	cgc	cgc	atc	tat	624
Leu	Ile	Ala	Gly	Ile	Val	Tyr	Ala	Thr	Trp	Val	Ala	Arg	Arg	Ile	Tyr	
atc	ccc	gtc	ccc	gaa	atc	gca	gcc	tcg	atg	acc	cta	aaa	tcc	gcc	gag	672
Ile	Pro	Val	Pro	Glu	Ile	Ala	Ala	Ser	Met	Thr	Leu	Lys	Ser	Ala	Glu	
tca	ccc	ggc	gcg	ccg	ccg	ccc	gtg	gcc	gtc	gtc	ctg	ctc	ctg	ttg		720
Ser	Pro	Gly	Ala	Pro	Pro	Pro	Val	Ala	Val	Val	Val	Leu	Leu	Leu	Leu	
225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	
ctc	ccg	gtc	acg	ctc	acc	ttc	ggc	gcg	act	atg	gcc	agc	ttg	cgc	aat	768
Leu	Pro	Val	Thr	Leu	Thr	Phe	Gly	Ala	Thr	Met	Ala	Ser	Leu	Arg	Asn	
att	ccc	ttc	cgc	gga	gtc	gca	gtc	ttc	ctc	ggg	cat	ccg	tac	acc	gcg	816
Ile	Pro	Phe	Arg	Gly	Val	Ala	Val	Phe	Leu	Gly	His	Pro	Tyr	Thr	Ala	
ctc	acc	gtc	acc	acc	ctg	atc	gcc	ctc	tac	tgc	ttc	ggc	ctg	cgc	cgc	864
Leu	Thr	Val	Thr	Thr	Leu	Ile	Ala	Leu	Tyr	Cys	Phe	Gly	Leu	Arg	Arg	
gga	ttg	tcg	cgc	gac	cag	gtg	ctc	aaa	atg	gcc	acg	gac	tcg	ctg	ctc	912
Gly	Leu	Ser	Arg	Asp	Gln	Val	Leu	Lys	Met	Ala	Thr	Asp	Ser	Leu	Leu	
290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	
ccc	gtc	ggc	gga	ctg	atg	atc	atc	ggc	ggc	ggc	ggc	gga	ctg	aaa		960
Pro	Val	Gly	Gly	Leu	Met	Cys	Ile	Ile	Gly	Gly	Gly	Gly	Ala	Leu	Lys	
305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	
cag	gtg	atc	gtg	gat	tcc	ggc	gtt	gga	act	tac	gcc	ggt	aag	ctg	ctg	1008
Gln	Val	Ile	Val	Asp	Ser	Gly	Val	Gly	Thr	Tyr	Ala	Gly	Lys	Leu	Leu	
atg	acc	agc	gcg	atc	tcg	ccg	ctg	atc	gtg	gtc	tgg	ctg	atc	gcc	gcc	1056
Met	Thr	Ser	Ala	Ile	Ser	Pro	Leu	Ile	Val	Val	Trp	Leu	Ile	Ala	Ala	
tgc	atg	cgc	ctc	gcg	cag	ggc	tcc	gcg	act	gtc	gcc	atc	atc	acg	gcc	1104
Cys	Met	Arg	Leu	Ala	Gln	Gly	Ser	Ala	Thr	Val	Ala	Ile	Ile	Thr	Ala	
gcc	ggc	atc	gcc	gcg	ccg	ctg	gtc	aag	gga	ctg	ccc	ggc	tac	tcg	ccc	1152
Ala	Gly	Ile	Ala	Ala	Pro	Leu	Val	Lys	Gly	Leu	Pro	Gly	Tyr	Ser	Pro	
gac	gag	ttg	atc	ctc	gcc	ctc	tgc	tgc	ggc	ggc	ggc	gga	ttt	tcc	cag	1200
Asp	Glu	Leu	Ile	Leu	Ala	Leu	Cys	Cys	Gly	Gly	Ser	Ala	Phe	Ser	Gln	
385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	
gtc	agc	gat	tcg	ggc	ttc	tgg	atg	gtc	acc	aat	tac	ttc	ggc	acc	acc	1248
Val	Ser	Asp	Ser	Gly	Phe	Trp	Met	Val	Thr	Asn	Tyr	Phe	Gly	Thr	Thr	
gtc	gcc	cag	acg	ctg	aag	acc	tgg	acc	acc	atg	aag	atc	atc	gcc	tcc	1296
Val	Ala	Gln	Thr	Leu	Lys	Thr	Trp	Thr	Thr	Met	Lys	Ile	Ile	Ala	Ser	
ctg	ctg	ggg	ctc	gcc	atc	atg	ctc	acc	gcg	cat	gcg	ctg	cta	cga		1341
Leu	Leu	Gly	Leu	Ala	Ile	Met	Leu	Thr	Ala	His	Ala	Leu	Leu	Arg		
435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	
tag																1344

<210> 10205
 <211> 447
 <212> PRT
 <213> Solibacter usitatus Ellin6076

PF59083SeqList PF59083.txt

<400> 10205

```

Met Pro Ala Asn Gly Thr Tyr Leu Ile Cys Ile Thr Val Ala Thr Leu
1      5      10      15
Ala Cys Leu Leu Leu Ile Leu Val Gly Lys Leu His Ala Phe Leu
20      25      30
Ala Leu Leu Ile Ser Ser Met Phe Met Gly Leu Ala Ala Gly Met Ala
35      40      45
Pro Glu Lys Val Leu Lys Ser Ile Gln Thr Gly Phe Gly Asp Ala Leu
50      55      60
Gly Phe Ile Ala Val Val Ile Gly Leu Gly Ala Met Ile Gly Arg Phe
65      70      75      80
Leu Glu Tyr Ser Gly Gly Gly Arg Ala Leu Ala Asp Trp Leu Leu Val
85      90      95
Lys Phe Gly Lys Asn His Ala Ala Trp Ala Val Leu Ile Ala Ser Phe
100     105     110
Leu Val Gly Leu Pro Ile Phe Phe Glu Val Gly Phe Ile Ile Leu Ile
115     120     125
Pro Ile Val Trp Ser Leu Thr Arg Glu Thr Lys Arg Ser Leu Leu Phe
130     135     140
Tyr Gly Leu Pro Met Ala Ala Leu Thr Met Thr His Ser Leu Val
145     150     155     160
Pro Pro His Pro Ala Pro Ala Ala Ala Ala Gln Leu Met Gly Gly Asp
165     170     175
Leu Ala His Thr Ile Ile Tyr Gly Val Leu Met Ser Ile Pro Met Thr
180     185     190
Leu Ile Ala Gly Ile Val Tyr Ala Thr Trp Val Ala Arg Arg Ile Tyr
195     200     205
Ile Pro Val Pro Glu Ile Ala Ala Ser Met Thr Leu Lys Ser Ala Glu
210     215     220
Ser Pro Gly Ala Pro Pro Pro Val Ala Val Val Val Leu Leu Leu Leu
225     230     235     240
Leu Pro Val Thr Leu Thr Phe Gly Ala Thr Met Ala Ser Leu Arg Asn
245     250     255
Ile Pro Phe Arg Gly Val Ala Val Phe Leu Gly His Pro Tyr Thr Ala
260     265     270
Leu Thr Val Thr Thr Leu Ile Ala Leu Tyr Cys Phe Gly Leu Arg Arg
275     280     285
Gly Leu Ser Arg Asp Gln Val Leu Lys Met Ala Thr Asp Ser Leu Leu
290     295     300
Pro Val Gly Gly Leu Met Cys Ile Ile Gly Gly Gly Gly Ala Leu Lys
305     310     315     320
Gln Val Ile Val Asp Ser Gly Val Gly Thr Tyr Ala Gly Lys Leu Leu
325     330     335
Met Thr Ser Ala Ile Ser Pro Leu Ile Val Val Trp Leu Ile Ala Ala
340     345     350
Cys Met Arg Leu Ala Gln Gly Ser Ala Thr Val Ala Ile Ile Thr Ala
355     360     365
Ala Gly Ile Ala Ala Pro Leu Val Lys Gly Leu Pro Gly Tyr Ser Pro
370     375     380
Asp Glu Leu Ile Leu Ala Leu Cys Cys Gly Gly Ser Ala Phe Ser Gln
385     390     395     400
Val Ser Asp Ser Gly Phe Trp Met Val Thr Asn Tyr Phe Gly Thr Thr
405     410     415
Val Ala Gln Thr Leu Lys Thr Trp Thr Thr Met Lys Ile Ile Ala Ser
420     425     430
Leu Leu Gly Leu Ala Ile Met Leu Thr Ala His Ala Leu Leu Arg
435     440     445

```

<210> 10206

<211> 1446

<212> DNA

<213> Mycobacterium smegmatis str. MC2 155

<220>

<221> CDS

<222> (1)..(1446)

<223> transl_table=11

PF59083SeqList PF59083.txt

```

<400> 10206
gtg gac gcc att gat ccg gca tac ggc acc acc acc ctt ctg ctg atc      48
Met Asp Ala Ile Asp Pro Ala Tyr Gly Thr Thr Thr Leu Leu Leu Ile
1      5      10      15
gcg gca gcc gcg gtg gcg gtg ctg ctg ttc ctc atc atc aag gtg aag      96
Ala Ala Ala Val Ala Val Leu Leu Phe Leu Ile Ile Lys Val Lys
20      25      30
ctg cac gcg ttc gtc gcc ctg gta ctg gtg agc ctg ttg acc gca ctg      144
Leu His Ala Phe Val Ala Leu Val Leu Val Ser Leu Leu Thr Ala Leu
35      40      45
gcc gcc ggt atc ccc gtg gcc gat gtg cca agc gcc ctg tca tcc ggg      192
Ala Ala Gly Ile Pro Val Ala Asp Val Pro Ser Ala Leu Ser Ser Gly
50      55      60
ttc tcc agc acg ctc ggc tcc gtg gcc ctg ctc gtc ggt ttc ggt gtc      240
Phe Ser Ser Thr Leu Gly Ser Val Ala Leu Leu Val Gly Phe Gly Val
65      70      75      80
atg atc ggg cgt ctt ctc gaa acc acc ggg ggt gca cag gtt ctc gcc      288
Met Ile Gly Arg Leu Leu Glu Thr Thr Gly Gly Ala Gln Val Leu Ala
85      90      95
gac acg ctc atc ggc ccg ttc ggc gag aag ccg gct ccc ctc gcg ctc      336
Asp Thr Leu Ile Gly Arg Phe Gly Glu Lys Arg Ala Pro Leu Ala Leu
100      105      110
ggc gtg gcg gcg ttg ctg ttc ggt ttc ccg atc ttc ttc gac gcc ggc      384
Gly Val Ala Ala Leu Leu Phe Gly Phe Pro Ile Phe Phe Asp Ala Gly
115      120      125
ctg gtc gtc ttc ctg ccg atc atc atg acg gtg gcc cgc cgt ttc ggc      432
Leu Val Val Phe Leu Pro Ile Ile Met Thr Val Ala Arg Arg Phe Gly
130      135      140
gga tcg ctg ctg ctg tac gca ttc ccc gca gcg ggc gcg ttc gcg gcc      480
Gly Ser Leu Leu Leu Tyr Ala Phe Pro Ala Ala Gly Ala Phe Ala Ala
145      150      155      160
atg cac gcc ctg gta ccg ccg cat ccc ggt ccg gtc gcg gcg gcc gaa      528
Met His Ala Leu Val Pro Pro His Pro Gly Pro Val Ala Ala Ala Glu
165      170      175
ttg ctc ggt gcc aac atc ggt ctg acg ttg atc gtg ggc gtc ccc gtg      576
Leu Leu Gly Ala Asn Ile Gly Leu Thr Leu Ile Val Gly Val Pro Val
180      185      190
gcg gtg gtg tcg tgg tac gtc ggc gcg ttc ctg gtg tcc cag gtg atc      624
Ala Val Val Ser Trp Tyr Val Gly Ala Phe Leu Val Ser Gln Val Ile
195      200      205
ggt cgg cgc gtg cac atc gac att ccc acg tca ctg ttc ggc gag atc      672
Gly Arg Arg Val His Ile Asp Ile Pro Thr Ser Leu Phe Gly Glu Ile
210      215      220
aac ggt ggg cgc gat atc gac gcc acg ggc acg gag gcc gac gcc gac      720
Asn Gly Gly Arg Asp Ile Asp Ala Thr Gly Thr Glu Ala Asp Ala Asp
225      230      235      240
ggg gcc ggc gcc aca ggg gcc tcg agg acc gcc acc cgg gcc acc ccg      768
Gly Ala Gly Ala Thr Gly Ala Ser Arg Thr Ala Thr Arg Ala Thr Pro
245      250      255
tcg ttc ctg acc gtc ctg ggt gtg ctg ttg ctg ccc ttc gtg ctg atc      816
Ser Phe Leu Thr Val Leu Gly Val Leu Leu Leu Pro Phe Val Leu Ile
260      265      270
tcc tgc aac acg gtg gtc gcc acc ctg cag acc gca ggg gtg atc ccc      864
Ser Cys Asn Thr Val Val Ala Thr Leu Gln Thr Ala Gly Val Ile Pro
275      280      285
gaa gag gcc acg tgg gcg gag tac ctc aaa ctg atc ggc acc acg tcg      912
Glu Glu Ala Thr Trp Ala Glu Tyr Leu Lys Leu Ile Gly Thr Thr Ser
290      295      300
atc gcc ctg ctg atc acc gtc atc gtc gcc acc ctg gta ctc gga ttg      960
Ile Ala Leu Leu Ile Thr Val Ile Val Ala Thr Thr Val Leu Gly Leu
305      310      315      320
cgc ggc agg tcg atg gcc acc gtc acc gac atc ctc gac aac gca ctc      1008
Arg Gly Arg Ser Met Ala Thr Val Thr Asp Ile Leu Asp Asn Ala Leu
325      330      335
ggc ccg atc tgc gcg atc atc ctg atc acc ggc gcg ggc ggc atg ttc      1056
Gly Pro Ile Cys Ala Ile Ile Leu Ile Thr Gly Ala Gly Gly Met Phe
340      345      350
ggg ggt gtg ctg cgc acc agc ggc atc ggt gac gcc ctg agc ggt tcg      1104
Gly Gly Val Leu Arg Thr Ser Gly Ile Gly Asp Ala Leu Ser Gly Ser
350

```

PF59083SeqList PF59083.txt

ctg	tcc	gac	ctc	gga	atc	tcg	ctg	atc	ctg	cag	gcc	ttc	ctc	atc	tcc	1152
Leu	Ser	Asp	Leu	Gly	Ile	Ser	Leu	Ile	Leu	Gln	Ala	Phe	Leu	Ile	Ser	
	370					375				380						
acg	ctg	ctg	cgc	gtc	gca	cag	ggg	tcg	gcg	acg	gtc	gca	ttg	acc	acc	1200
Thr	Leu	Leu	Arg	Val	Ala	Gln	Gly	Ser	Ala	Thr	Val	Ala	Leu	Thr	Thr	
	385				390					395					400	
acc	gcg	ggg	ctc	ctc	agc	gca	gcc	gtc	gcc	gcc	gcc	gga	ctg	agc	agc	1248
Thr	Ala	Gly	Leu	Leu	Ser	Ala	Ala	Val	Ala	Ala	Ala	Gly	Leu	Ser	Ser	
				405					410					415		
ctg	cag	ctg	acc	gcg	ctg	gtg	atg	gcg	atc	gcc	gcg	ggc	gcc	acg	gtg	1296
Leu	Gln	Leu	Thr	Ala	Leu	Val	Met	Ala	Ile	Ala	Ala	Gly	Ala	Thr	Val	
			420					425					430			
ctc	tcg	cac	gtc	aac	gac	tcc	ggc	ttc	tgg	ttg	gtc	agc	cgg	ttc	ttc	1344
Leu	Ser	His	Val	Asn	Asp	Ser	Gly	Phe	Trp	Leu	Val	Ser	Arg	Phe	Phe	
		435					440					445				
ggc	atg	gat	gtc	aag	acc	acg	ctc	aag	acc	tgg	acg	ctg	ctg	gag	acg	1392
Gly	Met	Asp	Val	Lys	Thr	Thr	Leu	Lys	Thr	Trp	Thr	Leu	Leu	Glu	Thr	
	450					455				460						
acg	ctg	ggc	gtg	aca	gcg	ttc	gtg	atc	agc	ctc	ggc	ctg	tgg	gcc	ata	1440
Thr	Leu	Gly	Val	Thr	Ala	Phe	Val	Ile	Ser	Leu	Gly	Leu	Trp	Ala	Ile	
	465				470					475					480	
ggc	tga															1446
Gly																

<210> 10207

<211> 481

<212> PRT

<213> Mycobacterium smegmatis str. MC2 155

<400> 10207

Met	Asp	Ala	Ile	Asp	Pro	Ala	Tyr	Gly	Thr	Thr	Thr	Leu	Leu	Leu	Ile	
1				5					10					15		
Ala	Ala	Ala	Ala	Val	Ala	Val	Leu	Leu	Phe	Leu	Ile	Ile	Lys	Val	Lys	
			20					25					30			
Leu	His	Ala	Phe	Val	Ala	Leu	Val	Leu	Val	Ser	Leu	Leu	Thr	Ala	Leu	
		35					40					45				
Ala	Ala	Gly	Ile	Pro	Val	Ala	Asp	Val	Pro	Ser	Ala	Leu	Ser	Ser	Gly	
	50					55				60						
Phe	Ser	Ser	Thr	Leu	Gly	Ser	Val	Ala	Leu	Leu	Val	Gly	Phe	Gly	Val	
65					70				75						80	
Met	Ile	Gly	Arg	Leu	Leu	Glu	Thr	Thr	Gly	Gly	Ala	Gln	Val	Leu	Ala	
				85					90					95		
Asp	Thr	Leu	Ile	Gly	Arg	Phe	Gly	Glu	Lys	Arg	Ala	Pro	Leu	Ala	Leu	
			100					105					110			
Gly	Val	Ala	Ala	Leu	Leu	Phe	Gly	Phe	Pro	Ile	Phe	Phe	Asp	Ala	Gly	
		115					120					125				
Leu	Val	Val	Phe	Leu	Pro	Ile	Ile	Met	Thr	Val	Ala	Arg	Arg	Phe	Gly	
	130					135					140					
Gly	Ser	Leu	Leu	Leu	Tyr	Ala	Phe	Pro	Ala	Ala	Gly	Ala	Phe	Ala	Ala	
145					150				155						160	
Met	His	Ala	Leu	Val	Pro	Pro	His	Pro	Gly	Pro	Val	Ala	Ala	Ala	Glu	
				165					170					175		
Leu	Leu	Gly	Ala	Asn	Ile	Gly	Leu	Thr	Leu	Ile	Val	Gly	Val	Pro	Val	
			180					185					190			
Ala	Val	Val	Ser	Trp	Tyr	Val	Gly	Ala	Phe	Leu	Val	Ser	Gln	Val	Ile	
		195					200					205				
Gly	Arg	Arg	Val	His	Ile	Asp	Ile	Pro	Thr	Ser	Leu	Phe	Gly	Glu	Ile	
	210					215					220					
Asn	Gly	Gly	Arg	Asp	Ile	Asp	Ala	Thr	Gly	Thr	Glu	Ala	Asp	Ala	Asp	
225					230				235						240	
Gly	Ala	Gly	Ala	Thr	Gly	Ala	Ser	Arg	Thr	Ala	Thr	Arg	Ala	Thr	Pro	
			245						250					255		
Ser	Phe	Leu	Thr	Val	Leu	Gly	Val	Leu	Leu	Pro	Phe	Val	Leu	Ile		
			260					265					270			
Ser	Cys	Asn	Thr	Val	Val	Ala	Thr	Leu	Gln	Thr	Ala	Gly	Val	Ile	Pro	
		275					280					285				
Glu	Glu	Ala	Thr	Trp	Ala	Glu	Tyr	Leu	Lys	Leu	Ile	Gly	Thr	Thr	Ser	

PF59083SeqList PF59083.txt

290	Ile	Ala	Leu	Leu	Ile	Thr	Val	Ile	Val	Ala	Thr	Leu	Val	Leu	Gly	Leu
305	Arg	Gly	Arg	Ser	Met	Ala	Thr	Val	Thr	Asp	Ile	Leu	Asp	Asn	Ala	Leu
					325					330					335	
	Gly	Pro	Ile	Cys	Ala	Ile	Ile	Leu	Ile	Thr	Gly	Ala	Gly	Gly	Met	Phe
				340					345					350		
	Gly	Gly	Val	Leu	Arg	Thr	Ser	Gly	Ile	Gly	Asp	Ala	Leu	Ser	Gly	Ser
			355					360					365			
	Leu	Ser	Asp	Leu	Gly	Ile	Ser	Leu	Ile	Leu	Gln	Ala	Phe	Leu	Ile	Ser
							375					380				
	Thr	Leu	Leu	Arg	Val	Ala	Gln	Gly	Ser	Ala	Thr	Val	Ala	Leu	Thr	Thr
385						390					395					400
	Thr	Ala	Gly	Leu	Leu	Ser	Ala	Ala	Val	Ala	Ala	Ala	Gly	Leu	Ser	Ser
					405					410					415	
	Leu	Gln	Leu	Thr	Ala	Leu	Val	Met	Ala	Ile	Ala	Ala	Gly	Ala	Thr	Val
				420					425					430		
	Leu	Ser	His	Val	Asn	Asp	Ser	Gly	Phe	Trp	Leu	Val	Ser	Arg	Phe	Phe
			435					440					445			
	Gly	Met	Asp	Val	Lys	Thr	Thr	Leu	Lys	Thr	Trp	Thr	Leu	Leu	Glu	Thr
							455					460				
	Thr	Leu	Gly	Val	Thr	Ala	Phe	Val	Ile	Ser	Leu	Gly	Leu	Trp	Ala	Ile
465						470					475					480
	Gly															

<210> 10208
 <211> 1386
 <212> DNA
 <213> Neisseria meningitidis FAM18

<220>
 <221> CDS
 <222> (1)..(1386)
 <223> transl_table=11

<400> 10208	
atg gac ggc tgg aca cag acg ctg tcc gcg caa acc ctg ttg ggc att	48
Met Asp Gly Trp Thr Gln Thr Leu Ser Ala Gln Thr Leu Leu Gly Ile	
1 5 10 15	
tcg gcg gcg gca atc atc ctc att ctg att tta atc gtc aaa ttc cgc	96
Ser Ala Ala Ala Ile Ile Leu Ile Leu Ile Leu Ile Val Lys Phe Arg	
20 25 30	
atc cac gcg ctg ctg aca ctg gtc atc gtc agc ctg ctg acg gct ttg	144
Ile His Ala Leu Leu Thr Leu Val Ile Val Ser Leu Leu Thr Ala Leu	
35 40 45	
gca acc ggt ttg ccc aca ggc agc att gtc aac gac gta ctg gtc aaa	192
Ala Thr Gly Leu Pro Thr Gly Ser Ile Val Asn Asp Val Leu Val Lys	
50 55 60	
aac ttc ggc ggc acg ctc ggc gtg gcg ctt ctg gtc ggc ctg ggc	240
Asn Phe Gly Gly Thr Leu Gly Gly Val Ala Leu Leu Val Gly Leu Gly	
65 70 75 80	
gca atg ctc gga cgt ttg gtc gaa aca tcc ggc ggc gca cag tcg ctg	288
Ala Met Leu Gly Arg Leu Val Glu Thr Ser Gly Gly Ala Gln Ser Leu	
85 90 95	
gcg gac gcg ctg atc cgg atg ttc ggc gaa aaa cgc gca ccg ttc gcg	336
Ala Asp Ala Leu Ile Arg Met Phe Gly Glu Lys Arg Ala Pro Phe Ala	
100 105 110	
ctg ggc gtt gcc tcg ctg att ttc ggc ttc ccg att ttc ttc gat gcc	384
Leu Gly Val Ala Ser Leu Ile Phe Gly Phe Pro Ile Phe Phe Asp Ala	
115 120 125	
gga cta atc gtc atg ctg ccc atc gtg ttc gcc acc gca cgg cgc atg	432
Gly Leu Ile Val Met Leu Pro Ile Val Phe Ala Thr Ala Arg Arg Met	
130 135 140	
aaa cag gac gta ctg ccc gcg ctt gcc tcc atc ggc gca ttt tcc	480
Lys Gln Asp Val Leu Pro Phe Ala Leu Ala Ser Ile Gly Ala Phe Ser	
145 150 155 160	
gtc atg cac gtc ttc ctg ccg ccc cat ccg ggc ccg att gcc gct tcc	528
Val Met His Val Phe Leu Pro Pro His Pro Gly Pro Ile Ala Ala Ser	

PF59083SeqList PF59083.txt

165																170																175																576
gaa Glu	ttt Phe	tac Tyr	ggc Gly 180	gcg Ala	aac Asn	atc Ile	ggc Gly	caa Gln 185	ggt Val	ttg Leu	att Ile	ttg Leu	ggt Gly 190	ctg Leu	ccg Pro																																	
			acc Thr	gcc Ala	ttc Phe 195	aca Thr	tgg Trp	tat Tyr	ttc Phe 200	agc Ser	ggt Gly	tat Tyr	atg Met	ctc Leu 205	ggc Gly	aaa Lys	gtg Val											624																				
			ttg Leu	ggg Gly 210	cgc Arg	acc Thr	atc Ile	cat His	ggt Val 215	ccc Pro	ggt Val	ccc Pro	gaa Glu	ctg Leu 220	ctc Leu	agc Ser	ggc Gly	ggc Gly																														
			acg Thr 225	caa Gln	gac Asp	aac Asn	gac Asp 230	ctg Leu	ccg Pro	aaa Lys	gaa Glu	cct Pro	gcc Ala 235	aaa Lys	gca Ala	gga Gly	acg Thr 240	gtc Val											720																			
			gtc Val	gcc Ala	atc Ile	atg Met	ctg Leu 245	att Ile	ccc Pro	atg Met	ctg Leu	ctg Leu 250	att Ile	ttc Phe	ctg Leu	aat Asn	acc Thr 255	ggc Gly																														
			gta Val	tcg Ser	gcc Ala 260	ctc Leu	atc Ile	agc Ser	gaa Glu	aaa Lys	ctc Leu 265	gta Val	agt Ser	gcg Ala	gac Asp	gaa Glu 270	acc Thr	tgg Trp											816																			
			gtt Val	cag Gln 275	acg Thr	gca Ala	aaa Lys	ata Ile	atc Ile	ggt Gly 280	tcg Ser	aca Thr	ccg Pro	atc Ile	gcc Ala 285	ctt Leu	ctg Leu	att Ile																														
			tcc Ser	gta Val 290	ttg Leu	gtc Val	gca Ala	ctg Leu	ttt Phe 295	gtc Val	ttg Leu	gga Gly	cgc Arg	aaa Lys 300	cgc Arg	ggc Gly	gaa Glu	agc Ser											912																			
			ggc Gly 305	agc Ser	gcg Ala	ttg Leu	gaa Glu 310	aaa Lys	acc Thr	gtg Val	gac Asp	ggc Gly	gca Ala 315	ctc Leu	gcc Ala	ccc Pro	gtc Val	tgt Cys 320																														
			tcc Ser	gtg Val	att Ile	ctg Leu	att Ile 325	acc Thr	ggc Gly	gcg Ala	ggc Gly	ggt Gly 330	atg Met	ttc Phe	ggc Gly	ggc Gly	gtt Val 335	ttg Leu											1008																			
			cgc Arg	gct Ala	tcc Ser	ggc Gly 340	atc Ile	ggc Gly	aag Lys	gca Ala	ctc Leu 345	gcc Ala	gac Asp	agc Ser	atg Met	gcg Ala 350	gat Asp	ttg Leu																														
			ggc Gly	att Ile	ccc Pro 355	gtc Val	ctt Leu	ttg Leu	ggc Gly 360	tgt Cys	ttc Phe	ctt Leu	gtc Val	gcc Ala 365	ttg Leu	gca Ala	ctg Leu	cgt Arg											1104																			
			atc Ile	gcg Ala 370	caa Gln	ggt Gly	tcg Ser	gca Ala 375	acc Thr	gtc Val	gcc Ala	ctg Leu	acc Thr 380	acc Ala	gct Ala	gcc Ala	gcg Ala	ctg Leu																														
			atg Met 385	gct Ala	cct Pro	gcc Ala	gtt Val 390	gcc Ala	gcc Ala	gcc Ala	ggc Gly	ttt Phe 395	acc Thr 400	gac Asp	tgg Trp	cag Gln	ctc Leu	gcc Ala 405											1200																			
			tgt Cys	atc Ile	gta Val	ttg Leu	gca Ala 405	acg Thr	gcg Ala	gca Ala	ggt Gly	tcg Ser 410	gtc Val	ggc Gly	tgc Cys	agc Ser	cac His 415	ttc Phe																														
			aac Asn	gac Asp	tcc Ser	ggc Gly 420	ttc Phe	tgg Trp	ctg Leu	gtc Val	ggc Gly 425	cgc Arg	ctc Leu	ttg Leu	gac Asp	atg Met 430	gac Asp	gta Val											1296																			
			ccg Pro	acc Thr 435	acg Thr	ctg Leu	aaa Lys	acc Thr	tgg Trp	acg Thr 440	gtc Val	aac Asn	caa Gln	acc Thr	ctc Leu 445	atc Ile	gca Ala	ctc Leu																														
			atc Ile	ggc Gly 450	ttt Phe	gcc Ala	ttg Leu	tcc Ser	gca Ala 455	ctg Leu	ctg Leu	ttc Phe	tcc Ser	atc Ile 460	gtc Val	tga											1386																					

<210> 10209
<211> 461
<212> PRT
<213> *Neisseria meningitidis* FAM18

```

<400> 10209
Met Asp Gly Trp Thr Gln Thr Leu Ser Ala Gln Thr Leu Leu Gly Ile
1          5          10          15
Ser Ala Ala Ala Ile Ile Leu Ile Leu Ile Leu Ile Val Lys Phe Arg
          20          25          30
Ile His Ala Leu Leu Thr Leu Val Ile Val Ser Leu Leu Thr Ala Leu
          35          40          45
Ala Thr Gly Leu Pro Thr Gly Ser Ile Val Asn Asp Val Leu Val Lys
Seite 10809

```

PF59083SeqList PF59083.txt

```

50      55      60
Asn Phe Gly Gly Thr Leu Gly Gly Val Ala Leu Leu Val Gly Leu Gly
65      70      75      80
Ala Met Leu Gly Arg Leu Val Glu Thr Ser Gly Gly Ala Gln Ser Leu
85      90      95
Ala Asp Ala Leu Ile Arg Met Phe Gly Glu Lys Arg Ala Pro Phe Ala
100      105      110
Leu Gly Val Ala Ser Leu Ile Phe Gly Phe Pro Ile Phe Phe Asp Ala
115      120      125
Gly Leu Ile Val Met Leu Pro Phe Ile Val Phe Ala Thr Ala Arg Arg Met
130      135      140
Lys Gln Asp Val Leu Pro Phe Ala Leu Ala Ser Ile Gly Ala Phe Ser
145      150      155      160
Val Met His Val Phe Leu Pro Pro His Pro Gly Pro Ile Ala Ala Ser
165      170      175
Glu Phe Tyr Gly Ala Asn Ile Gly Gln Val Leu Ile Leu Gly Leu Pro
180      185      190
Thr Ala Phe Ile Thr Trp Tyr Phe Ser Gly Tyr Met Leu Gly Lys Val
195      200      205
Leu Gly Arg Thr Ile His Val Pro Val Pro Glu Leu Leu Ser Gly Gly
210      215      220
Thr Gln Asp Asn Asp Leu Pro Lys Glu Pro Ala Lys Ala Gly Thr Val
225      230      235      240
Val Ala Ile Met Leu Ile Pro Met Leu Leu Ile Phe Leu Asn Thr Gly
245      250      255
Val Ser Ala Leu Ile Ser Glu Lys Leu Val Ser Ala Asp Glu Thr Trp
260      265      270
Val Gln Thr Ala Lys Ile Ile Gly Ser Thr Pro Ile Ala Leu Leu Ile
275      280      285
Ser Val Leu Val Ala Leu Phe Val Leu Gly Arg Lys Arg Gly Glu Ser
290      295      300
Gly Ser Ala Leu Glu Lys Thr Val Asp Gly Ala Leu Ala Pro Val Cys
305      310      315      320
Ser Val Ile Leu Ile Thr Gly Ala Gly Gly Met Phe Gly Gly Val Leu
325      330      335
Arg Ala Ser Gly Ile Gly Lys Ala Leu Ala Asp Ser Met Ala Asp Leu
340      345      350
Gly Ile Pro Val Leu Leu Gly Cys Phe Leu Val Ala Leu Ala Leu Arg
355      360      365
Ile Ala Gln Gly Ser Ala Thr Val Ala Leu Thr Thr Ala Ala Ala Leu
370      375      380
Met Ala Pro Ala Val Ala Ala Ala Gly Phe Thr Asp Trp Gln Leu Ala
385      390      395      400
Cys Ile Val Leu Ala Thr Ala Ala Gly Ser Val Gly Cys Ser His Phe
405      410      415
Asn Asp Ser Gly Phe Trp Leu Val Gly Arg Leu Leu Asp Met Asp Val
420      425      430
Pro Thr Thr Leu Lys Thr Trp Thr Val Asn Gln Thr Leu Ile Ala Leu
435      440      445
Ile Gly Phe Ala Leu Ser Ala Leu Leu Phe Ser Ile Val
450      455      460

```

<210> 10210

<211> 1347

<212> DNA

<213> Exiguobacterium sibiricum 255-15

<220>

<221> CDS

<222> (1)..(1347)

<223> transl_table=11

<400> 10210

```

atg cca tta gtc att gtt gct atc ggg att att ctg tta ctc gtt tta
Met Pro Leu Val Ile Val Ala Ile Gly Ile Ile Leu Leu Leu Val Leu
1      5      10      15
att atg ggg tta aaa tta aac acg ttc gtt tct tta atc atc gtc tcg
Ile Met Gly Leu Lys Leu Asn Thr Phe Val Ser Leu Ile Ile Val Ser
20      25      30

```

48

96

PF59083SeqList PF59083.txt																
ttc	gtc	gtc	gct	tta	ctg	ctt	gga	atg	ccg	ctt	gat	caa	atc	gtc	acg	144
Phe	Val	Val	Ala	Leu	Leu	Leu	Gly	Met	Pro	Leu	Asp	Gln	Ile	Val	Thr	
		35					40					45				
acg	att	gaa	gcc	ggt	ctc	ggc	ggc	acg	ctt	ggt	cac	ctc	gcc	tta	atc	192
Thr	Ile	Glu	Ala	Gly	Leu	Gly	Gly	Thr	Leu	Gly	His	Leu	Ala	Leu	Ile	
		50					55				60					
ttc	gga	ctt	ggt	gcc	atg	ctc	ggg	aaa	ttg	att	gcc	gat	gca	ggc	ggt	240
Phe	Gly	Leu	Gly	Ala	Met	Leu	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Gly	Gly	
		65			70				75					80		
gcg	caa	cgg	atc	gcg	atg	acg	ctt	gtc	gcg	aag	ttt	ggg	gaa	aag	aac	288
Ala	Gln	Arg	Ile	Ala	Met	Thr	Leu	Val	Ala	Lys	Phe	Gly	Glu	Lys	Asn	
				85					90					95		
atc	caa	tgg	gct	gtc	gtt	gtc	gcc	tca	ttc	atc	atc	ggg	att	gcg	tta	336
Ile	Gln	Trp	Ala	Val	Val	Val	Ala	Ser	Phe	Ile	Ile	Gly	Ile	Ala	Leu	
			100					105					110			
ttc	ttt	gaa	gtc	ggc	ttg	gtg	ttg	ttg	att	cca	atc	gtc	ttc	gcc	atc	384
Phe	Phe	Glu	Val	Gly	Leu	Val	Leu	Leu	Ile	Pro	Ile	Val	Phe	Ala	Ile	
		115					120					125				
tca	cgt	cag	tta	cgc	gtc	tcg	atc	ttg	tat	ctc	ggg	att	ccg	atg	gtt	432
Ser	Arg	Gln	Leu	Arg	Val	Ser	Ile	Leu	Tyr	Leu	Gly	Ile	Pro	Met	Val	
		130				135					140					
gct	gcc	ctt	tcc	gtc	aca	cac	ggc	ttt	ctt	ccg	cct	cac	ccg	ggc	ccg	480
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
		145			150				155					160		
acc	gtt	att	gcc	gga	gaa	tac	gga	gct	gac	ctt	ggg	caa	gtt	ctc	tta	528
Thr	Val	Ile	Ala	Gly	Glu	Tyr	Gly	Ala	Asp	Leu	Gly	Gln	Val	Leu	Leu	
				165					170					175		
tac	ggc	ttt	att	gta	gcc	gta	ccg	acc	gtc	atc	atc	gcc	ggg	ccg	atc	576
Tyr	Gly	Phe	Ile	Val	Ala	Val	Pro	Thr	Val	Ile	Ile	Ala	Gly	Pro	Ile	
			180					185					190			
ttt	acg	aaa	atc	gcg	aaa	cga	atc	gtt	ccg	gat	tca	ttc	aag	aaa	acc	624
Phe	Thr	Lys	Ile	Ala	Lys	Arg	Ile	Val	Pro	Asp	Ser	Phe	Lys	Lys	Thr	
		195				200						205				
ggc	aac	atc	gct	tca	ctc	ggg	gaa	caa	aaa	gaa	ttt	aat	ctc	gac	gag	672
Gly	Asn	Ile	Ala	Ser	Leu	Gly	Glu	Gln	Lys	Glu	Phe	Asn	Leu	Asp	Glu	
		210				215					220					
aca	cca	gga	ttc	ggt	atc	agt	gtc	ttc	aca	gcg	atg	ctg	cct	gtc	ctc	720
Thr	Pro	Gly	Phe	Gly	Ile	Ser	Val	Phe	Thr	Ala	Met	Leu	Pro	Val	Leu	
		225			230				235					240		
ctg	atg	tcg	atc	gcg	acg	att	tta	acg	tta	ttg	caa	aaa	acg	ctt	ggt	768
Leu	Met	Ser	Ile	Ala	Thr	Ile	Leu	Thr	Leu	Leu	Gln	Lys	Thr	Leu	Gly	
				245					250					255		
tgg	gaa	agt	aac	agt	gtt	tta	tct	gcc	gtt	caa	ttc	atc	gga	aac	gca	816
Trp	Glu	Ser	Asn	Ser	Val	Leu	Ser	Ala	Val	Gln	Phe	Ile	Gly	Asn	Ala	
			260					265					270			
tcg	acg	gcg	atg	ctg	att	tcc	ttg	ctt	ttc	gct	atc	tac	acg	atg	gga	864
Ser	Thr	Ala	Met	Leu	Ile	Ser	Leu	Leu	Phe	Ala	Ile	Tyr	Thr	Met	Gly	
		275				280						285				
ctg	gcg	cgt	cag	att	ccc	att	aaa	acc	gtc	atg	gat	tct	tgt	acg	acg	912
Leu	Ala	Arg	Gln	Ile	Pro	Ile	Lys	Thr	Val	Met	Asp	Ser	Cys	Thr	Thr	
		290			295						300					
gcc	atc	aca	caa	atc	gga	atg	atg	cta	ctg	atc	atc	ggc	ggc	ggc	ggt	960
Ala	Ile	Thr	Gln	Ile	Gly	Met	Met	Leu	Leu	Ile	Ile	Gly	Gly	Gly	Gly	
		305			310					315				320		
gcc	ttt	aag	cag	gtc	ctg	att	gac	ggg	ggg	gtc	ggg	aaa	ttc	gtc	gct	1008
Ala	Phe	Lys	Gln	Val	Leu	Ile	Asp	Gly	Gly	Val	Gly	Lys	Phe	Val	Ala	
				325				330						335		
cag	atg	ttt	gaa	gat	acg	aca	tta	tca	ccg	att	tta	ctg	gcg	tgg	atc	1056
Gln	Met	Phe	Glu	Asp	Thr	Thr	Leu	Ser	Pro	Ile	Leu	Leu	Ala	Trp	Ile	
			340					345					350			
atc	gca	gcc	atc	tta	cgg	att	tca	ctt	ggt	tcg	gca	acc	gtc	gct	tca	1104
Ile	Ala	Ala	Ile	Leu	Arg	Ile	Ser	Leu	Gly	Ser	Ala	Thr	Val	Ala	Ser	
		355				360						365				
ctg	acg	aca	gcc	ggt	ctc	gtc	att	ccg	ttg	ctc	ggg	caa	tcg	gat	gtc	1152
Leu	Thr	Thr	Ala	Gly	Leu	Val	Ile	Pro	Leu	Leu	Gly	Gln	Ser	Asp	Val	
		370				375					380					
aat	ctg	gcg	ctc	gtc	gtt	ctc	gca	aca	gga	gcc	ggc	agt	ttg	atc	gct	1200
Asn	Leu	Ala	Leu	Val	Val	Leu	Ala	Thr	Gly	Ala	Gly	Ser	Leu	Ile	Ala	
		385			390					395				400		

PF59083SeqList PF59083.txt																
tca	cac	gtc	aac	gac	gcc	gga	ttc	tgg	atg	ttt	aaa	gag	tat	ttc	gga	1248
Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Met	Phe	Lys	Glu	Tyr	Phe	Gly	
				405				410						415		
tta	acc	atg	aaa	gaa	act	ttt	gcg	acg	tgg	acc	ttg	ctt	gag	aca	atc	1296
Leu	Thr	Met	Lys	Glu	Thr	Phe	Ala	Thr	Trp	Thr	Leu	Leu	Glu	Thr	Ile	
			420					425					430			
att	tcc	gtc	ttc	gga	ctt	gga	ttc	gtc	ctt	ctg	ctc	agt	ctc	gtc	gtc	1344
Ile	Ser	Val	Phe	Gly	Leu	Gly	Phe	Val	Leu	Leu	Leu	Ser	Leu	Val	Val	
		435					440					445				
taa																1347

<210> 10211
 <211> 448
 <212> PRT
 <213> Exiguobacterium sibiricum 255-15

<400> 10211

Met	Pro	Leu	Val	Ile	Val	Ala	Ile	Gly	Ile	Ile	Leu	Leu	Leu	Val	Leu
1				5					10					15	
Ile	Met	Gly	Leu	Lys	Leu	Asn	Thr	Phe	Val	Ser	Leu	Ile	Ile	Val	Ser
			20					25					30		
Phe	Val	Val	Ala	Leu	Leu	Leu	Gly	Met	Pro	Leu	Asp	Gln	Ile	Val	Thr
		35					40					45			
Thr	Ile	Glu	Ala	Gly	Leu	Gly	Gly	Thr	Leu	Gly	His	Leu	Ala	Leu	Ile
	50					55					60				
Phe	Gly	Leu	Gly	Ala	Met	Leu	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Gly	Gly
65					70					75					80
Ala	Gln	Arg	Ile	Ala	Met	Thr	Leu	Val	Ala	Lys	Phe	Gly	Glu	Lys	Asn
			85						90					95	
Ile	Gln	Trp	Ala	Val	Val	Val	Ala	Ser	Phe	Ile	Ile	Gly	Ile	Ala	Leu
			100					105					110		
Phe	Phe	Glu	Val	Gly	Leu	Val	Leu	Ile	Pro	Ile	Val	Phe	Ala	Ile	
		115					120				125				
Ser	Arg	Gln	Leu	Arg	Val	Ser	Ile	Leu	Tyr	Leu	Gly	Ile	Pro	Met	Val
	130					135					140				
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro
145					150					155					160
Thr	Val	Ile	Ala	Gly	Glu	Tyr	Gly	Ala	Asp	Leu	Gly	Gln	Val	Leu	Leu
			165					170					175		
Tyr	Gly	Phe	Ile	Val	Ala	Val	Pro	Thr	Val	Ile	Ile	Ala	Gly	Pro	Ile
		180						185					190		
Phe	Thr	Lys	Ile	Ala	Lys	Arg	Ile	Val	Pro	Asp	Ser	Phe	Lys	Lys	Thr
		195					200					205			
Gly	Asn	Ile	Ala	Ser	Leu	Gly	Glu	Gln	Lys	Glu	Phe	Asn	Leu	Asp	Glu
	210					215					220				
Thr	Pro	Gly	Phe	Gly	Ile	Ser	Val	Phe	Thr	Ala	Met	Leu	Pro	Val	Leu
225					230					235					240
Leu	Met	Ser	Ile	Ala	Thr	Ile	Leu	Thr	Leu	Leu	Gln	Lys	Thr	Leu	Gly
			245						250					255	
Trp	Glu	Ser	Asn	Ser	Val	Leu	Ser	Ala	Val	Gln	Phe	Ile	Gly	Asn	Ala
			260					265					270		
Ser	Thr	Ala	Met	Leu	Ile	Ser	Leu	Phe	Ala	Ile	Tyr	Thr	Met	Gly	
		275					280				285				
Leu	Ala	Arg	Gln	Ile	Pro	Ile	Lys	Thr	Val	Met	Asp	Ser	Cys	Thr	Thr
	290					295					300				
Ala	Ile	Thr	Gln	Ile	Gly	Met	Met	Leu	Leu	Ile	Ile	Gly	Gly	Gly	Gly
305					310					315					320
Ala	Phe	Lys	Gln	Val	Leu	Ile	Asp	Gly	Gly	Val	Gly	Lys	Phe	Val	Ala
			325					330						335	
Gln	Met	Phe	Glu	Asp	Thr	Thr	Leu	Ser	Pro	Ile	Leu	Leu	Ala	Trp	Ile
			340					345					350		
Ile	Ala	Ala	Ile	Leu	Arg	Ile	Ser	Leu	Gly	Ser	Ala	Thr	Val	Ala	Ser
		355					360					365			
Leu	Thr	Thr	Ala	Gly	Leu	Val	Ile	Pro	Leu	Leu	Gly	Gln	Ser	Asp	Val
	370					375					380				
Asn	Leu	Ala	Leu	Val	Val	Leu	Ala	Thr	Gly	Ala	Gly	Ser	Leu	Ile	Ala
385					390				395						400

PF59083SeqList PF59083.txt

Ser His Val Asn Asp Ala Gly Phe Trp Met Phe Lys Glu Tyr Phe Gly
 405 410 415
 Leu Thr Met Lys Glu Thr Phe Ala Thr Trp Thr Leu Leu Glu Thr Ile
 420 425 430
 Ile Ser Val Phe Gly Leu Gly Phe Val Leu Leu Leu Ser Leu Val Val
 435 440 445

<210> 10212
 <211> 1365
 <212> DNA
 <213> Escherichia coli B

<220>
 <221> CDS
 <222> (1)..(1365)
 <223> transl_table=11

<400> 10212
 atg tcc aca att aca ttg tta tgc att gcg tta act ggc gta atc atg 48
 Met Ser Thr Ile Thr Leu Leu Cys Ile Ala Leu Thr Gly Val Ile Met 15
 1 5 10
 ctg ttg ctg ctg gtc atc aag gca aag gta caa cca ttc gtt gct ctg 96
 Leu Leu Leu Leu Val Ile Lys Ala Lys Val Gln Pro Phe Val Ala Leu 20 25 30
 ctc ctc gtc agc ctg tta gtc gca ctt gcg gcg ggt ata ccg gcg ggc 144
 Leu Leu Val Ser Leu Leu Val Ala Leu Ala Gly Ile Pro Ala Gly 35 40 45
 gaa gtg ggt aaa gtg atg atc gcc ggg atg ggc ggt gtg ctt ggt tcc 192
 Glu Val Gly Lys Val Met Ile Ala Gly Met Gly Gly Val Leu Gly Ser 50 55 60
 gtc act att att att ggt ctg ggc gct atg ctg ggg cgt atg atc gaa 240
 Val Thr Ile Ile Ile Gly Leu Gly Ala Met Leu Gly Arg Met Ile Glu 65 70 75 80
 cac tct ggt ggt gca gag tca ctg gct aat tat ttc agt cgc aag tta 288
 His Ser Gly Gly Ala Glu Ser Leu Ala Asn Tyr Phe Ser Arg Lys Leu 85 90 95
 ggt gac aaa cga act atc gct gcg ctg act ctg gca gcg ttc ttc ctc 336
 Gly Asp Lys Arg Thr Ile Ala Ala Leu Thr Leu Ala Ala Phe Phe Leu 100 105 110
 ggt att ccc gtc ttc ttt gat gtc ggc ttt att att ctt gcg cca atc 384
 Gly Ile Pro Val Phe Phe Asp Val Gly Phe Ile Ile Leu Ala Pro Ile 115 120 125
 att tac ggt ttt gcc aag gtt gcc aaa ata tcg cca ctc aaa ttt ggc 432
 Ile Tyr Gly Phe Ala Lys Val Ala Lys Ile Ser Pro Leu Lys Phe Gly 130 135 140
 ctg cct gtc gct ggg gtc atg ctc act gtt cac gtg gcg gta ccg ccg 480
 Leu Pro Val Ala Gly Val Met Leu Thr Val His Val Ala Val Pro Pro 145 150 155 160
 cat cca ggc cct gtc gcc gca gcg ggg tta ctc cac gca gac atc ggc 528
 His Pro Gly Pro Val Ala Ala Ala Gly Leu His Ala Asp Ile Gly 165 170 175
 tgg cta acc atc atc ggt att gcg att tct att ccc gta ggg gtt gtt 576
 Trp Leu Thr Ile Ile Gly Ile Ala Ile Ser Ile Pro Val Gly Val Val 180 185 190
 ggc tac ttt gca gcg aaa ata atc aat aag cgc caa tat gcg atg tca 624
 Gly Tyr Phe Ala Ala Lys Ile Ile Asn Lys Arg Gln Tyr Ala Met Ser 195 200 205
 gta gaa gta ctg gaa cag atg caa ctg gct ccg gcc agt gag gaa ggc 672
 Val Glu Val Leu Glu Gln Met Gln Leu Ala Pro Ala Ser Glu Glu Gly 210 215 220
 gcg aca aaa tta agc gat aaa ata aat cca ccg ggc gtc gcg ctg gtc 720
 Ala Thr Lys Leu Ser Asp Lys Ile Asn Pro Pro Gly Val Ala Leu Val 225 230 235 240
 acc tcg cta att gtt att cct atc gcg att atc atg gcg ggt acg gtt 768
 Thr Ser Leu Ile Val Ile Pro Ile Ala Ile Met Ala Gly Thr Val 245 250 255
 tcc gca aca ctg atg ccg cct tcg cat ccc ctg ctt ggt acg cta cag 816
 Ser Ala Thr Leu Met Pro Pro Ser His Pro Leu Leu Gly Thr Leu Gln 260 265 270

PF59083SeqList PF59083.txt

ctg atc ggc tca cca atg gta gct cta atg att gcg ctg gtg ctg gca	864
Leu Ile Gly Ser Pro Met Val Ala Leu Met Ile Ala Leu Val Leu Ala	
275 280 285	
ttc tgg tta ttg gct tta cgt cgc ggc tgg agc tta caa cac acc agc	912
Phe Trp Leu Leu Ala Leu Arg Arg Gly Trp Ser Leu Gln His Thr Ser	
290 295 300	
gac att atg ggc tca gcc ctt ccc act gcg gcg gta gtg att ttg gtt	960
Asp Ile Met Gly Ser Ala Leu Pro Thr Ala Ala Val Val Ile Leu Val	
305 310 315 320	
act ggt gct gga ggg gta ttt ggc aaa gtg ctg gtg gaa tcg ggc gtc	1008
Thr Gly Ala Gly Val Phe Gly Lys Val Leu Val Glu Ser Gly Val	
325 330 335	
ggc aaa gcc ctt gcc aac atg cta caa atg att gac ctg cct ctg tta	1056
Gly Lys Ala Leu Ala Asn Met Leu Gln Met Ile Asp Leu Pro Leu Leu	
340 345 350	
cca gcc gca ttt att att tca ctg gcg ctg cgt gca tcg cag ggg tca	1104
Pro Ala Ala Phe Ile Ile Ser Leu Ala Leu Arg Ala Ser Gln Gly Ser	
355 360 365	
gca acc gta gca atc ctg aca acc ggc ggg tta ctc tca gaa gcg gtg	1152
Ala Thr Val Ala Ile Leu Thr Thr Gly Gly Leu Leu Ser Glu Ala Val	
370 375 380	
atg gga ttg aat ccg att cag tgc gta ttg gtg acg ctg gca gcc tgc	1200
Met Gly Leu Asn Pro Ile Gln Cys Val Leu Val Thr Leu Ala Ala Cys	
385 390 395 400	
ttt ggt ggg ctt ggc gcg tca cat att aat gac tca ggg ttc tgg att	1248
Phe Gly Gly Leu Gly Ala Ser His Ile Asn Asp Ser Gly Phe Trp Ile	
405 410 415	
gtg acc aaa tat ctg ggg ttg tcg gta gca gac ggt ctg aaa acc tgg	1296
Val Thr Lys Tyr Leu Gly Leu Ser Val Ala Asp Gly Leu Lys Thr Trp	
420 425 430	
aca gtg tta acg acc att ctc ggt ttt acc gga ttc tta att acc tgg	1344
Thr Val Leu Thr Thr Ile Leu Gly Phe Thr Gly Phe Leu Ile Thr Trp	
435 440 445	
tgc gta tgg gcg gta att tga	1365
Cys Val Trp Ala Val Ile	
450	

<210> 10213
 <211> 454
 <212> PRT
 <213> Escherichia coli B

<400> 10213

Met Ser Thr Ile Thr Leu Leu Cys Ile Ala Leu Thr Gly Val Ile Met	
1 5 10 15	
Leu Leu Leu Leu Val Ile Lys Ala Lys Val Gln Pro Phe Val Ala Leu	
20 25 30	
Leu Leu Val Ser Leu Leu Val Ala Leu Ala Ala Gly Ile Pro Ala Gly	
35 40 45	
Glu Val Gly Lys Val Met Ile Ala Gly Met Gly Gly Val Leu Gly Ser	
50 55 60	
Val Thr Ile Ile Ile Gly Leu Gly Ala Met Leu Gly Arg Met Ile Glu	
65 70 75 80	
His Ser Gly Gly Ala Glu Ser Leu Ala Asn Tyr Phe Ser Arg Lys Leu	
85 90 95	
Gly Asp Lys Arg Thr Ile Ala Ala Leu Thr Leu Ala Ala Phe Phe Leu	
100 105 110	
Gly Ile Pro Val Phe Phe Asp Val Gly Phe Ile Ile Leu Ala Pro Ile	
115 120 125	
Ile Tyr Gly Phe Ala Lys Val Ala Lys Ile Ser Pro Leu Lys Phe Gly	
130 135 140	
Leu Pro Val Ala Gly Val Met Leu Thr Val His Val Ala Val Pro Pro	
145 150 155 160	
His Pro Gly Pro Val Ala Ala Ala Gly Leu His Ala Asp Ile Gly	
165 170 175	
Trp Leu Thr Ile Ile Gly Ile Ala Ile Ser Ile Pro Val Gly Val Val	
180 185 190	
Gly Tyr Phe Ala Ala Lys Ile Ile Asn Lys Arg Gln Tyr Ala Met Ser	
195 200 205	

PF59083SeqList PF59083.txt

Val	Glu	Val	Leu	Glu	Gln	Met	Gln	Leu	Ala	Pro	Ala	Ser	Glu	Glu	Gly
210						215					220				
Ala	Thr	Lys	Leu	Ser	Asp	Lys	Ile	Asn	Pro	Pro	Gly	Val	Ala	Leu	Val
225					230					235					240
Thr	Ser	Leu	Ile	Val	Ile	Pro	Ile	Ala	Ile	Ile	Met	Ala	Gly	Thr	Val
				245					250					255	
Ser	Ala	Thr	Leu	Met	Pro	Pro	Ser	His	Pro	Leu	Leu	Gly	Thr	Leu	Gln
				260				265					270		
Leu	Ile	Gly	Ser	Pro	Met	Val	Ala	Leu	Met	Ile	Ala	Leu	Val	Leu	Ala
		275					280					285			
Phe	Trp	Leu	Leu	Ala	Leu	Arg	Arg	Gly	Trp	Ser	Leu	Gln	His	Thr	Ser
290						295					300				
Asp	Ile	Met	Gly	Ser	Ala	Leu	Pro	Thr	Ala	Ala	Val	Val	Ile	Leu	Val
305					310					315					320
Thr	Gly	Ala	Gly	Gly	Val	Phe	Gly	Lys	Val	Leu	Val	Glu	Ser	Gly	Val
				325				330						335	
Gly	Lys	Ala	Leu	Ala	Asn	Met	Leu	Gln	Met	Ile	Asp	Leu	Pro	Leu	Leu
				340				345					350		
Pro	Ala	Ala	Phe	Ile	Ile	Ser	Leu	Ala	Leu	Arg	Ala	Ser	Gln	Gly	Ser
		355					360					365			
Ala	Thr	Val	Ala	Ile	Leu	Thr	Thr	Gly	Gly	Leu	Leu	Ser	Glu	Ala	Val
		370				375					380				
Met	Gly	Leu	Asn	Pro	Ile	Gln	Cys	Val	Leu	Val	Thr	Leu	Ala	Ala	Cys
385					390					395					400
Phe	Gly	Gly	Leu	Gly	Ala	Ser	His	Ile	Asn	Asp	Ser	Gly	Phe	Trp	Ile
				405				410						415	
Val	Thr	Lys	Tyr	Leu	Gly	Leu	Ser	Val	Ala	Asp	Gly	Leu	Lys	Thr	Trp
			420					425					430		
Thr	Val	Leu	Thr	Thr	Ile	Leu	Gly	Phe	Thr	Gly	Phe	Leu	Ile	Thr	Trp
		435					440					445			
Cys	Val	Trp	Ala	Val	Ile										
450															

<210> 10214
 <211> 1404
 <212> DNA
 <213> Pseudomonas putida GB-1

<220>
 <221> CDS
 <222> (1)..(1404)
 <223> transl_table=11

<400> 10214	
atg gtt gca aac caa caa gaa gct cgc acg gaa gcg atc agc gat aga	48
Met Val Ala Asn Gln Gln Glu Ala Arg Thr Glu Ala Ile Ser Asp Arg	
1 5 10 15	
gat aac tac acg atg act cca acg ttc tca tta atc gtt ctg ggc act	96
Asp Asn Tyr Thr Met Thr Pro Thr Phe Ser Leu Ile Val Leu Gly Thr	
20 25 30	
gca ata ctg ctg atc gtg gtc atg atc agc aag ctc aag gtc cac ccc	144
Ala Ile Leu Leu Ile Val Val Met Ile Ser Lys Leu Lys Val His Pro	
35 40 45	
ttc ctg gca ctg ctg gcc gca agc ctg gtg gtg ggc att ggt acc ggc	192
Phe Leu Ala Leu Leu Ala Ala Ser Leu Val Val Gly Ile Gly Thr Gly	
50 55 60	
atg ccg ccg acg gcc atg gtt gcc gcg ttc gaa aaa ggc atg ggc agc	240
Met Pro Pro Thr Ala Met Val Ala Ala Phe Glu Lys Gly Met Gly Ser	
65 70 75 80	
acg ctg ggc ttt ctt gcc ggc atc atc ggc ctg ggc agt atc ctc ggc	288
Thr Leu Gly Phe Leu Ala Gly Ile Ile Gly Leu Gly Ser Ile Leu Gly	
85 90 95	
aaa ctg ctg gaa gag tcg ggt ggg gcc agg cgc atc gcc acc acg ctg	336
Lys Leu Leu Glu Glu Ser Gly Gly Ala Arg Arg Ile Ala Thr Thr Leu	
100 105 110	
ctg aac ctg ttg ggt gaa cgc aat gct tca tgg gcc atg atg ctg gtg	384
Leu Asn Leu Leu Gly Glu Arg Asn Ala Ser Trp Ala Met Met Leu Val	
115 120 125	
ggc ttc atc gct ggc atc ccg gta ttt ttc gag gtc ggc ttc gtg ctg	432

PF59083SeqList PF59083.txt

Gly	Phe	Ile	Ala	Gly	Ile	Pro	Val	Phe	Phe	Glu	Val	Gly	Phe	Val	Leu	
130	130					135					140					
ctc	att	ccg	ctg	atc	tac	gtg	ggt	gcc	cgg	caa	acc	cgc	atc	agc	atg	480
Leu	Ile	Pro	Leu	Ile	Tyr	Val	Val	Ala	Arg	Gln	Thr	Arg	Ile	Ser	Met	
145					150					155					160	
ctg	tac	ctc	ggc	gtc	ccg	ctg	gcc	acc	tcg	ctg	atg	gtg	gtg	cac	tgc	528
Leu	Tyr	Leu	Gly	Val	Pro	Leu	Ala	Thr	Ser	Leu	Met	Val	Val	His	Cys	
			165						170					175		
att	ctg	ccg	cca	cac	cca	gct	gct	acg	gcg	att	acc	ggc	atg	ctc	aat	576
Ile	Leu	Pro	Pro	His	Pro	Ala	Ala	Thr	Ala	Ile	Thr	Gly	Met	Leu	Asn	
			180						185				190			
gcc	gat	atc	ggc	acg	gtc	atc	ctc	tat	ggc	ctg	atc	gtt	ggc	ttg	ccc	624
Ala	Asp	Ile	Gly	Thr	Val	Ile	Leu	Tyr	Gly	Leu	Ile	Val	Gly	Leu	Pro	
		195					200					205				
act	gcc	atc	atc	gcc	ggc	ccg	gtc	tgg	gta	cgc	ttc	gcc	tgc	aag	cgc	672
Thr	Ala	Ile	Ile	Ala	Gly	Pro	Val	Trp	Val	Arg	Phe	Ala	Cys	Lys	Arg	
	210					215					220					
ggc	gca	aca	caa	gcg	caa	gat	acc	ttc	ctt	tcg	gca	cgt	acc	gag	gcc	720
Gly	Ala	Thr	Gln	Ala	Gln	Asp	Thr	Phe	Leu	Ser	Ala	Arg	Thr	Glu	Ala	
225					230					235					240	
cag	gtc	gat	gac	cag	ccg	ctg	cct	gct	ttc	ggc	att	acc	ctc	gcc	acc	768
Gln	Val	Asp	Asp	Gln	Pro	Leu	Pro	Ala	Phe	Gly	Ile	Thr	Leu	Ala	Thr	
			245						250					255		
gta	ctg	ctg	ccg	ttg	ctg	ctg	atg	gtc	ggc	aaa	acc	ttg	gcc	gtc	atg	816
Val	Leu	Leu	Pro	Leu	Leu	Leu	Met	Val	Gly	Lys	Thr	Leu	Ala	Val	Met	
			260				265						270			
gtg	ctg	gca	aag	ggc	tcc	acg	ctg	tac	gag	tgg	gtg	gcc	ttc	gtt	ggc	864
Val	Leu	Ala	Lys	Gly	Ser	Thr	Leu	Tyr	Glu	Trp	Val	Ala	Phe	Val	Gly	
		275				280						285				
aac	cca	ctg	atc	gcc	ctg	gcg	ctg	tcg	gtt	atg	ttc	ggc	tac	tgg	gca	912
Asn	Pro	Leu	Ile	Ala	Leu	Ala	Leu	Ser	Val	Met	Phe	Gly	Tyr	Trp	Ala	
	290					295					300					
ctg	ggc	ctg	cgc	cgc	ggc	ctg	gac	atg	gcg	cag	ttg	ctc	aac	ctg	acc	960
Leu	Gly	Leu	Arg	Arg	Gly	Leu	Asp	Met	Ala	Gln	Leu	Leu	Asn	Leu	Thr	
305					310					315					320	
cag	cgc	tgc	ttc	ccg	ccc	ctg	gcc	ggt	att	ttg	ctg	att	atc	ggt	gcc	1008
Gln	Arg	Cys	Phe	Pro	Pro	Leu	Ala	Gly	Ile	Leu	Leu	Ile	Ile	Gly	Ala	
			325					330						335		
ggc	ggc	gcc	ttc	aac	gac	atg	ctg	gtc	ggt	agc	ggc	atc	ggc	aag	gcg	1056
Gly	Gly	Ala	Phe	Asn	Asp	Met	Leu	Val	Gly	Ser	Gly	Ile	Gly	Lys	Ala	
		340						345					350			
ctg	gct	gac	gtg	ctc	aac	cag	acc	cag	ctc	aac	ccg	atc	atc	ctc	gcc	1104
Leu	Ala	Asp	Val	Leu	Asn	Gln	Thr	Gln	Leu	Asn	Pro	Ile	Ile	Leu	Ala	
		355				360						365				
tgg	ctg	atc	gct	ggg	atc	atg	cac	ttc	gcg	gtc	ggt	tcg	gcc	acg	gtg	1152
Trp	Leu	Ile	Ala	Gly	Ile	Met	His	Phe	Ala	Val	Gly	Ser	Ala	Thr	Val	
		370				375					380					
gca	atg	atc	agc	gca	gcc	ggc	atg	gtc	atg	ccg	atc	ctg	gac	caa	cac	1200
Ala	Met	Ile	Ser	Ala	Ala	Gly	Met	Val	Met	Pro	Ile	Leu	Asp	Gln	His	
385					390					395					400	
ccc	gaa	tac	aac	cgg	gaa	atc	ctg	gtg	atc	gcc	atc	ggt	gca	ggc	gcc	1248
Pro	Glu	Tyr	Asn	Arg	Glu	Ile	Leu	Val	Ile	Ala	Ile	Gly	Ala	Gly	Ala	
			405					410						415		
atc	ggc	tgg	aca	cac	att	acc	gat	tcg	gcg	ttc	tgg	gtg	gtg	aag	gag	1296
Ile	Gly	Trp	Thr	His	Ile	Thr	Asp	Ser	Ala	Phe	Trp	Val	Val	Lys	Glu	
			420				425						430			
tat	ctg	ggg	ctg	tca	ctc	agc	gat	gcg	ttg	aaa	aaa	ttc	act	gcg	gcg	1344
Tyr	Leu	Gly	Leu	Ser	Leu	Ser	Asp	Ala	Leu	Lys	Lys	Phe	Thr	Ala	Ala	
		435				440						445				
aca	gtg	ctg	gcc	tcg	gtg	atc	gcc	ttg	tgc	ctg	acc	ctg	ctc	ctt	tca	1392
Thr	Val	Leu	Ala	Ser	Val	Ile	Ala	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Ser	
		450				455					460					
aaa	att	gtc	tga													1404
Lys	Ile	Val														
465																

<210> 10215

<211> 467

<212> PRT

<213> Pseudomonas putida GB-1

<400> 10215

```

Met Val Ala Asn Gln Gln Glu Ala Arg Thr Glu Ala Ile Ser Asp Arg
1      5      10      15
Asp Asn Tyr Thr Met Thr Pro Thr Phe Ser Leu Ile Val Leu Gly Thr
20      25      30
Ala Ile Leu Leu Ile Val Val Met Ile Ser Lys Leu Lys Val His Pro
35      40      45
Phe Leu Ala Leu Leu Ala Ala Ser Leu Val Val Gly Ile Gly Thr Gly
50      55      60
Met Pro Pro Thr Ala Met Val Ala Ala Phe Glu Lys Gly Met Gly Ser
65      70      75      80
Thr Leu Gly Phe Leu Ala Gly Ile Ile Gly Leu Gly Ser Ile Leu Gly
85      90      95
Lys Leu Leu Glu Ser Gly Gly Ala Arg Arg Ile Ala Thr Thr Leu
100      105      110
Leu Asn Leu Leu Gly Glu Arg Asn Ala Ser Trp Ala Met Met Leu Val
115      120      125
Gly Phe Ile Ala Gly Ile Pro Val Phe Phe Glu Val Gly Phe Val Leu
130      135      140
Leu Ile Pro Leu Ile Tyr Val Val Ala Arg Gln Thr Arg Ile Ser Met
145      150      155      160
Leu Tyr Leu Gly Val Pro Leu Ala Thr Ser Leu Met Val Val His Cys
165      170      175
Ile Leu Pro Pro His Pro Ala Ala Thr Ala Ile Thr Gly Met Leu Asn
180      185      190
Ala Asp Ile Gly Thr Val Ile Leu Tyr Gly Leu Ile Val Gly Leu Pro
195      200      205
Thr Ala Ile Ile Ala Gly Pro Val Trp Val Arg Phe Ala Cys Lys Arg
210      215      220
Gly Ala Thr Gln Ala Gln Asp Thr Phe Leu Ser Ala Arg Thr Glu Ala
225      230      235      240
Gln Val Asp Asp Gln Pro Leu Pro Ala Phe Gly Ile Thr Leu Ala Thr
245      250      255
Val Leu Leu Pro Leu Leu Leu Met Val Gly Lys Thr Leu Ala Val Met
260      265      270
Val Leu Ala Lys Gly Ser Thr Leu Tyr Glu Trp Val Ala Phe Val Gly
275      280      285
Asn Pro Leu Ile Ala Leu Ala Leu Ser Val Met Phe Gly Tyr Trp Ala
290      295      300
Leu Gly Leu Arg Arg Gly Leu Asp Met Ala Gln Leu Leu Asn Leu Thr
305      310      315      320
Gln Arg Cys Phe Pro Leu Ala Gly Ile Leu Leu Ile Ile Gly Ala
325      330      335
Gly Gly Ala Phe Asn Asp Met Leu Val Gly Ser Gly Ile Gly Lys Ala
340      345      350
Leu Ala Asp Val Leu Asn Gln Thr Gln Leu Asn Pro Ile Ile Leu Ala
355      360      365
Trp Leu Ile Ala Gly Ile Met His Phe Ala Val Gly Ser Ala Thr Val
370      375      380
Ala Met Ile Ser Ala Ala Gly Met Val Met Pro Ile Leu Asp Gln His
385      390      395      400
Pro Glu Tyr Asn Arg Glu Ile Leu Val Ile Ala Ile Gly Ala Gly Ala
405      410      415
Ile Gly Trp Thr His Ile Thr Asp Ser Ala Phe Trp Val Val Lys Glu
420      425      430
Tyr Leu Gly Leu Ser Leu Ser Asp Ala Leu Lys Lys Phe Thr Ala Ala
435      440      445
Thr Val Leu Ala Ser Val Ile Ala Leu Cys Leu Thr Leu Leu Ser
450      455      460
Lys Ile Val
465

```

<210> 10216

<211> 1386

<212> DNA

<213> Pseudomonas putida GB-1

PF59083SeqList PF59083.txt

<220>
<221> CDS
<222> (1)..(1386)
<223> transl_table=11

<400> 10216

atg acc ccc ttg gat ata cag ctg cta ctg acc gct ctg gtc agt gtc	48
Met Thr Pro Leu Asp Ile Gln Leu Leu Leu Thr Ala Leu Val Ser Val	
1 5 10 15	
ctg gtg ctg gtg gca ctc atc gtg tcg cgc ctg aag atg cac ccg ctg	96
Leu Val Leu Val Ala Leu Ile Val Ser Arg Leu Lys Met His Pro Leu	
20 25 30	
ctg gcc ttg ctg gtg gtg tcc att ggg gtg ggc ttc gct acc cgc atg	144
Leu Ala Leu Leu Val Val Ser Ile Gly Val Gly Phe Ala Thr Arg Met	
35 40 45	
gag cca ggc agc atc gtc tcc cac ttg ctt acc ggc gct gga aaa acc	192
Glu Pro Gly Ser Ile Val Ser His Leu Leu Thr Gly Ala Gly Lys Thr	
50 55 60	
ctg ggg gcc gtc ggg gtg gtg att gcc ctt ggc gcg atg ctc ggc aaa	240
Leu Gly Ala Val Gly Val Ile Ala Leu Gly Ala Met Leu Gly Lys	
65 70 75 80	
att ctg gct gac gct ggc gtc acc gag cag gtc gct gat gtc atc ctc	288
Ile Leu Ala Asp Ala Gly Val Thr Glu Gln Val Ala Asp Val Ile Leu	
85 90 95	
aag cgc acc tcg gac cgc atg att ccg tgg gcc atg atg ttg gtt gcc	336
Lys Arg Thr Ser Asp Arg Met Ile Pro Trp Ala Met Met Leu Val Ala	
100 105 110	
ttc gtc att ggc atc ccc atg ttt ttc gaa gtg ggc ctg gtg atc atg	384
Phe Val Ile Gly Ile Pro Met Phe Phe Glu Val Gly Leu Val Ile Met	
115 120 125	
ctg ccg ctg att ttc agc gtg gcg cgc aag ctg gaa agc aag gcc cgc	432
Leu Pro Leu Ile Phe Ser Val Ala Arg Lys Leu Glu Ser Lys Ala Arg	
130 135 140	
ttc aag ggc tct gca tac gtg tat gta ggc gtg ccg gtg att tcg gcg	480
Phe Lys Gly Ser Ala Tyr Val Tyr Val Gly Val Pro Val Ile Ser Ala	
145 150 155 160	
ctg gct gcc atg cac ggc atg gta ccg ccg cac cct ggc ccc ctg acc	528
Leu Ala Ala Met His Gly Met Val Pro Pro His Pro Gly Pro Leu Thr	
165 170 175	
gcc atc gcg gta ctc aag acc tcg gtt ggg gcc acc atg ctt tac ggc	576
Ala Ile Ala Val Leu Lys Thr Ser Val Gly Pro Thr Met Leu Tyr Gly	
180 185 190	
ttc ctg gcg gct atc ccg gca atg atc ctg ggc ggc ccg ctg tat ggc	624
Phe Leu Ala Ala Ile Pro Ala Met Ile Leu Gly Gly Pro Leu Tyr Gly	
195 200 205	
atg ttc att tcg ccg cgc atg agc act cgc cct gat cag gct ttg ctg	672
Met Phe Ile Ser Pro Arg Met Ser Thr Arg Pro Asp Gln Ala Leu Leu	
210 215 220	
gac cag ttc acc ctg gct gaa aaa gcc gac gat caa ccc cgc ccc ggc	720
Asp Gln Phe Thr Leu Ala Glu Lys Ala Asp Asp Gln Pro Arg Pro Gly	
225 230 235 240	
gta gcg atc ggc atg ctg gcc gcg ttg ctg ccg gcg att ctg atg ctg	768
Val Ala Ile Gly Met Leu Ala Ala Leu Leu Pro Ala Ile Leu Met Leu	
245 250 255	
gtg cat gcc gtc gcc gag atg ctg cta ccc aag ggc aac ccg ttg ctg	816
Val His Ala Val Ala Glu Met Leu Leu Pro Lys Gly Asn Pro Leu Leu	
260 265 270	
gag ctg gcc agt ttc ctc ggc aac ccg ctg atc gcc atg ttg ctg ggc	864
Glu Leu Ala Ser Phe Leu Gly Asn Pro Leu Ile Ala Met Leu Leu Gly	
275 280 285	
gtg ctg ttc gcc ggc gcc agc ctg gta ctg gcg cgc ggc ggt gac gcc	912
Val Leu Phe Ala Gly Ala Ser Leu Val Leu Ala Arg Gly Gly Asp Ala	
290 295 300	
gaa cac ctg cgc gat gca ctg ggc aaa agc ctc aag cct atc gcc tcg	960
Glu His Leu Arg Asp Ala Leu Gly Lys Ser Leu Lys Pro Ile Ala Ser	
305 310 315 320	
atc atc atg atc atc gcc ggc ggc ggg gct ttt cag gag atg ctg acc	1008
Ile Ile Met Ile Ile Ala Gly Gly Gly Ala Phe Gln Glu Met Leu Thr	
325 330 335	

PF59083SeqList PF59083.txt

agc	gcc	aag	gtg	ggg	gat	gcc	att	gtg	cac	ctg	act	cag	caa	tcg	gcc	1056
Ser	Ala	Lys	Val	Gly	Asp	Ala	Ile	Val	His	Leu	Thr	Gln	Gln	Ser	Ala	
			340					345					350			
ttc	ccg	ccc	ttg	atg	ctg	ggg	tgg	ttg	atc	gcg	atg	ttg	ctt	tcg	gtg	1104
Phe	Pro	Pro	Leu	Met	Leu	Gly	Trp	Leu	Ile	Ala	Met	Leu	Leu	Ser	Val	
		355					360					365				
tct	acc	ggc	tcc	gcc	acg	gta	ggg	atc	gtt	ggg	gct	gcc	ggc	ttg	ctg	1152
Ser	Thr	Gly	Ser	Ala	Thr	Val	Gly	Ile	Val	Gly	Ala	Ala	Gly	Leu	Leu	
	370					375				380						
gca	ccg	ctg	gcg	ggg	gcc	gac	ccc	agc	ctc	aac	ctg	ccg	ttg	ctg	gcc	1200
Ala	Pro	Leu	Ala	Gly	Ala	Asp	Pro	Ser	Leu	Asn	Leu	Pro	Leu	Leu	Ala	
385					390					395					400	
ttg	tcc	atc	ggc	tgt	ggc	tcg	ctg	ttc	ttc	aac	tat	gcg	aac	cat	gca	1248
Leu	Ser	Ile	Gly	Cys	Gly	Ser	Leu	Phe	Phe	Asn	Tyr	Ala	Asn	His	Ala	
			405					410						415		
ggg	ttc	tgg	atg	gtg	aaa	gag	tcc	ttt	ggg	atg	acc	atg	ggc	gaa	gcc	1296
Gly	Phe	Trp	Met	Val	Lys	Glu	Ser	Phe	Gly	Met	Thr	Met	Gly	Glu	Ala	
		420					425						430			
acc	agg	acc	atc	tcg	gtg	gtg	cag	tcc	atc	gtg	gcg	gtg	gtc	ggg	ttg	1344
Thr	Arg	Thr	Ile	Ser	Val	Val	Gln	Ser	Ile	Val	Ala	Val	Val	Gly	Leu	
		435					440					445				
att	gtg	gtg	ctg	gtc	ttg	aat	gcg	gca	att	act	gtg	agt	tga			1386
Ile	Val	Val	Leu	Val	Leu	Asn	Ala	Ala	Ile	Thr	Val	Ser				
	450					455					460					

<210> 10217

<211> 461

<212> PRT

<213> Pseudomonas putida GB-1

<400> 10217

Met	Thr	Pro	Leu	Asp	Ile	Gln	Leu	Leu	Leu	Thr	Ala	Leu	Val	Ser	Val	
1				5				10						15		
Leu	Val	Leu	Val	Ala	Leu	Ile	Val	Ser	Arg	Leu	Lys	Met	His	Pro	Leu	
			20					25					30			
Leu	Ala	Leu	Leu	Val	Val	Ser	Ile	Gly	Val	Gly	Phe	Ala	Thr	Arg	Met	
		35					40					45				
Glu	Pro	Gly	Ser	Ile	Val	Ser	His	Leu	Leu	Thr	Gly	Ala	Gly	Lys	Thr	
	50					55					60					
Leu	Gly	Ala	Val	Gly	Val	Ile	Ala	Leu	Gly	Ala	Met	Leu	Gly	Lys		
65				70					75					80		
Ile	Leu	Ala	Asp	Ala	Gly	Val	Thr	Glu	Gln	Val	Ala	Asp	Val	Ile	Leu	
			85				90							95		
Lys	Arg	Thr	Ser	Asp	Arg	Met	Ile	Pro	Trp	Ala	Met	Met	Leu	Val	Ala	
			100				105						110			
Phe	Val	Ile	Gly	Ile	Pro	Met	Phe	Phe	Glu	Val	Gly	Leu	Val	Ile	Met	
		115				120						125				
Leu	Pro	Leu	Ile	Phe	Ser	Val	Ala	Arg	Lys	Leu	Glu	Ser	Lys	Ala	Arg	
	130					135					140					
Phe	Lys	Gly	Ser	Ala	Tyr	Val	Tyr	Val	Gly	Val	Pro	Val	Ile	Ser	Ala	
145					150				155					160		
Leu	Ala	Ala	Met	His	Gly	Met	Val	Pro	Pro	His	Pro	Gly	Pro	Leu	Thr	
			165						170					175		
Ala	Ile	Ala	Val	Leu	Lys	Thr	Ser	Val	Gly	Pro	Thr	Met	Leu	Tyr	Gly	
		180					185						190			
Phe	Leu	Ala	Ala	Ile	Pro	Ala	Met	Ile	Leu	Gly	Gly	Pro	Leu	Tyr	Gly	
		195				200						205				
Met	Phe	Ile	Ser	Pro	Arg	Met	Ser	Thr	Arg	Pro	Asp	Gln	Ala	Leu	Leu	
	210					215					220					
Asp	Gln	Phe	Thr	Leu	Ala	Glu	Lys	Ala	Asp	Asp	Gln	Pro	Arg	Pro	Gly	
225					230					235					240	
Val	Ala	Ile	Gly	Met	Leu	Ala	Ala	Leu	Leu	Pro	Ala	Ile	Leu	Met	Leu	
			245						250					255		
Val	His	Ala	Val	Ala	Glu	Met	Leu	Leu	Pro	Lys	Gly	Asn	Pro	Leu	Leu	
		260						265					270			
Glu	Leu	Ala	Ser	Phe	Leu	Gly	Asn	Pro	Leu	Ile	Ala	Met	Leu	Leu	Gly	
		275				280						285				
Val	Leu	Phe	Ala	Gly	Ala	Ser	Leu	Val	Leu	Ala	Arg	Gly	Gly	Asp	Ala	
	290					295					300					

PF59083SeqList PF59083.txt

Glu His Leu Arg Asp Ala Leu Gly Lys Ser Leu Lys Pro Ile Ala Ser
 305 310 315 320
 Ile Ile Met Ile Ile Ala Gly Gly Gly Ala Phe Gln Glu Met Leu Thr
 325 330 335
 Ser Ala Lys Val Gly Asp Ala Ile Val His Leu Thr Gln Gln Ser Ala
 340 345 350
 Phe Pro Pro Leu Met Leu Gly Trp Leu Ile Ala Met Leu Leu Ser Val
 355 360 365
 Ser Thr Gly Ser Ala Thr Val Gly Ile Val Gly Ala Ala Gly Leu Leu
 370 375 380
 Ala Pro Leu Ala Gly Ala Asp Pro Ser Leu Asn Leu Pro Leu Leu Ala
 385 390 395 400
 Leu Ser Ile Gly Cys Gly Ser Leu Phe Phe Asn Tyr Ala Asn His Ala
 405 410 415
 Gly Phe Trp Met Val Lys Glu Ser Phe Gly Met Thr Met Gly Glu Ala
 420 425 430
 Thr Arg Thr Ile Ser Val Val Gln Ser Ile Val Ala Val Val Gly Leu
 435 440 445
 Ile Val Val Leu Val Leu Asn Ala Ala Ile Thr Val Ser
 450 455 460

<210> 10218

<211> 1344

<212> DNA

<213> Marinobacter sp. ELB17

<220>

<221> CDS

<222> (1)..(1344)

<223> transl_table=11

<400> 10218

atg cac atg gtt ttt att tta atc gct ctt att gcg ttc att gtg ttc	48
Met His Met Val Phe Ile Leu Ile Ala Leu Ile Ala Phe Ile Val Phe	
1 5 10 15	
gca acg agc aaa ttg cgc ctc aac cct ttc att aca ctt ttg ctg gca	96
Ala Thr Ser Lys Leu Arg Leu Asn Pro Phe Ile Thr Leu Leu Leu Ala	
20 25 30	
tcg ttc att gcc gcg ttc gca ttt ggc ctg ccg ctc gat gcc atc gaa	144
Ser Phe Ile Ala Ala Phe Ala Phe Gly Leu Pro Leu Asp Ala Ile Glu	
35 40 45	
tca acg att cgc ggt ggt ttt ggt aaa att ctc ggc tac atc ggc ctg	192
Ser Thr Ile Arg Gly Gly Phe Gly Lys Ile Leu Gly Tyr Ile Gly Leu	
50 55 60	
gtt atc gtt ttg ggt acc atc ggt gtc att ctt gag cgc acc ggt	240
Val Ile Val Leu Gly Thr Ile Ile Gly Val Ile Leu Glu Arg Thr Gly	
65 70 75 80	
gcc gct att gtg atg gct gag acg atc att aaa tgt ttg ggt aaa aaa	288
Ala Ala Ile Val Met Ala Glu Thr Ile Ile Lys Cys Leu Gly Lys Lys	
85 90 95	
ttc cct acc atg acg atg tcc atc gtt ggt ttt att gtg tct att ccg	336
Phe Pro Thr Met Thr Met Ser Ile Val Gly Phe Ile Val Ser Ile Pro	
100 105 110	
gtg ttt tgt gat tcc ggt ttt gtc att ctc aac agc ctg aag cgc tcc	384
Val Phe Cys Asp Ser Gly Phe Val Ile Leu Asn Ser Leu Lys Arg Ser	
115 120 125	
atg gcg aga acc ctt agc gta tcc ccc gtc gca atg acg gtg gca ctt	432
Met Ala Arg Thr Leu Ser Val Ser Pro Val Ala Met Thr Val Ala Leu	
130 135 140	
tct acc ggt cta ttt gca acc cac acc ctt gta cca ccc acg ccc ggc	480
Ser Thr Gly Leu Phe Ala Thr His Thr Leu Val Pro Pro Thr Pro Gly	
145 150 155 160	
ccg att gcg gcc gca ggc aac ctg ggg ttg gaa aac aac ttg ggg ctg	528
Pro Ile Ala Ala Ala Gly Asn Leu Gly Leu Glu Asn Asn Leu Gly Leu	
165 170 175	
gtt atc ggc gtc ggc ctt gtt ttc gcc ata atc gcg gcg atg gcg ggt	576
Val Ile Gly Val Gly Leu Val Phe Ala Ile Ile Ala Ala Met Ala Gly	
180 185 190	
ttg gtt tgg gcc tat ttc tca cga aac ctg ccc agt aca gaa ctg gat	624

PF59083SeqList PF59083.txt

Leu	Val	Trp	Ala	Tyr	Phe	Ser	Arg	Asn	Leu	Pro	Ser	Thr	Glu	Leu	Asp	
cta	aca	gaa	gaa	gcg	ttt	gag	gaa	ggg	aaa	gag	cat	tac	ggg	gaa	ctg	672
Leu	Thr	Glu	Glu	Ala	Phe	Glu	Glu	Gly	Lys	Glu	His	Tyr	Gly	Glu	Leu	
	210					215					220					
cct	ggc	cca	tg	aaa	gcc	ttt	gct	cct	att	ttt	gta	ccc	att	gcc	ctt	720
Pro	Gly	Pro	Trp	Lys	Ala	Phe	Ala	Pro	Ile	Phe	Val	Pro	Ile	Ala	Leu	
225					230					235					240	
att	tgt	ttg	ggc	tca	gta	gcc	agt	tac	cca	acc	gcc	ccg	ctg	ggg	gat	768
Ile	Cys	Leu	Gly	Ser	Val	Ala	Ser	Tyr	Pro	Thr	Ala	Pro	Leu	Gly	Asp	
				245					250					255		
ggg	ttt	ctt	tat	gaa	gcg	ctg	aat	ttt	ctt	ggg	aag	ccg	cta	aat	gct	816
Gly	Phe	Leu	Tyr	Glu	Ala	Leu	Asn	Phe	Leu	Gly	Lys	Pro	Leu	Asn	Ala	
			260					265					270			
ctg	ttg	att	ggc	ctt	ggg	ttt	gca	gta	ctg	ctg	att	caa	ggg	aat	gag	864
Leu	Leu	Ile	Gly	Leu	Gly	Phe	Ala	Val	Leu	Leu	Ile	Gln	Gly	Asn	Glu	
			275				280					285				
aaa	ctc	aaa	gga	ttt	gcc	cgt	cac	acc	gaa	aaa	ggg	ctg	ggt	gtc	tcg	912
Lys	Leu	Lys	Gly	Phe	Ala	Arg	His	Thr	Glu	Lys	Gly	Leu	Val	Val	Ser	
	290					295					300					
gca	ccg	att	att	ctg	att	acc	ggg	gca	ggg	ggc	gca	ttc	ggg	gct	gtg	960
Ala	Pro	Ile	Ile	Leu	Ile	Thr	Gly	Ala	Gly	Gly	Ala	Phe	Gly	Ala	Val	
305					310					315					320	
ctg	gcc	gca	aca	ccg	ctg	ggg	gat	ttc	ctt	ggc	cag	aac	ctg	tct	aca	1008
Leu	Ala	Ala	Thr	Pro	Leu	Gly	Asp	Phe	Leu	Gly	Gln	Asn	Leu	Ser	Thr	
				325				330						335		
ttg	ggc	ttg	ggg	ggt	atc	atg	cct	ttc	att	gtg	gcc	gct	gca	ctc	aaa	1056
Leu	Gly	Leu	Gly	Val	Ile	Met	Pro	Phe	Ile	Val	Ala	Ala	Ala	Leu	Lys	
			340				345					350				
tcg	gca	caa	ggg	tct	tca	acc	gtc	gcc	ctg	ggt	acc	gct	tct	gca	ctg	1104
Ser	Ala	Gln	Gly	Ser	Ser	Thr	Val	Ala	Leu	Val	Thr	Ala	Ser	Ala	Leu	
		355				360					365					
ggt	gcc	ccg	ttg	ttg	ccg	caa	ttg	gga	ttg	gac	tca	gat	atg	ggc	cg	1152
Val	Ala	Pro	Leu	Leu	Pro	Gln	Leu	Gly	Leu	Asp	Ser	Asp	Met	Gly	Arg	
		370				375					380					
gta	cta	acg	ggt	atg	gcc	ggt	ggt	gct	ggc	gca	atg	acc	gtc	tcc	cac	1200
Val	Leu	Thr	Val	Met	Ala	Val	Gly	Ala	Gly	Ala	Met	Thr	Val	Ser	His	
385					390				395						400	
gcc	aac	gac	agc	tat	ttt	tg	gtg	gta	tcc	cag	ttc	agt	aaa	atg	gac	1248
Ala	Asn	Asp	Ser	Tyr	Phe	Trp	Val	Val	Ser	Gln	Phe	Ser	Lys	Met	Asp	
				405				410						415		
ggt	gca	acg	gca	tat	cg	tca	cac	aca	gca	gca	aca	ctt	ttt	atg	ggc	1296
Val	Ala	Thr	Ala	Tyr	Arg	Ser	His	Thr	Ala	Ala	Thr	Leu	Phe	Met	Gly	
			420				425						430			
ctg	gta	aca	att	act	gcc	gtg	tg	cta	gca	tcc	ctg	gca	gct	ctg		1341
Leu	Val	Thr	Ile	Thr	Ala	Val	Trp	Leu	Ala	Ser	Leu	Ala	Ala	Leu		
		435				440						445				
taa																1344

<210> 10219
 <211> 447
 <212> PRT
 <213> Marinobacter sp. ELB17

<400> 10219
 Met His Met Val Phe Ile Leu Ile Ala Leu Ile Ala Phe Ile Val Phe
 1 5 10 15
 Ala Thr Ser Lys Leu Arg Leu Asn Pro Phe Ile Thr Leu Leu Leu Ala
 20 25 30
 Ser Phe Ile Ala Ala Phe Ala Phe Gly Leu Pro Leu Asp Ala Ile Glu
 35 40 45
 Ser Thr Ile Arg Gly Gly Phe Gly Lys Ile Leu Gly Tyr Ile Gly Leu
 50 55 60
 Val Ile Val Leu Gly Thr Ile Ile Gly Val Ile Leu Glu Arg Thr Gly
 65 70 75 80
 Ala Ala Ile Val Met Ala Glu Thr Ile Ile Lys Cys Leu Gly Lys Lys
 85 90 95

PF59083SeqList PF59083.txt

Phe Pro Thr Met Thr Met Ser Ile Val Gly Phe Ile Val Ser Ile Pro
 100 105 110
 Val Phe Cys Asp Ser Gly Phe Val Ile Leu Asn Ser Leu Lys Arg Ser
 115 120 125
 Met Ala Arg Thr Leu Ser Val Ser Pro Val Ala Met Thr Val Ala Leu
 130 135 140
 Ser Thr Gly Leu Phe Ala Thr His Thr Leu Val Pro Pro Thr Pro Gly
 145 150 155 160
 Pro Ile Ala Ala Ala Gly Asn Leu Gly Leu Glu Asn Asn Leu Gly Leu
 165 170 175
 Val Ile Gly Val Gly Leu Val Phe Ala Ile Ile Ala Ala Met Ala Gly
 180 185 190
 Leu Val Trp Ala Tyr Phe Ser Arg Asn Leu Pro Ser Thr Glu Leu Asp
 195 200 205
 Leu Thr Glu Glu Ala Phe Glu Gly Lys Glu His Tyr Gly Glu Leu
 210 215 220
 Pro Gly Pro Trp Lys Ala Phe Ala Pro Ile Phe Val Pro Ile Ala Leu
 225 230 235 240
 Ile Cys Leu Gly Ser Val Ala Ser Tyr Pro Thr Ala Pro Leu Gly Asp
 245 250 255
 Gly Phe Leu Tyr Glu Ala Leu Asn Phe Leu Gly Lys Pro Leu Asn Ala
 260 265 270
 Leu Leu Ile Gly Leu Gly Phe Ala Val Leu Leu Ile Gln Gly Asn Glu
 275 280 285
 Lys Leu Lys Gly Phe Ala Arg His Thr Glu Lys Gly Leu Val Val Ser
 290 295 300
 Ala Pro Ile Ile Leu Ile Thr Gly Ala Gly Gly Ala Phe Gly Ala Val
 305 310 315 320
 Leu Ala Ala Thr Pro Leu Gly Asp Phe Leu Gly Gln Asn Leu Ser Thr
 325 330 335
 Leu Gly Leu Gly Val Ile Met Pro Phe Ile Val Ala Ala Ala Leu Lys
 340 345 350
 Ser Ala Gln Gly Ser Ser Thr Val Ala Leu Val Thr Ala Ser Ala Leu
 355 360 365
 Val Ala Pro Leu Leu Pro Gln Leu Gly Leu Asp Ser Asp Met Gly Arg
 370 375 380
 Val Leu Thr Val Met Ala Val Gly Ala Gly Ala Met Thr Val Ser His
 385 390 395 400
 Ala Asn Asp Ser Tyr Phe Trp Val Val Ser Gln Phe Ser Lys Met Asp
 405 410 415
 Val Ala Thr Ala Tyr Arg Ser His Thr Ala Ala Thr Leu Phe Met Gly
 420 425 430
 Leu Val Thr Ile Thr Ala Val Trp Leu Ala Ser Leu Ala Ala Leu
 435 440 445

<210> 10220
 <211> 1395
 <212> DNA
 <213> Enterobacter sakazakii

<220>
 <221> CDS
 <222> (1)..(1395)
 <223> transl_table=11

<400> 10220
 atg ttg agg ata ata acg atg aca gaa acc act ttc gct tat agc gcc 48
 Met Leu Arg Ile Ile Thr Met Thr Glu Thr Phe Ala Tyr Ser Ala
 1 5 10 15
 ggt acg ctg ctt ggc att gct gcc ggt gcc gtc gta ctg ctg gta 96
 Gly Thr Leu Leu Gly Ile Ala Ala Gly Ala Val Val Leu Leu Val
 20 25 30
 ctt atc atg cgc ttt aaa gtg cat gct ttt ctt gcg ctt acc ctg gtc 144
 Leu Ile Met Arg Phe Lys Val His Ala Phe Leu Ala Thr Leu Val
 35 40 45
 agt atc gtg gtg gcg ctg ttg acc aaa gtg ccg ttt gat aaa gtc gtg 192
 Ser Ile Val Val Ala Leu Leu Thr Lys Val Pro Phe Asp Lys Val Val
 50 55 60
 cct acg ctg ctg acc ggt ttt ggc agt acg ctt gcg ggc gtt gcg ctg 240

PF59083SeqList PF59083.txt

Pro 65	Thr	Leu	Leu	Thr	Gly 70	Phe	Gly	Ser	Thr	Leu 75	Ala	Gly	Val	Ala	Leu 80	
ctg	gtg	ggc	atc	ggc	gcg	atg	att	ggc	cgt	ctg	ctg	gaa	gtg	tcc	ggc	288
Leu	Val	Gly	Ile	Gly 85	Ala	Met	Ile	Gly	Arg 90	Leu	Leu	Glu	Val	Ser 95	Gly	
ggc	gcg	aaa	gtg	ctg	gcc	gat	acg	ctg	att	aac	aaa	ttc	ggg	gaa	cac	336
Gly	Ala	Lys	Val	Leu	Ala	Asp	Thr	Leu	Ile	Asn	Lys	Phe	Gly 110	Glu	His	
cgc	gcg	ccc	ttc	gcg	ctc	ggc	gtc	gcc	tcg	ctg	ctg	ttt	ggc	ttc	cct	384
Arg	Ala	Pro 115	Phe	Ala	Leu	Gly	Val 120	Ala	Ser	Leu	Leu	Phe	Gly 125	Phe	Pro	
atc	ttc	ttt	gac	gcg	ggg	ctt	gtc	gtc	atg	ctg	ccg	att	atc	ttc	agc	432
Ile	Phe 130	Phe	Asp	Ala	Gly 135	Leu	Val	Val	Met	Leu	Pro 140	Ile	Ile	Phe	Ser	
gtg	gcg	aaa	gag	ttt	ggc	ggc	tcg	acg	ctg	aaa	tac	gcc	ttc	ccg	gag	480
Val 145	Ala	Lys	Arg	Phe	Gly 150	Gly	Ser	Thr	Leu	Lys 155	Tyr	Ala	Phe	Pro	Ala 160	
gag	ggc	gag	ttt	gag	gcc	atg	cat	gag	ctg	gtg	ccg	ccg	cat	ccg	ggc	528
Ala	Gly	Ala	Phe	Ala 165	Ala	Met	His	Ala	Leu 170	Val	Pro	Pro	His	Pro 175	Gly	
ccg	gtt	gcc	gag	agc	gaa	ctg	ctg	ggg	gag	aac	atc	ggg	ctg	ctg	gtg	576
Pro	Val	Ala 180	Ala	Ser	Glu	Leu	Leu	Gly 185	Ala	Asn	Ile	Gly 190	Leu	Leu	Val	
att	gtc	ggg	ctg	att	atc	gag	atc	ccg	acc	tgg	tat	ttt	ggc	ggc	tat	624
Ile	Val	Gly 195	Leu	Ile	Ile	Ala 200	Ile	Pro	Thr	Trp	Tyr	Phe 205	Gly	Gly	Tyr	
ctg	tat	ggg	cag	tac	gcc	ggg	aaa	aaa	ttc	gac	att	aag	ctg	ccc	tct	672
Leu	Tyr 210	Gly	Gln	Tyr	Ala 215	Gly	Lys	Lys	Phe	Asp 220	Ile	Lys	Leu	Pro	Ser	
tct	ttc	ctt	ggc	gaa	gtg	gac	gcc	gat	ccg	acg	cac	gag	ccg	ccg	tca	720
Ser 225	Phe	Leu	Gly	Glu	Val 230	Asp	Ala	Asp	Pro	Thr 235	His	Arg	Pro	Pro	Ser 240	
ttc	ggc	atg	gtg	atc	acc	atc	ctg	ctg	ctg	ccg	ctg	ctg	ctg	att	ttc	768
Phe	Gly	Met	Val 245	Ile	Thr	Ile	Leu	Leu	Leu 250	Pro	Leu	Leu	Leu	Ile 255	Phe	
ctt	gat	acc	ggc	ctc	aac	acc	gcc	aaa	gtg	ctg	ggc	tgg	gtc	agc	gcc	816
Leu	Asp	Thr 260	Gly	Leu	Asn	Thr	Ala 265	Lys	Val	Leu	Gly	Trp	Val 270	Ser	Ala	
gat	aac	agc	gtg	gag	aac	ttc	ctg	cgt	atg	ctc	ggg	aaa	acc	ccg	gtc	864
Asp	Asn	Ser 275	Val	Ala	Asn	Phe 280	Leu	Arg	Met	Leu	Gly	Lys 285	Thr	Pro	Val	
gag	ctg	ctg	att	acc	gtc	ttt	ttc	gag	ctg	atg	gtg	ttc	agc	gag	aac	912
Ala	Leu 290	Leu	Ile	Thr	Val 295	Phe	Phe	Ala	Leu	Met	Val 300	Phe	Ser	Arg	Asn	
cac	agc	gag	cag	cat	ctg	gag	aaa	att	tgc	gac	ggc	gag	ctt	ggc	cct	960
His 305	Ser	Arg	Gln	His	Leu 310	Glu	Lys	Ile	Cys	Asp 315	Gly	Ala	Leu	Gly	Pro 320	
atc	tgc	ggc	atc	att	ctg	gtg	acc	ggc	gca	ggc	ggc	atg	ttc	ggc	ggc	1008
Ile	Cys	Gly	Ile	Ile 325	Leu	Val	Thr	Gly	Ala 330	Gly	Gly	Met	Phe	Gly 335	Gly	
gtg	ctg	gag	gcc	agc	ggc	atc	ggc	gac	gag	ctg	gag	ggc	gtg	ctc	tca	1056
Val	Leu	Arg	Ala 340	Ser	Gly	Ile	Gly	Asp	Ala 345	Leu	Ala	Gly	Val 350	Leu	Ser	
gac	acc	ggc	atg	ccg	gtg	att	ctc	gag	gag	ttt	gtt	atc	tcc	acc	gag	1104
Asp	Thr	Gly 355	Met	Pro	Val	Ile	Leu 360	Ala	Ala	Phe	Val	Ile	Ser	Thr	Ala	
ctg	gag	gtg	gag	cag	ggc	tcg	gag	acg	gtc	gag	ctg	acg	acc	acc	gcc	1152
Leu	Arg 370	Val	Ala	Gln	Gly	Ser 375	Ala	Thr	Val	Ala	Leu	Thr	Thr	Thr	Ala	
gag	ctg	gtc	gag	ccg	atg	gtg	cag	gag	acg	ccg	ggc	tta	agc	cag	ttc	1200
Ala 385	Leu	Val	Ala	Pro	Met 390	Val	Gln	Ala	Thr	Pro 395	Gly	Leu	Ser	Gln	Phe 400	
gac	ctt	tgc	ttt	att	gtt	atc	gcc	atc	gag	ggc	ggc	gag	acg	gtg	ctc	1248
Asp	Leu	Cys	Phe	Ile 405	Val	Ile	Ala	Ile	Ala 410	Gly	Gly	Ala	Thr	Val 415	Leu	
tca	cac	gtc	aac	gag	tcc	ggg	ttc	tgg	cta	gtg	ggc	cgt	ttc	ctt	gaa	1296
Ser	His	Val	Asn	Asp	Ser	Gly	Phe	Trp	Leu	Val	Gly	Arg	Phe	Leu	Glu	
atg	gac	gag	aaa	acc	acg	ctg	aaa	acc	tgg	acc	gtg	atg	gaa	acc	ctg	1344

PF59083SeqList PF59083.txt

Met Asp Glu Lys Thr Thr Leu Lys Thr Trp Thr Val Met Glu Thr Leu
 435 440 445
 ctg ggc acc atc gcc ttc ctg ctg gca gcc gtg ggg agc att ctg ctt
 Leu Gly Thr Ile Ala Phe Leu Leu Ala Ala Val Gly Ser Ile Leu Leu
 450 455 460
 taa

1392

1395

<210> 10221

<211> 464

<212> PRT

<213> Enterobacter sakazakii

<400> 10221

Met Leu Arg Ile Ile Thr Met Thr Glu Thr Thr Phe Ala Tyr Ser Ala
 1 5 10 15
 Gly Thr Leu Leu Gly Ile Ala Ala Gly Ala Val Val Leu Leu Leu Val
 20 25 30
 Leu Ile Met Arg Phe Lys Val His Ala Phe Leu Ala Leu Thr Leu Val
 35 40 45
 Ser Ile Val Val Ala Leu Leu Thr Lys Val Pro Phe Asp Lys Val Val
 50 55 60
 Pro Thr Leu Leu Thr Gly Phe Gly Ser Thr Leu Ala Gly Val Ala Leu
 65 70 75 80
 Leu Val Gly Ile Gly Ala Met Ile Gly Arg Leu Leu Glu Val Ser Gly
 85 90 95
 Gly Ala Lys Val Leu Ala Asp Thr Leu Ile Asn Lys Phe Gly Glu His
 100 105 110
 Arg Ala Pro Phe Ala Leu Gly Val Ala Ser Leu Leu Phe Gly Phe Pro
 115 120 125
 Ile Phe Phe Asp Ala Gly Leu Val Val Met Leu Pro Ile Ile Phe Ser
 130 135 140
 Val Ala Lys Arg Phe Gly Ser Thr Leu Lys Tyr Ala Phe Pro Ala
 145 150 155 160
 Ala Gly Ala Phe Ala Ala Met His Ala Leu Val Pro Pro His Pro Gly
 165 170 175
 Pro Val Ala Ala Ser Glu Leu Leu Gly Ala Asn Ile Gly Leu Leu Val
 180 185 190
 Ile Val Gly Leu Ile Ile Ala Ile Pro Thr Trp Tyr Phe Gly Gly Tyr
 195 200 205
 Leu Tyr Gly Gln Tyr Ala Gly Lys Lys Phe Asp Ile Lys Leu Pro Ser
 210 215 220
 Ser Phe Leu Gly Glu Val Asp Ala Asp Pro Thr His Arg Pro Pro Ser
 225 230 235 240
 Phe Gly Met Val Ile Thr Ile Leu Leu Leu Pro Leu Leu Leu Ile Phe
 245 250 255
 Leu Asp Thr Gly Leu Asn Thr Ala Lys Val Leu Gly Trp Val Ser Ala
 260 265 270
 Asp Asn Ser Val Ala Asn Phe Leu Arg Met Leu Gly Lys Thr Pro Val
 275 280 285
 Ala Leu Leu Ile Thr Val Phe Phe Ala Leu Met Val Phe Ser Arg Asn
 290 295 300
 His Ser Arg Gln His Leu Glu Lys Ile Cys Asp Gly Ala Leu Gly Pro
 305 310 315 320
 Ile Cys Gly Ile Ile Leu Val Thr Gly Ala Gly Gly Met Phe Gly Gly
 325 330 335
 Val Leu Arg Ala Ser Gly Ile Gly Asp Ala Leu Ala Gly Val Leu Ser
 340 345 350
 Asp Thr Gly Met Pro Val Ile Leu Ala Ala Phe Val Ile Ser Thr Ala
 355 360 365
 Leu Arg Val Ala Gln Gly Ser Ala Thr Val Ala Leu Thr Thr Thr Ala
 370 375 380
 Ala Leu Val Ala Pro Met Val Gln Ala Thr Pro Gly Leu Ser Gln Phe
 385 390 395 400
 Asp Leu Cys Phe Ile Val Ile Ala Ile Ala Gly Gly Ala Thr Val Leu
 405 410 415
 Ser His Val Asn Asp Ser Gly Phe Trp Leu Val Gly Arg Phe Leu Glu
 420 425 430

PF59083SeqList PF59083.txt

Met Asp Glu Lys Thr Thr Leu Lys Thr Trp Thr Val Met Glu Thr Leu
 435 440 445
 Leu Gly Thr Ile Ala Phe Leu Leu Ala Ala Val Gly Ser Ile Leu Leu
 450 455 460

<210> 10222
 <211> 1320
 <212> DNA
 <213> Escherichia coli B

<220>
 <221> CDS
 <222> (1)..(1320)
 <223> transl_table=11

<400> 10222
 atg cca tta atc att att gcg gca ggc gtc gcg ctg ctt ctt atc ctg 48
 Met Pro Leu Ile Ile Ile Ala Ala Gly Val Ala Leu Leu Leu Ile Leu
 1 5 10 15
 atg atc gtc ttt aaa gtt aac ggc ttt att gcc ctc gtt ctg gta gct 96
 Met Ile Val Phe Lys Val Asn Gly Phe Ile Ala Leu Val Leu Val Ala
 20 25 30
 gcc gtc gtc gga ttt gcc gaa ggg atg gat gca cag gcc gtc ctg cac 144
 Ala Val Val Gly Phe Ala Glu Gly Met Asp Ala Gln Ala Val Leu His
 35 40 45
 tct ata caa aat ggt atc ggc agc acg ctc ggc ggg ctg gca atg atc 192
 Ser Ile Gln Asn Gly Ile Gly Ser Thr Leu Gly Gly Leu Ala Met Ile
 50 55 60
 ctc ggt ttc ggg gcc atg tta ggc aag ctg att tct gat acg ggt gcg 240
 Leu Gly Phe Gly Ala Met Leu Gly Lys Leu Ile Ser Asp Thr Gly Ala
 65 70 75 80
 gca caa cgt atc gcc act acg ctg att gct act ttt ggt aaa aaa cgc 288
 Ala Gln Arg Ile Ala Thr Thr Leu Ile Ala Thr Phe Gly Lys Lys Arg
 85 90 95
 gtg caa tgg gcg cta gtg atc acc ggt ctg gtt gtg ggc ctc gcc atg 336
 Val Gln Trp Ala Leu Val Ile Thr Gly Leu Val Val Gly Leu Ala Met
 100 105 110
 ttt ttt gaa gtg ggt ttt gtc ctg ctg ttg ccg ttg gta ttt acc atc 384
 Phe Phe Glu Val Gly Phe Val Leu Leu Leu Pro Leu Val Phe Thr Ile
 115 120 125
 gta gca tca tca gga tta ccc ctg ttg tat gtt ggc gta cca atg gta 432
 Val Ala Ser Ser Gly Leu Pro Leu Leu Tyr Val Gly Val Pro Met Val
 130 135 140
 gca gcg ctc tct gta acc cac tgt ttt ctg ccg cca cat cca ggg cct 480
 Ala Ala Leu Ser Val Thr His Cys Phe Leu Pro Pro His Pro Gly Pro
 145 150 155 160
 act gcc atc gcg act atc ttt gag gct aat ctc gga acg act tta ctg 528
 Thr Ala Ile Ala Thr Ile Phe Glu Ala Asn Leu Gly Thr Thr Leu Leu
 165 170 175
 tat gga ttt atc att acc att ccg aca gtt att gtc gca gga ccg ctg 576
 Tyr Gly Phe Ile Ile Thr Ile Pro Thr Val Ile Val Ala Gly Pro Leu
 180 185 190
 ttt tct aaa ctg cta act cgc ttt gag aaa gca cca ccg gaa ggc tta 624
 Phe Ser Lys Leu Leu Thr Arg Phe Glu Lys Ala Pro Pro Glu Gly Leu
 195 200 205
 ttt aat cct cat ctg ttt agc gaa gag gag atg ccc tcc ttc tgg aac 672
 Phe Asn Pro His Leu Phe Ser Glu Glu Glu Met Pro Ser Phe Trp Asn
 210 215 220
 agt att ttc gct gcc gtg atc ccg gtc atc ctg atg gct atc gcc gcc 720
 Ser Ile Phe Ala Ala Val Ile Pro Val Ile Leu Met Ala Ile Ala Ala
 225 230 235 240
 gtt tgt gaa att acg tta ccg aaa act aac acc gtg cgc ctc ttc ttt 768
 Val Cys Glu Ile Thr Leu Pro Lys Thr Asn Thr Val Arg Leu Phe Phe
 245 250 255
 gaa ttt gtc ggt aac cct gcc gtt gcg ctg ttt att gcc att gtt att 816
 Glu Phe Val Gly Asn Pro Ala Val Ala Leu Phe Ile Ala Ile Val Ile
 260 265 270
 gcg att ttc aca ctg ggc cga cgt aat gga cgc acc atc gag caa atc 864
 Ala Ile Phe Thr Leu Gly Arg Arg Asn Gly Arg Thr Ile Glu Gln Ile

PF59083SeqList PF59083.txt

275	280	285	
atg gat atc att ggg gat tct ata ggc gct atc gcg atg att gtg ttt	Met Asp Ile Ile Gly Asp Ser Ile Gly Ala Ile Ala Met Ile Val Phe	912	
290	295	300	
att atc gct ggc ggc ggc ggc ttt aag cag gta tta gta gat agc ggt	Ile Ile Ala Gly Gly Gly Ala Phe Lys Gln Val Val Val Asp Ser Gly	960	
305	310	315	
gtc ggg cac tat att tca cac tta atg acc gga act aca ctt tcg ccg	Val Gly His Tyr Ile Ser His Leu Met Thr Gly Thr Thr Leu Ser Pro	1008	
325	330	335	
tta ttg atg tgc tgg act gtt gcg gcg ctg ttg cgt atc gct ctg ggc	Leu Leu Met Cys Trp Thr Val Ala Ala Leu Leu Arg Ile Ala Leu Gly	1056	
340	345	350	
tct gcc acc gtc gcg gcc att acc acc gcg ggt gtg gtg ttg ccg att	Ser Ala Thr Val Ala Ala Ile Thr Thr Ala Gly Val Val Leu Pro Ile	1104	
355	360	365	
atc aac gtt acc cat gcc gat ccc gct tta atg gta ctg gca acc ggt	Ile Asn Val Thr His Ala Asp Pro Ala Leu Met Val Leu Ala Thr Gly	1152	
370	375	380	
gcg ggc agc gtg atc gcg tca cac gta aac gac cct ggc ttc tgg cta	Ala Gly Ser Val Ile Ala Ser His Val Asn Asp Pro Gly Phe Trp Leu	1200	
385	390	395	
ttt aaa ggg tat ttt aat ctg acg gtt ggt gaa acg ttg cgt acc tgg	Phe Lys Gly Tyr Phe Asn Leu Thr Val Gly Glu Thr Leu Arg Thr Trp	1248	
405	410	415	
acg gtg atg gaa acc ctt att tct att atg ggt ttg ctg ggc gtg tta	Thr Val Met Glu Thr Leu Ile Ser Ile Met Gly Leu Leu Gly Val Leu	1296	
420	425	430	
gcc att aac gcc gta ttg cac tga	Ala Ile Asn Ala Val Leu His	1320	
435			

<210> 10223

<211> 439

<212> PRT

<213> Escherichia coli B

<400> 10223

Met Pro Leu Ile Ile Ile Ala Ala Gly Val Ala Leu Leu Leu Ile Leu	1 5 10 15
Met Ile Val Phe Lys Val Asn Gly Phe Ile Ala Leu Val Leu Val Ala	20 25 30
Ala Val Val Gly Phe Ala Glu Gly Met Asp Ala Gln Ala Val Leu His	35 40 45
Ser Ile Gln Asn Gly Ile Gly Ser Thr Leu Gly Gly Leu Ala Met Ile	50 55 60
Leu Gly Phe Gly Ala Met Leu Gly Lys Leu Ile Ser Asp Thr Gly Ala	65 70 75 80
Ala Gln Arg Ile Ala Thr Thr Leu Ile Ala Thr Phe Gly Lys Lys Arg	85 90 95
Val Gln Trp Ala Leu Val Ile Thr Gly Leu Val Val Gly Leu Ala Met	100 105 110
Phe Phe Glu Val Gly Phe Val Leu Leu Leu Pro Leu Val Phe Thr Ile	115 120 125
Val Ala Ser Ser Gly Leu Pro Leu Leu Tyr Val Gly Val Pro Met Val	130 135 140
Ala Ala Leu Ser Val Thr His Cys Phe Leu Pro Pro His Pro Gly Pro	145 150 155 160
Thr Ala Ile Ala Thr Ile Phe Glu Ala Asn Leu Gly Thr Thr Leu Leu	165 170 175
Tyr Gly Phe Ile Ile Thr Ile Pro Thr Val Ile Val Ala Gly Pro Leu	180 185 190
Phe Ser Lys Leu Leu Thr Arg Phe Glu Lys Ala Pro Pro Glu Gly Leu	195 200 205
Phe Asn Pro His Leu Phe Ser Glu Glu Glu Met Pro Ser Phe Trp Asn	210 215 220
Ser Ile Phe Ala Ala Val Ile Pro Val Ile Leu Met Ala Ile Ala Ala	225 230 235 240
Val Cys Glu Ile Thr Leu Pro Lys Thr Asn Thr Val Arg Leu Phe Phe	

PF59083SeqList PF59083.txt

245 250 255
 Glu Phe Val Gly Asn Pro Ala Val Ala Leu Phe Ile Ala Ile Val Ile
 260 265 270
 Ala Ile Phe Thr Leu Gly Arg Arg Asn Gly Arg Thr Ile Glu Gln Ile
 275 280 285
 Met Asp Ile Ile Gly Asp Ser Ile Gly Ala Ile Ala Met Ile Val Phe
 290 295 300
 Ile Ile Ala Gly Gly Gly Ala Phe Lys Gln Val Leu Val Asp Ser Gly
 305 310 315 320
 Val Gly His Tyr Ile Ser His Leu Met Thr Gly Thr Thr Leu Ser Pro
 325 330 335
 Leu Leu Met Cys Trp Thr Val Ala Ala Leu Leu Arg Ile Ala Leu Gly
 340 345 350
 Ser Ala Thr Val Ala Ala Ile Thr Thr Ala Gly Val Val Leu Pro Ile
 355 360 365
 Ile Asn Val Thr His Ala Asp Pro Ala Leu Met Val Leu Ala Thr Gly
 370 375 380
 Ala Gly Ser Val Ile Ala Ser His Val Asn Asp Pro Gly Phe Trp Leu
 385 390 395 400
 Phe Lys Gly Tyr Phe Asn Leu Thr Val Gly Glu Thr Leu Arg Thr Trp
 405 410 415
 Thr Val Met Glu Thr Leu Ile Ser Ile Met Gly Leu Leu Gly Val Leu
 420 425 430
 Ala Ile Asn Ala Val Leu His
 435

<210> 10224
 <211> 1365
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1365)
 <223> transl_table=11

<400> 10224
 atg tcc aca att aca ttg tta tgc att gcg tta gct ggc gta atc atg 48
 Met Ser Thr Ile Thr Leu Leu Cys Ile Ala Leu Ala Gly Val Ile Met 15
 1 5 10
 ctg ttg ctg ctg gtc atc aag gca aag gta caa cca ttc gtt gct ctg 96
 Leu Leu Leu Leu Val Ile Lys Ala Lys Val Gln Pro Phe Val Ala Leu 20 25 30
 ctc ctc gtc agc ctg tta gtc gca ctt gcg gcg ggt ata ccg gcg ggc 144
 Leu Leu Val Ser Leu Leu Val Ala Leu Ala Ala Gly Ile Pro Ala Gly 35 40 45
 gaa gtg ggt aaa gtg atg atc gcc ggg atg ggc ggt gtg ctt ggt tcc 192
 Glu Val Gly Lys Val Met Ile Ala Gly Met Gly Gly Val Leu Gly Ser 50 55 60
 gtc act att att att ggt ggc gct atg ctg ggg cgt atg atc gaa 240
 Val Thr Ile Ile Ile Gly Leu Gly Ala Met Leu Gly Arg Met Ile Glu 65 70 75 80
 cac tct ggt ggt gca gag tca ctg gct aat tat ttc agt cgc aag tta 288
 His Ser Gly Gly Ala Glu Ser Leu Ala Asn Tyr Phe Ser Arg Lys Leu 85 90 95
 ggt gac aaa cga act atc gct gcg ctg act ctg gca gcg ttc ttc ctc 336
 Gly Asp Lys Arg Thr Ile Ala Ala Leu Thr Leu Ala Ala Phe Phe Leu 100 105 110
 ggt att ccc gtc ttc ttt gat gtc ggc ttt att att ctt gcg cca atc 384
 Gly Ile Pro Val Phe Phe Asp Val Gly Phe Ile Ile ctt Ala Pro Ile 115 120 125
 att tac ggt ttt gcc aag gtt gcc aaa ata tcg cca ctc aaa ttt ggc 432
 Ile Tyr Gly Phe Ala Lys Val Ala Lys Ile Ser Pro Leu Lys Phe Gly 130 135 140
 ctg cct gtc gct gga atc atg cta act gtt cat gtg gcg gta ccg ccg 480
 Leu Pro Val Ala Gly Ile Met Leu Thr Val His Val Ala Val Pro Pro 145 150 155 160
 cat cca ggc cct gtc gcc gca gcg ggg tta ctc cac gca gac atc ggc 528
 His Pro Gly Pro Val Ala Ala Ala Gly Leu Leu His Ala Asp Ile Gly

PF59083SeqList PF59083.txt

					165					170					175		
tgg	cta	acc	atc	atc	ggt	att	gcg	att	tct	att	ccc	gta	ggg	att	gtt		576
Trp	Leu	Thr	Ile	Ile	Gly	Ile	Ala	Ile	Ser	Ile	Pro	Val	Gly	Ile	Val		
			180						185								
ggc	tac	ttt	gca	gcg	aaa	ata	atc	aat	acg	cg	caa	tat	gcg	atg	tcg		624
Gly	Tyr	Phe	Ala	Ala	Lys	Ile	Ile	Asn	Thr	Arg	Gln	Tyr	Ala	Met	Ser		
		195						200				205					
gtg	gaa	gta	ctg	gaa	cag	atg	caa	ctg	gct	ccg	gcc	agt	gag	gaa	ggc		672
Val	Glu	Val	Leu	Glu	Gln	Met	Gln	Leu	Ala	Pro	Ala	Ser	Glu	Glu	Gly		
	210					215					220						
gca	aca	aaa	tta	agc	gat	aaa	ata	aat	cca	ccg	ggc	gtc	gcg	ctg	gtc		720
Ala	Thr	Lys	Leu	Ser	Asp	Lys	Ile	Asn	Pro	Pro	Gly	Val	Ala	Leu	Val		
225					230					235					240		
acc	tcg	cta	att	ggt	att	cct	atc	gcg	att	atc	atg	gcg	ggg	acg	ggt		768
Thr	Ser	Leu	Ile	Val	Ile	Pro	Ile	Ala	Ile	Ile	Met	Ala	Gly	Thr	Val		
			245						250					255			
tcc	gca	aca	ctg	atg	ccg	cct	tcg	cat	ccc	ctg	ctt	ggg	acg	cta	cag		816
Ser	Ala	Thr	Leu	Met	Pro	Pro	Ser	His	Pro	Leu	Leu	Gly	Thr	Leu	Gln		
			260					265					270				
ctg	atc	ggc	tca	cca	atg	gta	gct	cta	atg	att	gcg	ctg	gtg	ctg	gca		864
Leu	Ile	Gly	Ser	Pro	Met	Val	Ala	Leu	Met	Ile	Ala	Leu	Val	Leu	Ala		
		275				280						285					
ttc	tgg	tta	ttg	gct	tta	cgt	cg	ggc	tgg	agc	tta	caa	cac	acc	agc		912
Phe	Trp	Leu	Leu	Ala	Leu	Arg	Arg	Gly	Trp	Ser	Leu	Gln	His	Thr	Ser		
	290					295					300						
gac	att	atg	ggc	tca	gcc	ctt	ccc	act	gcg	gcg	gta	gtg	att	ttg	ggt		960
Asp	Ile	Met	Gly	Ser	Ala	Leu	Pro	Thr	Ala	Ala	Val	Val	Ile	Leu	Val		
305					310				315						320		
act	ggg	gct	gga	ggg	gta	ttt	ggc	aaa	gtg	ctg	gtg	gaa	tcg	ggc	gtc		1008
Thr	Gly	Ala	Gly	Gly	Val	Phe	Gly	Lys	Val	Leu	Val	Glu	Ser	Gly	Val		
			325						330					335			
ggc	aaa	gcc	ctt	gcc	aat	atg	cta	caa	atg	att	gac	ctg	cct	ctg	tta		1056
Gly	Lys	Ala	Leu	Ala	Asn	Met	Leu	Gln	Met	Ile	Asp	Leu	Pro	Leu	Leu		
		340						345					350				
cca	gcc	gca	ttt	att	att	tca	ctg	gct	ctg	cgt	gca	tcg	cag	ggg	tca		1104
Pro	Ala	Ala	Phe	Ile	Ile	Ser	Leu	Ala	Leu	Arg	Ala	Ser	Gln	Gly	Ser		
		355					360					365					
gca	acc	gta	gca	atc	ctg	aca	acc	ggc	ggg	tta	ctc	tca	gaa	gcg	gtg		1152
Ala	Thr	Val	Ala	Ile	Leu	Thr	Thr	Gly	Gly	Leu	Leu	Ser	Glu	Ala	Val		
	370					375					380						
atg	gga	ttg	aat	ccg	att	cag	tgc	gta	ttg	gtg	acg	ctg	gca	gcc	tgc		1200
Met	Gly	Leu	Asn	Pro	Ile	Gln	Cys	Val	Leu	Val	Thr	Leu	Ala	Ala	Cys		
385					390					395					400		
ttt	ggg	ggg	ctt	ggc	gcg	tca	cat	att	aat	gac	tca	ggg	ttc	ttg	att		1248
Phe	Gly	Gly	Leu	Gly	Ala	Ser	His	Ile	Asn	Asp	Ser	Gly	Phe	Trp	Ile		
			405						410					415			
gtg	acc	aaa	tat	ctg	ggg	ttg	tcg	gta	gca	gac	ggg	ctg	aaa	acc	ttg		1296
Val	Thr	Lys	Tyr	Leu	Gly	Leu	Ser	Val	Ala	Asp	Gly	Leu	Lys	Thr	Trp		
			420					425					430				
aca	gtg	tta	acg	acc	att	ctc	ggg	ttt	acc	gga	ttc	tta	att	acc	ttg		1344
Thr	Val	Leu	Thr	Thr	Ile	Leu	Gly	Phe	Thr	Gly	Phe	Leu	Ile	Thr	Trp		
		435					440					445					
tgc	gta	tgg	gcg	gta	att	tga											1365
Cys	Val	Trp	Ala	Val	Ile												
	450																

<210> 10225

<211> 454

<212> PRT

<213> Escherichia coli

<400> 10225

Met	Ser	Thr	Ile	Thr	Leu	Leu	Cys	Ile	Ala	Leu	Ala	Gly	Val	Ile	Met
1				5					10					15	
Leu	Leu	Leu	Leu	Val	Ile	Lys	Ala	Lys	Val	Gln	Pro	Phe	Val	Ala	Leu
			20					25					30		
Leu	Leu	Val	Ser	Leu	Leu	Val	Ala	Leu	Ala	Ala	Gly	Ile	Pro	Ala	Gly
		35					40				45				
Glu	Val	Gly	Lys	Val	Met	Ile	Ala	Gly	Met	Gly	Gly	Val	Leu	Gly	Ser

PF59083SeqList PF59083.txt

50 55 60
 Val Thr Ile Ile Ile Gly Leu Gly Ala Met Leu Gly Arg Met Ile Glu
 65 70 75 80
 His Ser Gly Gly Ala Glu Ser Leu Ala Asn Tyr Phe Ser Arg Lys Leu
 85 90 95
 Gly Asp Lys Arg Thr Ile Ala Ala Leu Thr Leu Ala Ala Phe Phe Leu
 100 105 110
 Gly Ile Pro Val Phe Phe Asp Val Gly Phe Ile Ile Leu Ala Pro Ile
 115 120 125
 Ile Tyr Gly Phe Ala Lys Val Ala Lys Ile Ser Pro Leu Lys Phe Gly
 130 135 140
 Leu Pro Val Ala Gly Ile Met Leu Thr Val His Val Ala Val Pro Pro
 145 150 155 160
 His Pro Gly Pro Val Ala Ala Ala Gly Leu Leu His Ala Asp Ile Gly
 165 170 175
 Trp Leu Thr Ile Gly Ile Ala Ile Ser Ile Pro Val Gly Ile Val
 180 185 190
 Gly Tyr Phe Ala Ala Lys Ile Ile Asn Thr Arg Gln Tyr Ala Met Ser
 195 200 205
 Val Glu Val Leu Glu Gln Met Gln Leu Ala Pro Ala Ser Glu Glu Gly
 210 215 220
 Ala Thr Lys Leu Ser Asp Lys Ile Asn Pro Pro Gly Val Ala Leu Val
 225 230 235 240
 Thr Ser Leu Ile Val Ile Pro Ile Ala Ile Ile Met Ala Gly Thr Val
 245 250 255
 Ser Ala Thr Leu Met Pro Pro Ser His Pro Leu Leu Gly Thr Leu Gln
 260 265 270
 Leu Ile Gly Ser Pro Met Val Ala Leu Met Ile Ala Leu Val Leu Ala
 275 280 285
 Phe Trp Leu Leu Ala Leu Arg Arg Gly Trp Ser Leu Gln His Thr Ser
 290 295 300
 Asp Ile Met Gly Ser Ala Leu Pro Thr Ala Ala Val Val Ile Leu Val
 305 310 315 320
 Thr Gly Ala Gly Gly Val Phe Gly Lys Val Leu Val Glu Ser Gly Val
 325 330 335
 Gly Lys Ala Leu Ala Asn Met Leu Gln Met Ile Asp Leu Pro Leu Leu
 340 345 350
 Pro Ala Ala Phe Ile Ile Ser Leu Ala Leu Arg Ala Ser Gln Gly Ser
 355 360 365
 Ala Thr Val Ala Ile Leu Thr Thr Gly Gly Leu Leu Ser Glu Ala Val
 370 375 380
 Met Gly Leu Asn Pro Ile Gln Cys Val Leu Val Thr Leu Ala Ala Cys
 385 390 395 400
 Phe Gly Gly Leu Gly Ala Ser His Ile Asn Asp Ser Gly Phe Trp Ile
 405 410 415
 Val Thr Lys Tyr Leu Gly Leu Ser Val Ala Asp Gly Leu Lys Thr Trp
 420 425 430
 Thr Val Leu Thr Thr Ile Leu Gly Phe Thr Gly Phe Leu Ile Thr Trp
 435 440 445
 Cys Val Trp Ala Val Ile
 450

<210> 10226
 <211> 1365
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1365)
 <223> transl_table=11

<400> 10226	
atg tcc aca att aca ttg tta tgc att gcg tta gct ggc gta atc atg	48
Met Ser Thr Ile Thr Leu Leu Cys Ile Ala Leu Ala Gly Val Ile Met	
1 5 10 15	
ctg ttg cta ctg gtc atc aag gca aag gta caa cca ttc gtt gct ctg	96
Leu Leu Leu Leu Val Ile Lys Ala Lys Val Gln Pro Phe Val Ala Leu	
20 25 30	

PF59083SeqList PF59083.txt

ctc	ctc	gtc	agc	ctg	tta	gtc	gca	ctt	gcg	gcg	ggg	ata	ccg	gcg	ggc	144
Leu	Leu	Val	Ser	Leu	Leu	Val	Ala	Leu	Ala	Ala	Gly	Ile	Pro	Ala	Gly	
		35					40					45				
gaa	gtg	ggg	aaa	gtg	atg	atc	gcc	ggg	atg	ggc	ggg	gtg	ctt	ggg	tcc	192
Glu	Val	Gly	Lys	Val	Met	Ile	Ala	Gly	Met	Gly	Gly	Val	Leu	Gly	Ser	
	50					55					60					
gtc	act	att	att	att	ggg	ctg	ggc	gct	atg	ctg	ggg	cgt	atg	atc	gaa	240
Val	Thr	Ile	Ile	Ile	Gly	Leu	Gly	Ala	Met	Leu	Gly	Arg	Met	Ile	Glu	
65					70					75					80	
cac	tct	ggg	ggg	gca	gag	tca	ctg	gct	aat	tat	ttc	agt	cgc	aag	cta	288
His	Ser	Gly	Gly	Ala	Glu	Ser	Leu	Ala	Asn	Tyr	Phe	Ser	Arg	Lys	Leu	
				85					90					95		
ggg	gac	aaa	cga	act	atc	gct	gcg	ctg	act	ctg	gca	gcg	ttc	ttc	ctc	336
Gly	Asp	Lys	Arg	Thr	Ile	Ala	Ala	Leu	Thr	Leu	Ala	Ala	Phe	Phe	Leu	
		100						105					110			
ggg	att	ccc	gtc	ttc	ttt	gat	gtc	ggc	ttt	att	att	ctt	gcg	cca	atc	384
Gly	Ile	Pro	Val	Phe	Phe	Asp	Val	Gly	Phe	Ile	Ile	Leu	Ala	Pro	Ile	
		115					120					125				
att	tac	ggg	ttt	gcc	aag	gtt	gcc	aaa	ata	tca	cca	ctc	aaa	ttt	ggc	432
Ile	Tyr	Gly	Phe	Ala	Lys	Val	Ala	Lys	Ile	Ser	Pro	Leu	Lys	Phe	Gly	
	130					135					140					
ctg	cct	gtc	gct	ggg	atc	atg	ctc	act	gtt	cac	gtg	gcg	gta	ccg	ccg	480
Leu	Pro	Val	Ala	Gly	Ile	Met	Leu	Thr	Val	His	Val	Ala	Val	Pro	Pro	
145					150					155					160	
cat	cca	ggc	cct	gtc	gcc	gca	gcg	ggg	tta	ctc	cac	gca	gac	atc	ggc	528
His	Pro	Gly	Pro	Val	Ala	Ala	Ala	Gly	Leu	Leu	His	Ala	Asp	Ile	Gly	
				165					170					175		
tgg	cta	acc	atc	atc	ggg	att	gcg	att	tct	att	ccc	gta	ggg	att	gtt	576
Trp	Leu	Thr	Ile	Ile	Gly	Ile	Ala	Ile	Ser	Ile	Pro	Val	Gly	Ile	Val	
		180						185					190			
ggc	tac	ttt	gca	gcg	aaa	ata	atc	aat	aag	cgc	caa	tat	gcg	atg	tcg	624
Gly	Tyr	Phe	Ala	Ala	Lys	Ile	Ile	Asn	Lys	Arg	Gln	Tyr	Ala	Met	Ser	
		195				200						205				
gtc	gag	gta	ctg	gaa	cag	atg	caa	ctg	gct	ccg	gcc	agt	gag	gaa	ggc	672
Val	Glu	Val	Leu	Glu	Gln	Met	Gln	Leu	Ala	Pro	Ala	Ser	Glu	Glu	Gly	
	210					215					220					
gcg	aca	aaa	tta	agc	gat	aaa	ata	aat	cca	ccg	ggc	gtc	gcg	ctg	gtc	720
Ala	Thr	Lys	Leu	Ser	Asp	Lys	Ile	Asn	Pro	Pro	Gly	Val	Ala	Leu	Val	
225					230					235					240	
acc	tcg	cta	att	gtt	att	cct	atc	gcg	att	atc	atg	gcg	ggg	acg	gtt	768
Thr	Ser	Leu	Ile	Val	Ile	Pro	Ile	Ala	Ile	Ile	Met	Ala	Gly	Thr	Val	
				245					250					255		
tcc	gca	aca	ctg	atg	ccg	cct	tcg	cat	ccc	ctg	ctt	ggg	acg	cta	cag	816
Ser	Ala	Thr	Leu	Met	Pro	Pro	Ser	His	Pro	Leu	Leu	Gly	Thr	Leu	Gln	
		260						265					270			
ctg	atc	ggc	tca	cca	atg	gta	gct	cta	atg	att	gcg	ctg	gtg	ctg	gca	864
Leu	Ile	Gly	Ser	Pro	Met	Val	Ala	Leu	Met	Ile	Ala	Leu	Val	Leu	Ala	
		275				280						285				
ttc	tgg	tta	ttg	gct	tta	cgt	cgc	ggc	tgg	agc	tta	caa	cac	acc	agc	912
Phe	Trp	Leu	Leu	Ala	Leu	Arg	Arg	Gly	Trp	Ser	Leu	Gln	His	Thr	Ser	
	290					295					300					
gac	att	atg	ggc	tca	gcc	ctt	ccc	act	gcg	gcg	gta	gtg	att	ttg	gtt	960
Asp	Ile	Met	Gly	Ser	Ala	Leu	Pro	Thr	Ala	Ala	Val	Val	Ile	Leu	Val	
305					310					315					320	
act	ggg	gct	gga	ggg	gta	ttt	ggc	aaa	gtg	ctg	gtg	gaa	tcg	ggc	gtc	1008
Thr	Gly	Ala	Gly	Gly	Val	Phe	Gly	Lys	Val	Leu	Val	Glu	Ser	Gly	Val	
				325					330					335		
ggg	aaa	gcc	ctt	gcc	aac	atg	tta	caa	atg	att	gac	ctg	cct	ctg	tta	1056
Gly	Lys	Ala	Leu	Ala	Asn	Met	Leu	Gln	Met	Ile	Asp	Leu	Pro	Leu	Leu	
		340						345					350			
cca	gcc	gca	ttt	att	att	tca	ctg	gcg	ctg	cgt	gca	tcg	cag	ggg	tca	1104
Pro	Ala	Ala	Phe	Ile	Ile	Ser	Leu	Ala	Leu	Arg	Ala	Ser	Gln	Gly	Ser	
		355						360				365				
gca	acc	gta	gca	atc	ctg	aca	acc	ggc	ggg	tta	ctc	tca	gaa	gcg	gtg	1152
Ala	Thr	Val	Ala	Ile	Leu	Thr	Thr	Gly	Gly	Leu	Leu	Ser	Glu	Ala	Val	
		370				375					380					
atg	gga	ttg	aat	cca	att	cag	tgc	gta	ttg	gtg	acg	ctg	gca	gcc	tgc	1200
Met	Gly	Leu	Asn	Pro	Ile	Gln	Cys	Val	Leu	Val	Thr	Leu	Ala	Ala	Cys	
385					390					395					400	

PF59083SeqList PF59083.txt

ttt ggt ggg ctt ggc gcg tca cat att aat gac tca ggg ttc tgg att	1248
Phe Gly Gly Leu Gly Ala Ser His Ile Asn Asp Ser Gly Phe Trp Ile	
gtg acc aaa tat ctg ggg ttg tcg gta gca gac ggg ctg aaa acc tgg	1296
Val Thr Lys Tyr Leu Gly Leu Ser Val Ala Asp Gly Leu Lys Thr Trp	
aca gtg tta acg acc att ctc ggt ttt acc gga ttc tta att acc tgg	1344
Thr Val Leu Thr Thr Ile Leu Gly Phe Thr Gly Phe Leu Ile Thr Trp	
tgc gta tgg gcg gta att tga	1365
Cys Val Trp Ala Val Ile	

<210> 10227
 <211> 454
 <212> PRT
 <213> Escherichia coli

<400> 10227

Met Ser Thr Ile Thr Leu Leu Cys Ile Ala Leu Ala Gly Val Ile Met	
1 5 10 15	
Leu Leu Leu Leu Val Ile Lys Ala Lys Val Gln Pro Phe Val Ala Leu	
20 25 30	
Leu Leu Val Ser Leu Leu Val Ala Leu Ala Ala Gly Ile Pro Ala Gly	
35 40 45	
Glu Val Gly Lys Val Met Ile Ala Gly Met Gly Gly Val Leu Gly Ser	
50 55 60	
Val Thr Ile Ile Ile Gly Leu Gly Ala Met Leu Gly Arg Met Ile Glu	
65 70 75 80	
His Ser Gly Gly Ala Glu Ser Leu Ala Asn Tyr Phe Ser Arg Lys Leu	
85 90 95	
Gly Asp Lys Arg Thr Ile Ala Ala Leu Thr Leu Ala Ala Phe Phe Leu	
100 105 110	
Gly Ile Pro Val Phe Phe Asp Val Gly Phe Ile Ile Leu Ala Pro Ile	
115 120 125	
Ile Tyr Gly Phe Ala Lys Val Ala Lys Ile Ser Pro Leu Lys Phe Gly	
130 135 140	
Leu Pro Val Ala Gly Ile Met Leu Thr Val His Val Ala Val Pro Pro	
145 150 155 160	
His Pro Gly Pro Val Ala Ala Ala Gly Leu His Ala Asp Ile Gly	
165 170 175	
Trp Leu Thr Ile Ile Gly Ile Ala Ile Ser Ile Pro Val Gly Ile Val	
180 185 190	
Gly Tyr Phe Ala Ala Lys Ile Ile Asn Lys Arg Gln Tyr Ala Met Ser	
195 200 205	
Val Glu Val Leu Glu Gln Met Gln Leu Ala Pro Ala Ser Glu Glu Gly	
210 215 220	
Ala Thr Lys Leu Ser Asp Lys Ile Asn Pro Pro Gly Val Ala Leu Val	
225 230 235 240	
Thr Ser Leu Ile Val Ile Pro Ile Ala Ile Ile Met Ala Gly Thr Val	
245 250 255	
Ser Ala Thr Leu Met Pro Pro Ser His Pro Leu Leu Gly Thr Leu Gln	
260 265 270	
Leu Ile Gly Ser Pro Met Val Ala Leu Met Ile Ala Leu Val Leu Ala	
275 280 285	
Phe Trp Leu Leu Ala Leu Arg Arg Gly Trp Ser Leu Gln His Thr Ser	
290 295 300	
Asp Ile Met Gly Ser Ala Leu Pro Thr Ala Ala Val Val Ile Leu Val	
305 310 315 320	
Thr Gly Ala Gly Gly Val Phe Gly Lys Val Leu Val Glu Ser Gly Val	
325 330 335	
Gly Lys Ala Leu Ala Asn Met Leu Gln Met Ile Asp Leu Pro Leu Leu	
340 345 350	
Pro Ala Ala Phe Ile Ile Ser Leu Ala Leu Arg Ala Ser Gln Gly Ser	
355 360 365	
Ala Thr Val Ala Ile Leu Thr Thr Gly Gly Leu Leu Ser Glu Ala Val	
370 375 380	
Met Gly Leu Asn Pro Ile Gln Cys Val Leu Val Thr Leu Ala Ala Cys	
385 390 395 400	

PF59083SeqList PF59083.txt

Phe Gly Gly Leu Gly Ala Ser His Ile Asn Asp Ser Gly Phe Trp Ile
 405 410 415
 Val Thr Lys Tyr Leu Gly Leu Ser Val Ala Asp Gly Leu Lys Thr Trp
 420 425 430
 Thr Val Leu Thr Thr Ile Leu Gly Phe Thr Gly Phe Leu Ile Thr Trp
 435 440 445
 Cys Val Trp Ala Val Ile
 450

<210> 10228
 <211> 1338
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1338)
 <223> transl_table=11

<400> 10228
 atg cac tct caa atc tgg gtt gtg agc acg ctg ctt atc agc atc gtg 48
 Met His Ser Gln Ile Trp Val Val Ser Thr Leu Leu Ile Ser Ile Val
 1 5 10 15
 tta att gta ctg acc atc gtg aag ttc aaa ttc cac ccg ttt ctg gcg 96
 Leu Ile Val Leu Thr Ile Val Lys Phe Lys Phe His Pro Phe Leu Ala
 20 25 30
 ctg ttg ctg gcc agc ttc ttc gtg gga acg atg atg ggc atg ggg cca 144
 Leu Leu Leu Ala Ser Phe Phe Val Gly Thr Met Met Gly Met Gly Pro
 35 40 45
 ctg gat atg gta aat gct att gaa agt gga att ggc gga acg ctg ggg 192
 Leu Asp Met Val Asn Ala Ile Glu Ser Gly Ile Gly Gly Thr Leu Gly
 50 55 60
 ttc ctc gca gcg gtt atc ggc ctt ggc acg ata ctg gga aaa atg atg 240
 Phe Leu Ala Ala Val Ile Gly Leu Gly Thr Ile Leu Gly Lys Met Met
 65 70 75 80
 gaa gta tcc ggg gcc gca gaa aga att ggt ctg aca ctt caa cgc tgc 288
 Glu Val Ser Gly Ala Ala Glu Arg Ile Gly Leu Thr Leu Gln Arg Cys
 85 90 95
 cgc tgg ctt tca gtt gat gtc att atg gtg ctg gtt ggc ctg att tgt 336
 Arg Trp Leu Ser Val Asp Val Ile Met Val Leu Val Gly Leu Ile Cys
 100 105 110
 ggc atc acg ctg ttt gtt gaa gtg ggc gtc gtg cta ttg att cct ctg 384
 Gly Ile Thr Leu Phe Val Glu Val Gly Val Val Leu Leu Ile Pro Leu
 115 120 125
 gct ttt tca att gcc aaa aaa acc aat acc tca tta aag ctt gcc 432
 Ala Phe Ser Ile Ala Lys Lys Thr Asn Thr Ser Leu Leu Lys Leu Ala
 130 135 140
 att ccg cta tgt acc gca ttg atg gca gtg cac tgc gtg gtt cct cca 480
 Ile Pro Leu Cys Thr Ala Leu Met Ala Val His Cys Val Val Pro Pro
 145 150 155 160
 cat ccg gct gct tta tat gtt gcc aat aag ctg ggc gca gat atc ggt 528
 His Pro Ala Ala Leu Tyr Val Ala Asn Lys Leu Gly Ala Asp Ile Gly
 165 170 175
 tcg gtg atc gtc tac ggt ttg ctg gtt ggg ctg atg gca tca ctg atc 576
 Ser Val Ile Val Tyr Gly Leu Leu Val Gly Leu Met Ala Ser Leu Ile
 180 185 190
 ggt ggc cca ctt ttc ctt aaa ttt ctg ggt caa cga ctg ccc ttt aaa 624
 Gly Gly Pro Leu Phe Leu Lys Phe Leu Gly Gln Arg Leu Pro Phe Lys
 195 200 205
 cct gta ccc aca gag ttt gca gat ctc aaa gtt cgc gat gaa aaa aca 672
 Pro Val Pro Thr Glu Phe Ala Asp Leu Lys Val Arg Asp Glu Lys Thr
 210 215 220
 cta ccg tca tta ggc gca acg tta ttc acc ata ctg cta ccc att gcg 720
 Leu Pro Ser Leu Gly Ala Thr Leu Phe Thr Ile Leu Leu Pro Ile Ala
 225 230 235 240
 ctg atg ttg gtt aaa acg att gcc gaa ttg aat atg gcg cgt gag agt 768
 Leu Met Leu Val Lys Thr Ile Ala Glu Leu Asn Met Ala Arg Glu Ser
 245 250 255
 ggt ttg tat atc ttg gtt gag ttt att ggc aac cct atc act gcc atg 816

PF59083SeqList PF59083.txt

Gly	Leu	Tyr	Ile	Leu	Val	Glu	Phe	Ile	Gly	Asn	Pro	Ile	Thr	Ala	Met	
260								265					270			
ttt	atc	gcc	gtg	ttt	gtc	gcc	tat	tat	gtg	ttg	ggt	ata	cgc	cag	cat	864
Phe	Ile	Ala	Val	Phe	Val	Ala	Tyr	Tyr	Val	Leu	Gly	Ile	Arg	Gln	His	
275							280					285				
atg	agc	atg	ggg	acg	atg	ctc	aca	cat	acg	gaa	aat	ggc	ttc	ggt	tct	912
Met	Ser	Met	Gly	Thr	Met	Leu	Thr	His	Thr	Glu	Asn	Gly	Phe	Gly	Ser	
290						295					300					
att	gct	aat	att	ttg	ctg	att	atc	ggg	gcc	gga	ggc	gca	ttc	aac	gcc	960
Ile	Ala	Asn	Ile	Leu	Leu	Ile	Ile	Gly	Ala	Gly	Gly	Ala	Phe	Asn	Ala	
305					310					315					320	
att	tta	aaa	agc	agc	agt	ctc	gct	gat	acg	ctg	gca	ggt	att	ctc	tcc	1008
Ile	Leu	Lys	Ser	Ser	Ser	Leu	Ala	Asp	Thr	Leu	Ala	Val	Ile	Leu	Ser	
			325					330						335		
aat	atg	cat	atg	cac	ccg	att	ctt	ctg	gcc	tgg	tta	gtg	gct	ctt	att	1056
Asn	Met	His	Met	His	Pro	Ile	Leu	Leu	Ala	Trp	Leu	Val	Ala	Leu	Ile	
			340					345					350			
ctg	cat	gcg	gca	gtg	ggc	tcc	gct	acc	gtg	gca	atg	atg	ggg	gca	acg	1104
Leu	His	Ala	Ala	Val	Gly	Ser	Ala	Thr	Val	Ala	Met	Met	Gly	Ala	Thr	
		355				360						365				
gca	att	ggt	gca	ccc	atg	ctg	ccg	ctg	tat	ccc	gac	atc	agc	ccg	gaa	1152
Ala	Ile	Val	Ala	Pro	Met	Leu	Pro	Leu	Tyr	Pro	Asp	Ile	Ser	Pro	Glu	
370						375					380					
att	att	gcg	att	gct	atc	ggt	tca	ggt	gca	att	ggc	tgc	act	atc	ggt	1200
Ile	Ile	Ala	Ile	Ala	Ile	Gly	Ser	Gly	Ala	Ile	Gly	Cys	Thr	Ile	Val	
385					390					395					400	
acg	gac	tcg	ctt	ttc	tgg	cta	gtg	aag	caa	tat	tgc	ggc	gct	acg	ctc	1248
Thr	Asp	Ser	Leu	Phe	Trp	Leu	Val	Lys	Gln	Tyr	Cys	Gly	Ala	Thr	Leu	
			405					410						415		
aat	gaa	aca	ttt	aaa	tac	tat	acg	aca	gcg	aca	ttt	atc	gct	tca	gtc	1296
Asn	Glu	Thr	Phe	Lys	Tyr	Tyr	Thr	Thr	Ala	Thr	Phe	Ile	Ala	Ser	Val	
			420					425					430			
gtc	gct	ctg	gcg	ggc	aca	ttc	ctg	ctg	tca	ttt	atc	atc	taa			1338
Val	Ala	Leu	Ala	Gly	Thr	Phe	Leu	Leu	Ser	Phe	Ile	Ile				
		435					440					445				

<210> 10229
 <211> 445
 <212> PRT
 <213> Escherichia coli

<400> 10229

Met	His	Ser	Gln	Ile	Trp	Val	Val	Ser	Thr	Leu	Leu	Ile	Ser	Ile	Val
1				5					10					15	
Leu	Ile	Val	Leu	Thr	Ile	Val	Lys	Phe	Lys	Phe	His	Pro	Phe	Leu	Ala
			20					25					30		
Leu	Leu	Leu	Ala	Ser	Phe	Phe	Val	Gly	Thr	Met	Met	Gly	Met	Gly	Pro
		35				40						45			
Leu	Asp	Met	Val	Asn	Ala	Ile	Glu	Ser	Gly	Ile	Gly	Gly	Thr	Leu	Gly
	50					55					60				
Phe	Leu	Ala	Ala	Val	Ile	Gly	Leu	Gly	Thr	Ile	Leu	Gly	Lys	Met	Met
65					70					75					80
Glu	Val	Ser	Gly	Ala	Ala	Glu	Arg	Ile	Gly	Leu	Thr	Leu	Gln	Arg	Cys
			85					90					95		
Arg	Trp	Leu	Ser	Val	Asp	Val	Ile	Met	Val	Leu	Val	Gly	Leu	Ile	Cys
			100					105					110		
Gly	Ile	Thr	Leu	Phe	Val	Glu	Val	Gly	Val	Val	Leu	Leu	Ile	Pro	Leu
		115				120						125			
Ala	Phe	Ser	Ile	Ala	Lys	Lys	Thr	Asn	Thr	Ser	Leu	Leu	Lys	Leu	Ala
		130				135						140			
Ile	Pro	Leu	Cys	Thr	Ala	Leu	Met	Ala	Val	His	Cys	Val	Val	Pro	Pro
145					150					155				160	
His	Pro	Ala	Ala	Leu	Tyr	Val	Ala	Asn	Lys	Leu	Gly	Ala	Asp	Ile	Gly
			165					170					175		
Ser	Val	Ile	Val	Tyr	Gly	Leu	Leu	Val	Gly	Leu	Met	Ala	Ser	Leu	Ile
			180					185					190		
Gly	Gly	Pro	Leu	Phe	Leu	Lys	Phe	Leu	Gly	Gln	Arg	Leu	Pro	Phe	Lys
		195					200					205			
Pro	Val	Pro	Thr	Glu	Phe	Ala	Asp	Leu	Lys	Val	Arg	Asp	Glu	Lys	Thr

PF59083SeqList PF59083.txt

```

210          215          220
Leu Pro Ser Leu Gly Ala Thr Leu Phe Thr Ile Leu Leu Pro Ile Ala
225          230          235
Leu Met Leu Val Lys Thr Ile Ala Glu Leu Asn Met Ala Arg Glu Ser
245          250          255
Gly Leu Tyr Ile Leu Val Glu Phe Ile Gly Asn Pro Ile Thr Ala Met
260          265          270
Phe Ile Ala Val Phe Val Ala Tyr Tyr Val Leu Gly Ile Arg Gln His
275          280          285
Met Ser Met Gly Thr Met Leu Thr His Thr Glu Asn Gly Phe Gly Ser
290          295          300
Ile Ala Asn Ile Leu Leu Ile Ile Gly Ala Gly Gly Ala Phe Asn Ala
305          310          315
Ile Leu Lys Ser Ser Ser Leu Ala Asp Thr Leu Ala Val Ile Leu Ser
325          330          335
Asn Met His Met His Pro Ile Leu Leu Ala Trp Leu Val Ala Leu Ile
340          345          350
Leu His Ala Ala Val Gly Ser Ala Thr Val Ala Met Met Gly Ala Thr
355          360          365
Ala Ile Val Ala Pro Met Leu Pro Leu Tyr Pro Asp Ile Ser Pro Glu
370          375          380
Ile Ile Ala Ile Ala Ile Gly Ser Gly Ala Ile Gly Cys Thr Ile Val
385          390          395
Thr Asp Ser Leu Phe Trp Leu Val Lys Gln Tyr Cys Gly Ala Thr Leu
405          410          415
Asn Glu Thr Phe Lys Tyr Tyr Thr Thr Ala Thr Phe Ile Ala Ser Val
420          425          430
Val Ala Leu Ala Gly Thr Phe Leu Leu Ser Phe Ile Ile
435          440          445

```

<210> 10230
 <211> 1347
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (1)..(1347)
 <223> transl_table=11

```

<400> 10230
atg cca tta ctg atc gta gca atc ggg att gtg gca tta ttg ctt ttg      48
Met Pro Leu Leu Ile Val Ala Ile Gly Ile Val Ala Leu Leu Leu Leu
1          5          10          15
att atg ggg tta aaa ctg aat acg ttt gtt tcc ttg att atc gta tcg      96
Ile Met Gly Leu Lys Leu Asn Thr Phe Val Ser Leu Ile Ile Val Ser
20          25          30
ttc ggg gtt gca ttg gcg ctt gga atg ccg ctt gac gac atc gtc aaa      144
Phe Gly Val Ala Leu Ala Leu Gly Met Pro Leu Asp Asp Ile Val Lys
35          40          45
acg att gaa gaa ggc ctt ggc gga acg ctc ggc cat atc gca ttg atc      192
Thr Ile Glu Glu Gly Leu Gly Gly Thr Leu Gly His Ile Ala Leu Ile
50          55          60
ttc ggg ctc ggc gcc atg ctg ggc agg ctg atc gcg gat tca ggg ggc      240
Phe Gly Leu Gly Ala Met Leu Gly Arg Leu Ile Ala Asp Ser Gly Gly
65          70          75          80
gct cag cgc att gcg atg acc ctc gtc aac aaa ttc gga gaa gaa aac      288
Ala Gln Arg Ile Ala Met Thr Leu Val Asn Lys Phe Gly Glu Glu Asn
85          90          95
atc caa tgg gcg gtc gtc atc gcc tcc ttt atc atc ggg gta gca tta      336
Ile Gln Trp Ala Val Val Ile Ala Ser Phe Ile Ile Gly Val Ala Leu
100          105          110
ttc ttc gaa gtc gca ttg gta tta ttg att cca att gta ttc gcc att      384
Phe Phe Glu Val Ala Leu Val Leu Leu Ile Pro Ile Val Phe Ala Ile
115          120          125
tca aaa gaa ttg gag ata tct att tca tac ctt gga att cca atg acg      432
Ser Lys Glu Leu Glu Ile Ser Ile Ser Tyr Leu Gly Ile Pro Met Thr
130          135          140
gcg gcc tta tcc gtc aca cac ggc ttc ctg ccc ccg cat ccg gga ccg      480

```

PF59083SeqList PF59083.txt

Ala 145	Ala	Leu	Ser	Val	Thr 150	His	Gly	Phe	Leu	Pro 155	Pro	His	Pro	Gly	Pro 160	
acg	gct	atc	gcg	gga	gag	ctc	ggc	gcc	aat	atc	ggg	gaa	gtg	ctg	ctc	528
Thr	Ala	Ile	Ala	Gly 165	Glu	Leu	Gly	Ala	Asn 170	Ile	Gly	Glu	Val	Leu 175	Leu	
tac	ggt	atc	att	ggt	gca	att	cca	acc	ggt	ctt	ttg	gcc	gga	cct	tta	576
Tyr	Gly	Ile	Ile	Val	Ala	Ile	Pro	Thr 185	Val	Leu	Leu	Ala	Gly 190	Pro	Leu	
ttt	acg	aaa	ctg	gcg	aaa	aaa	atc	gtc	ccg	caa	tca	ttt	gag	aaa	atg	624
Phe	Thr	Lys 195	Leu	Ala	Lys	Lys	Ile 200	Val	Pro	Gln	Ser	Phe 205	Glu	Lys	Met	
ggc	agc	atc	gct	tca	ctc	ggt	gag	cag	aaa	acg	ttc	aag	ctt	gaa	gag	672
Gly	Ser	Ile	Ala	Ser	Leu	Gly 215	Glu	Gln	Lys	Thr	Phe 220	Lys	Leu	Glu	Glu	
acg	ccc	ggc	ttc	ggc	atc	agc	gtc	ttc	aca	gct	atg	ctt	ccg	gtc	att	720
Thr	Pro	Gly	Phe	Gly	Ile 230	Ser	Val	Phe	Thr	Ala 235	Met	Leu	Pro	Val	Ile 240	
atc	atg	tct	att	tcg	act	gtt	att	acg	ctt	att	caa	gaa	acg	atg	ggc	768
Ile	Met	Ser	Ile	Ser 245	Thr	Val	Ile	Thr	Leu 250	Ile	Gln	Glu	Thr	Met 255	Gly	
ctt	gca	gac	aac	agc	ctg	ctg	gca	gcg	ggt	cgt	tta	atc	ggg	aat	gcc	816
Leu	Ala	Asp	Asn 260	Ser	Leu	Leu	Ala	Ala 265	Val	Arg	Leu	Ile	Gly 270	Asn	Ala	
tcg	act	tcg	atg	gtc	atc	tcc	ctg	ttg	gtc	gcg	atc	tat	acg	atg	ggg	864
Ser	Thr	Ser 275	Met	Val	Ile	Ser	Leu 280	Val	Ala	Ile	Tyr 285	Thr	Met	Gly		
atc	gcc	aga	aag	atc	ccg	atc	aaa	caa	gtg	atg	gat	tcc	tgt	tca	acc	912
Ile	Ala	Arg	Lys	Ile	Pro	Ile 295	Lys	Gln	Val	Met	Asp 300	Ser	Cys	Ser	Thr	
gcc	att	aca	caa	atc	gga	atg	atg	ctc	ttg	atc	atc	ggg	ggc	ggc	ggc	960
Ala	Ile	Thr	Gln	Ile	Gly 310	Met	Met	Leu	Leu	Ile 315	Ile	Gly	Gly	Gly	Gly 320	
gcc	ttc	aaa	caa	gtc	ttg	atc	aat	ggc	gga	gta	ggc	gac	tat	gta	gct	1008
Ala	Phe	Lys	Gln 325	Val	Leu	Ile	Asn	Gly	Gly 330	Val	Gly	Asp	Tyr	Val 335	Ala	
gaa	tta	ttc	aaa	gga	aca	gcc	atg	tcg	ccg	atc	ttg	ctc	gcc	tgg	gtc	1056
Glu	Leu	Phe	Lys 340	Gly	Thr	Ala	Met	Ser	Pro	Ile	Leu	Leu	Ala	Trp	Val	
atc	gcc	gca	att	ctg	cgc	atc	tcc	tta	gga	tcc	gcg	aca	ggt	gct	gca	1104
Ile	Ala	Ala 355	Ile	Leu	Arg	Ile	Ser 360	Leu	Gly	Ser	Ala	Thr 365	Val	Ala	Ala	
tta	agc	aca	acc	gga	ctc	gtt	ctt	ccg	atg	ctc	gga	caa	agc	gat	gtc	1152
Leu	Ser 370	Thr	Thr	Gly	Leu	Val 375	Leu	Pro	Met	Leu	Gly 380	Gln	Ser	Asp	Val	
aat	ctt	gcg	ctg	ggt	gtg	ctt	gca	aca	ggg	gcc	gga	agt	gta	atc	gct	1200
Asn	Leu	Ala	Leu	Val	Val 390	Leu	Ala	Thr	Gly	Ala 395	Gly	Ser	Val	Ile	Ala 400	
tcc	cat	gtc	aat	gac	gca	ggc	ttc	tgg	atg	ttc	aaa	gag	tat	ttc	gga	1248
Ser	His	Val	Asn	Asp 405	Ala	Gly	Phe	Trp	Met 410	Phe	Lys	Glu	Tyr	Phe 415	Gly	
cta	agc	atg	aaa	gag	aca	ttt	gcc	acc	tgg	aca	ctg	ctt	gaa	acc	att	1296
Leu	Ser	Met	Lys 420	Glu	Thr	Phe	Ala	Thr 425	Trp	Thr	Leu	Leu	Glu	Thr	Ile	
atc	gcg	gtg	gcc	gga	tta	gga	ttt	act	tta	ttg	tta	agc	cta	ttt	gta	1344
Ile	Ala	Val 435	Ala	Gly	Leu	Gly	Phe 440	Thr	Leu	Leu	Leu	Ser	Leu	Phe	Val	
taa																1347

<210> 10231

<211> 448

<212> PRT

<213> Bacillus licheniformis

<400> 10231

Met Pro Leu Leu Ile Val Ala Ile Gly Ile Val Ala Leu Leu Leu Leu
 1 5 10 15
 Ile Met Gly Leu Lys Leu Asn Thr Phe Val Ser Leu Ile Ile Val Ser
 Seite 10835

PF59083SeqList PF59083.txt

20 25 30
 Phe Gly Val Ala Leu Ala Leu Gly Met Pro Leu Asp Asp Ile Val Lys
 35 40 45
 Thr Ile Glu Glu Gly Leu Gly Gly Thr Leu Gly His Ile Ala Leu Ile
 50 55 60
 Phe Gly Leu Gly Ala Met Leu Gly Arg Leu Ile Ala Asp Ser Gly Gly
 65 70 75 80
 Ala Gln Arg Ile Ala Met Thr Leu Val Asn Lys Phe Gly Glu Glu Asn
 85 90 95
 Ile Gln Trp Ala Val Val Ile Ala Ser Phe Ile Ile Gly Val Ala Leu
 100 105 110
 Phe Phe Glu Val Ala Leu Val Leu Leu Ile Pro Ile Val Phe Ala Ile
 115 120 125
 Ser Lys Glu Leu Glu Ile Ser Ile Ser Tyr Leu Gly Ile Pro Met Thr
 130 135 140
 Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro His Pro Gly Pro
 145 150 155 160
 Thr Ala Ile Ala Gly Glu Leu Gly Ala Asn Ile Gly Glu Val Leu Leu
 165 170 175
 Tyr Gly Ile Ile Val Ala Ile Pro Thr Val Leu Leu Ala Gly Pro Leu
 180 185 190
 Phe Thr Lys Leu Ala Lys Lys Ile Val Pro Gln Ser Phe Glu Lys Met
 195 200 205
 Gly Ser Ile Ala Ser Leu Gly Glu Gln Lys Thr Phe Lys Leu Glu Glu
 210 215 220
 Thr Pro Gly Phe Gly Ile Ser Val Phe Thr Ala Met Leu Pro Val Ile
 225 230 235 240
 Ile Met Ser Ile Ser Thr Val Ile Thr Leu Ile Gln Glu Thr Met Gly
 245 250 255
 Leu Ala Asp Asn Ser Leu Leu Ala Ala Val Arg Leu Ile Gly Asn Ala
 260 265 270
 Ser Thr Ser Met Val Ile Ser Leu Leu Val Ala Ile Tyr Thr Met Gly
 275 280 285
 Ile Ala Arg Lys Ile Pro Ile Lys Gln Val Met Asp Ser Cys Ser Thr
 290 295 300
 Ala Ile Thr Gln Ile Gly Met Met Leu Leu Ile Ile Gly Gly Gly Gly
 305 310 315 320
 Ala Phe Lys Gln Val Leu Ile Asn Gly Gly Val Gly Asp Tyr Val Ala
 325 330 335
 Glu Leu Phe Lys Gly Thr Ala Met Ser Pro Ile Leu Leu Ala Trp Val
 340 345 350
 Ile Ala Ala Ile Leu Arg Ile Ser Leu Gly Ser Ala Thr Val Ala Ala
 355 360 365
 Leu Ser Thr Thr Gly Leu Val Leu Pro Met Leu Gly Gln Ser Asp Val
 370 375 380
 Asn Leu Ala Leu Val Val Leu Ala Thr Gly Ala Gly Ser Val Ile Ala
 385 390 395 400
 Ser His Val Asn Asp Ala Gly Phe Trp Met Phe Lys Glu Tyr Phe Gly
 405 410 415
 Leu Ser Met Lys Glu Thr Phe Ala Thr Trp Thr Leu Leu Glu Thr Ile
 420 425 430
 Ile Ala Val Ala Gly Leu Gly Phe Thr Leu Leu Leu Ser Leu Phe Val
 435 440 445

<210> 10232

<211> 1347

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1347)

<223> transl_table=11

<400> 10232

atg ccg tta atc atc gtt gca ctt ggg atc tta gca tta cta ttt ctg 48
 Met Pro Leu Ile Ile Val Ala Leu Gly Ile Leu Ala Leu Leu Phe Leu
 1 5 10 15
 att atg ggc tta aaa tta aac aca ttt att tcc ctg ctg gtc gta tcg 96
 440 445
 Seite 10836

PF59083SeqList PF59083.txt

Ile	Met	Gly	Leu	Lys	Leu	Asn	Thr	Phe	Ile	Ser	Leu	Leu	Val	Val	Ser	
20								25					30			
ttc	ggc	gtg	gca	ctg	gca	ctc	ggg	atg	ccg	ttc	gat	aaa	ggt	gtc	agc	144
Phe	Gly	Val	Ala	Leu	Ala	Leu	Gly	Met	Pro	Phe	Asp	Lys	Val	Val	Ser	
35							40					45				
tcc	atc	gaa	gca	gga	ata	ggg	ggg	act	ctt	ggc	cac	atc	gcg	ctc	atc	192
Ser	Ile	Glu	Ala	Gly	Ile	Gly	Gly	Thr	Leu	Gly	His	Ile	Ala	Leu	Ile	
50						55				60						
ttc	gga	ctc	ggt	gcg	atg	ctg	ggc	aaa	ctg	atc	gcg	gat	tca	gga	ggc	240
Phe	Gly	Leu	Gly	Ala	Met	Leu	Gly	Lys	Leu	Ile	Ala	Asp	Ser	Gly	Gly	
65					70					75				80		
gca	cag	cg	att	g	atg	acg	ctc	gtc	aac	aaa	ttc	ggt	gag	aaa	aat	288
Ala	Gln	Arg	Ile	Ala	Met	Thr	Leu	Val	Asn	Lys	Phe	Gly	Glu	Lys	Asn	
85								90						95		
att	caa	tgg	gcc	ggt	gtc	att	gcc	tca	ttc	att	att	ggg	att	g	tta	336
Ile	Gln	Trp	Ala	Val	Val	Ile	Ala	Ser	Phe	Ile	Ile	Gly	Ile	Ala	Leu	
100							105						110			
ttt	ttt	gaa	gta	gga	ctg	ggt	cta	tta	att	ccg	att	gtc	ttt	g	att	384
Phe	Phe	Glu	Val	Gly	Leu	Val	Leu	Leu	Ile	Pro	Ile	Val	Phe	Ala	Ile	
115							120					125				
tca	aga	gaa	ttg	aag	att	tct	att	tta	ttt	ctc	gga	atc	ccg	atg	gtc	432
Ser	Arg	Glu	Leu	Lys	Ile	Ser	Ile	Leu	Phe	Leu	Gly	Ile	Pro	Met	Val	
130						135					140					
gcg	gca	cta	tcc	gtc	aca	cac	ggt	ttc	ctg	ccg	ccg	cac	ccg	gga	cct	480
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
145					150					155				160		
acg	gcg	atc	gcc	ggt	gag	tat	ggc	gca	aac	att	gga	gaa	gtg	ctg	ctg	528
Thr	Ala	Ile	Ala	Gly	Glu	Tyr	Gly	Ala	Asn	Ile	Gly	Glu	Val	Leu	Leu	
165							170							175		
tac	ggc	ttt	atc	ggt	gct	ggt	ccg	aca	gtg	ctc	att	gca	ggg	ccg	tta	576
Tyr	Gly	Phe	Ile	Val	Ala	Val	Pro	Thr	Val	Leu	Ile	Ala	Gly	Pro	Leu	
180							185						190			
ttt	aca	aag	ttc	g	aaa	aaa	atc	ggt	cct	gca	tca	ttt	g	aaa	aac	624
Phe	Thr	Lys	Phe	Ala	Lys	Lys	Ile	Val	Pro	Ala	Ser	Phe	Ala	Lys	Asn	
195						200						205				
ggc	aat	att	gca	tca	ctc	ggc	aca	caa	aaa	aca	ttt	aac	ctt	gaa	gaa	672
Gly	Asn	Ile	Ala	Ser	Leu	Gly	Thr	Gln	Lys	Thr	Phe	Asn	Leu	Glu	Glu	
210						215					220					
aca	ccc	ggc	ttt	gga	atc	agt	gtc	ttt	act	gca	atg	ctc	ccg	att	atc	720
Thr	Pro	Gly	Phe	Gly	Ile	Ser	Val	Phe	Thr	Ala	Met	Leu	Pro	Ile	Ile	
225					230					235				240		
atc	atg	tcg	gtc	g	acc	att	atc	gac	ctg	ctt	caa	gaa	aca	atc	ggg	768
Ile	Met	Ser	Val	Ala	Thr	Ile	Ile	Asp	Leu	Leu	Gln	Glu	Thr	Ile	Gly	
245							250							255		
ttt	gca	gat	aac	gga	ggt	tta	gct	ttt	atc	aga	ttg	att	gga	aac	gca	816
Phe	Ala	Asp	Asn	Gly	Val	Leu	Ala	Phe	Ile	Arg	Leu	Ile	Gly	Asn	Ala	
260							265						270			
tcg	act	gct	atg	att	att	tcg	tta	ttg	gtc	gca	gtc	tat	aca	atg	ggc	864
Ser	Thr	Ala	Met	Ile	Ile	Ser	Leu	Leu	Val	Ala	Val	Tyr	Thr	Met	Gly	
275							280					285				
atc	aag	cg	aac	att	cca	gtc	aaa	acc	gtg	atg	gat	tct	tgt	tca	act	912
Ile	Lys	Arg	Asn	Ile	Pro	Val	Lys	Thr	Val	Met	Asp	Ser	Cys	Ser	Thr	
290						295					300					
gcc	att	tca	caa	atc	ggc	atg	atg	ctt	ttg	atc	atc	gga	gga	ggc	ggc	960
Ala	Ile	Ser	Gln	Ile	Gly	Met	Met	Leu	Leu	Ile	Ile	Gly	Gly	Gly	Gly	
305					310					315				320		
gcc	ttc	aaa	caa	gtg	ctg	atc	aac	ggc	ggt	gtc	ggc	gat	tac	gta	gca	1008
Ala	Phe	Lys	Gln	Val	Leu	Ile	Asn	Gly	Gly	Val	Gly	Asp	Tyr	Val	Ala	
325														335		
gac	tta	ttc	aaa	gga	acg	gca	tta	tcg	cca	atc	att	ctg	gca	tgg	ctc	1056
Asp	Leu	Phe	Lys	Gly	Thr	Ala	Leu	Ser	Pro	Ile	Ile	Leu	Ala	Trp	Leu	
340							345						350			
atc	gca	gcg	atc	ctg	cg	att	tct	cta	gga	tcg	gcg	act	ggt	gcc	gca	1104
Ile	Ala	Ile	Ile	Leu	Arg	Ile	Ser	Leu	Gly	Ser	Ala	Thr	Val	Ala	Ala	
355						360						365				
cta	agc	aca	aca	ggt	ctg	gtc	att	ccg	tta	ttg	ggc	cat	tct	gat	ggt	1152
Leu	Ser	Thr	Thr	Gly	Leu	Val	Ile	Pro	Leu	Leu	Gly	His	Ser	Asp	Val	
370						375					380					
aac	ctg	gcg	tta	gtc	gta	ctc	gca	aca	gga	gcc	agg	agc	gtc	atc	gct	1200

PF59083SeqList PF59083.txt

Asn	Leu	Ala	Leu	Val	Val	Leu	Ala	Thr	Gly	Ala	Gly	Ser	Val	Ile	Ala	
385					390					395					400	
tca	cac	gtc	aat	gac	gcc	ggc	ttc	tgg	atg	ttc	aag	gaa	tac	ttc	gga	1248
Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Met	Phe	Lys	Glu	Tyr	Phe	Gly	
				405					410					415		
tta	agc	atg	aaa	gaa	aca	ttc	gcc	aca	tgg	aca	ttg	ctg	gaa	acc	att	1296
Leu	Ser	Met	Lys	Glu	Thr	Phe	Ala	Thr	Trp	Thr	Leu	Leu	Glu	Thr	Ile	
			420					425					430			
att	tcc	gtt	gct	gga	ctg	gga	ttc	att	tta	ttg	tta	agt	tta	gtt	gta	1344
Ile	Ser	Val	Ala	Gly	Leu	Gly	Phe	Ile	Leu	Leu	Leu	Ser	Leu	Val	Val	
		435					440					445				
tga																1347

<210> 10233

<211> 448

<212> PRT

<213> Bacillus subtilis

<400> 10233

Met	Pro	Leu	Ile	Ile	Val	Ala	Leu	Gly	Ile	Leu	Ala	Leu	Leu	Phe	Leu	
1				5					10					15		
Ile	Met	Gly	Leu	Lys	Leu	Asn	Thr	Phe	Ile	Ser	Leu	Leu	Val	Val	Ser	
			20					25					30			
Phe	Gly	Val	Ala	Leu	Ala	Leu	Gly	Met	Pro	Phe	Asp	Lys	Val	Val	Ser	
		35					40					45				
Ser	Ile	Glu	Ala	Gly	Ile	Gly	Gly	Thr	Leu	Gly	His	Ile	Ala	Leu	Ile	
	50					55					60					
Phe	Gly	Leu	Gly	Ala	Met	Leu	Gly	Lys	Leu	Ile	Ala	Asp	Ser	Gly	Gly	
65					70					75					80	
Ala	Gln	Arg	Ile	Ala	Met	Thr	Leu	Val	Asn	Lys	Phe	Gly	Glu	Lys	Asn	
			85						90					95		
Ile	Gln	Trp	Ala	Val	Val	Ile	Ala	Ser	Phe	Ile	Ile	Gly	Ile	Ala	Leu	
			100					105					110			
Phe	Phe	Glu	Val	Gly	Leu	Val	Leu	Leu	Ile	Pro	Ile	Val	Phe	Ala	Ile	
		115					120					125				
Ser	Arg	Glu	Leu	Lys	Ile	Ser	Ile	Leu	Phe	Leu	Gly	Ile	Pro	Met	Val	
	130					135					140					
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
145					150					155					160	
Thr	Ala	Ile	Ala	Gly	Glu	Tyr	Gly	Ala	Asn	Ile	Gly	Glu	Val	Leu	Leu	
			165					170						175		
Tyr	Gly	Phe	Ile	Val	Ala	Val	Pro	Thr	Val	Leu	Ile	Ala	Gly	Pro	Leu	
			180					185					190			
Phe	Thr	Lys	Phe	Ala	Lys	Lys	Ile	Val	Pro	Ala	Ser	Phe	Ala	Lys	Asn	
		195					200					205				
Gly	Asn	Ile	Ala	Ser	Leu	Gly	Thr	Gln	Lys	Thr	Phe	Asn	Leu	Glu	Glu	
	210					215					220					
Thr	Pro	Gly	Phe	Gly	Ile	Ser	Val	Phe	Thr	Ala	Met	Leu	Pro	Ile	Ile	
225					230					235					240	
Ile	Met	Ser	Val	Ala	Thr	Ile	Ile	Asp	Leu	Leu	Gln	Glu	Thr	Ile	Gly	
			245					250						255		
Phe	Ala	Asp	Asn	Gly	Val	Leu	Ala	Phe	Ile	Arg	Leu	Ile	Gly	Asn	Ala	
			260					265					270			
Ser	Thr	Ala	Met	Ile	Ile	Ser	Leu	Leu	Val	Ala	Val	Tyr	Thr	Met	Gly	
		275					280					285				
Ile	Lys	Arg	Asn	Ile	Pro	Val	Lys	Thr	Val	Met	Asp	Ser	Cys	Ser	Thr	
	290					295					300					
Ala	Ile	Ser	Gln	Ile	Gly	Met	Met	Leu	Leu	Ile	Ile	Gly	Gly	Gly	Gly	
305					310					315					320	
Ala	Phe	Lys	Gln	Val	Leu	Ile	Asn	Gly	Gly	Val	Gly	Asp	Tyr	Val	Ala	
			325					330						335		
Asp	Leu	Phe	Lys	Gly	Thr	Ala	Leu	Ser	Pro	Ile	Ile	Leu	Ala	Trp	Leu	
			340					345					350			
Ile	Ala	Ala	Ile	Leu	Arg	Ile	Ser	Leu	Gly	Ser	Ala	Thr	Val	Ala	Ala	
		355					360					365				
Leu	Ser	Thr	Thr	Gly	Leu	Val	Ile	Pro	Leu	Leu	Gly	His	Ser	Asp	Val	
	370					375					380					

PF59083SeqList PF59083.txt

Asn Leu Ala Leu Val Val Leu Ala Thr Gly Ala Gly Ser Val Ile Ala
 385 390 395 400
 Ser His Val Asn Asp Ala Gly Phe Trp Met Phe Lys Glu Tyr Phe Gly
 405 410 415
 Leu Ser Met Lys Glu Thr Phe Ala Thr Trp Thr Leu Leu Glu Thr Ile
 420 425 430
 Ile Ser Val Ala Gly Leu Gly Phe Ile Leu Leu Leu Ser Leu Val Val
 435 440 445

<210> 10234
 <211> 1356
 <212> DNA
 <213> Zymomonas mobilis

<220>
 <221> CDS
 <222> (1)..(1356)
 <223> transl_table=11

<400> 10234
 atg cac tct aat gga aca atg ctc ctt tta tat gca ttg gcg tcc atc 48
 Met His Ser Asn Gly Thr Met Leu Leu Leu Tyr Ala Leu Ala Ser Ile
 1 5 10 15
 atc att ctt att ttg atg att gca aag tgg cgt cta aac cct ttt gtt 96
 Ile Ile Leu Ile Leu Met Ile Ala Lys Trp Arg Leu Asn Pro Phe Val
 20 25 30
 tcc ctt att tta gtt tca atc ggt atg ggt gcc gta acg ggc atg ccc 144
 Ser Leu Ile Leu Val Ser Ile Gly Met Gly Ala Val Thr Gly Met Pro
 35 40 45
 tta acc aaa gtt ttg tcg gcc ttt caa gat ggt ctt ggt tct ggt atc 192
 Leu Thr Lys Val Leu Ser Ala Phe Gln Asp Gly Leu Gly Ser Gly Ile
 50 55 60
 ggt tcc aca gcg agt gtt atc gca ctc ggc acc atg ctt ggt aag atc 240
 Gly Ser Thr Ala Ser Val Ile Ala Leu Gly Thr Met Leu Gly Lys Ile
 65 70 75 80
 ttg gct gag tct ggt ggt gcg gaa cgt atc gct acg acg acg atc aaa 288
 Leu Ala Glu Ser Gly Gly Ala Glu Arg Ile Ala Thr Thr Thr Ile Lys
 85 90 95
 atc ttt ggc ccc aaa ctt atc cac tgg gcg atg ctg gtc att gcc ttt 336
 Ile Phe Gly Pro Lys Leu Ile His Trp Ala Met Leu Val Ile Ala Phe
 100 105 110
 atc gtg ggt att ccg atc ttc tat cag gtc ggt ttt atc ctg ttg att 384
 Ile Val Gly Ile Pro Ile Phe Tyr Gln Val Gly Phe Ile Leu Leu Ile
 115 120 125
 ccg ctc gtc ttt acc tta gga cgt gcc agc ggg att tct ctt gtc aaa 432
 Pro Leu Val Phe Thr Leu Gly Arg Ala Ser Gly Ile Ser Leu Val Lys
 130 135 140
 tta acc att ccg ctt tgt gcc ggt ttg gcg acc gtt cat ggt ttg ctg 480
 Leu Thr Ile Pro Leu Cys Ala Gly Leu Ala Thr Val His Gly Leu Leu
 145 150 155 160
 cct ccg cat ccg ggt tca atg caa tgc gtt gaa atg ctc cat gct gat 528
 Pro Pro His Pro Gly Ser Met Gln Cys Val Glu Met Leu His Ala Asp
 165 170 175
 gtg ggt aaa acc att ctt tac ggt ttc atc gtc ggt ttc cct gcc gct 576
 Val Gly Lys Thr Ile Leu Tyr Gly Phe Ile Val Gly Phe Pro Ala Ala
 180 185 190
 atc ctt gcc ggt ccg ctt tac ggc aat tgg att acg cct cgc att cag 624
 Ile Leu Ala Gly Pro Leu Tyr Gly Asn Trp Ile Thr Pro Arg Ile Gln
 195 200 205 210
 ctg cct gcc cac aac cca ttt gca gaa agt ctt gaa ggt agc agc gat 672
 Leu Pro Ala His Asn Pro Phe Ala Glu Ser Leu Glu Gly Ser Ser Asp
 215 220 225
 cag gat aaa aat ttg ccg ggt ttc tgg ctg acg att ttc tcg att ttg 720
 Gln Asp Lys Asn Leu Pro Gly Phe Trp Leu Thr Ile Phe Ser Ile Leu
 230 235 240
 ctt cct gtt ttg ctg atg gtt ttt tcc agc ggc gcc aat atc ttc ctg 768
 Leu Pro Val Leu Leu Met Val Phe Ser Ser Gly Ala Asn Ile Phe Leu
 245 250 255
 ccc cac ggt aac aac att cgc gct ttc atg aac ttc atg ggt gat ccg 816

PF59083SeqList PF59083.txt

Pro	His	Gly	Asn	Asn	Ile	Arg	Ala	Phe	Met	Asn	Phe	Met	Gly	Asp	Pro	
260							265						270			
gtt	gtt	tcc	ttg	ctt	atc	gct	ttg	ctg	gtc	agc	atg	gtc	acc	ttg	ggt	864
Val	Val	Ser	Leu	Leu	Ile	Ala	Leu	Leu	Val	Ser	Met	Val	Thr	Leu	Gly	
275							280						285			
ttc	tgg	cgt	ggt	ttc	agc	agt	gct	gat	ctt	ctg	aaa	ttc	acc	aat	gac	912
Phe	Trp	Arg	Gly	Phe	Ser	Ser	Ala	Asp	Leu	Leu	Lys	Phe	Thr	Asn	Asp	
290						295					300					
tgc	ttg	ggc	ccg	acg	gct	ggc	att	ctg	ttg	ctg	atc	ggt	gct	ggt	ggc	960
Cys	Leu	Gly	Pro	Thr	Ala	Gly	Ile	Leu	Leu	Ile	Gly	Ala	Gly	Gly	Gly	
305					310					315					320	
gga	ttt	agt	gaa	att	ctg	tat	cgc	gcc	ggt	gtc	agt	aac	gcc	atg	gcc	1008
Gly	Phe	Ser	Glu	Ile	Leu	Tyr	Arg	Ala	Gly	Val	Ser	Asn	Ala	Met	Ala	
			325					330						335		
gat	ctg	tct	cac	gtc	atg	cat	ctg	tcc	ccg	att	atg	ctc	ggc	ttt	atc	1056
Asp	Leu	Ser	His	Val	Met	His	Leu	Ser	Pro	Ile	Met	Leu	Gly	Phe	Ile	
			340					345					350			
att	gcg	gcg	ggt	atc	cgc	gtt	gca	acc	ggt	tca	cag	acg	gtg	gca	atg	1104
Ile	Ala	Ala	Val	Ile	Arg	Val	Ala	Thr	Gly	Ser	Gln	Thr	Val	Ala	Met	
			355				360					365				
tcg	atg	tcc	ggc	ggt	atg	tta	gcc	ccg	atc	atc	ttc	agc	acc	ccg	ggc	1152
Ser	Met	Ser	Gly	Gly	Met	Leu	Ala	Pro	Ile	Ile	Phe	Ser	Thr	Pro	Gly	
			370			375						380				
ttc	cac	agc	cct	gaa	ttg	ctg	gtt	ctt	tcg	atc	ggt	gcc	ggt	tcg	tcc	1200
Phe	His	Ser	Pro	Glu	Leu	Val	Leu	Ser	Ile	Gly	Ala	Gly	Ser	Ser	Ser	
385					390				395						400	
att	ctg	tct	cac	gtc	aat	gac	ggt	gct	ttc	tgg	ctg	tta	aaa	gaa	tat	1248
Ile	Leu	Ser	His	Val	Asn	Asp	Gly	Ala	Phe	Trp	Leu	Leu	Lys	Glu	Tyr	
			405					410						415		
ctg	aat	atg	acg	gtc	agc	cag	acc	ttc	aag	acc	tgg	acg	gtt	tct	gtc	1296
Leu	Asn	Met	Thr	Val	Ser	Gln	Thr	Phe	Lys	Thr	Trp	Thr	Val	Ser	Val	
			420					425					430			
acc	atc	gct	tcg	att	gca	gcc	ctg	atc	ctc	acc	ttt	ggt	ctt	cag	gca	1344
Thr	Ile	Ala	Ser	Ile	Ala	Ala	Leu	Ile	Leu	Thr	Phe	Gly	Leu	Gln	Ala	
			435				440					445				
ttg	ggt	ctt	taa													1356
Leu	Gly	Leu														
450																

<210> 10235

<211> 451

<212> PRT

<213> Zymomonas mobilis

<400> 10235

Met	His	Ser	Asn	Gly	Thr	Met	Leu	Leu	Leu	Tyr	Ala	Leu	Ala	Ser	Ile	
1				5					10					15		
Ile	Ile	Leu	Ile	Leu	Met	Ile	Ala	Lys	Trp	Arg	Leu	Asn	Pro	Phe	Val	
			20					25					30			
Ser	Leu	Ile	Leu	Val	Ser	Ile	Gly	Met	Gly	Ala	Val	Thr	Gly	Met	Pro	
		35					40					45				
Leu	Thr	Lys	Val	Leu	Ser	Ala	Phe	Gln	Asp	Gly	Leu	Gly	Ser	Gly	Ile	
		50				55					60					
Gly	Ser	Thr	Ala	Ser	Val	Ile	Ala	Leu	Gly	Thr	Met	Leu	Gly	Lys	Ile	
65					70				75					80		
Leu	Ala	Glu	Ser	Gly	Gly	Ala	Glu	Arg	Ile	Ala	Thr	Thr	Thr	Ile	Lys	
			85					90						95		
Ile	Phe	Gly	Pro	Lys	Leu	Ile	His	Trp	Ala	Met	Leu	Val	Ile	Ala	Phe	
			100					105					110			
Ile	Val	Gly	Ile	Pro	Ile	Phe	Tyr	Gln	Val	Gly	Phe	Ile	Leu	Leu	Ile	
		115					120					125				
Pro	Leu	Val	Phe	Thr	Leu	Gly	Arg	Ala	Ser	Gly	Ile	Ser	Leu	Val	Lys	
		130				135					140					
Leu	Thr	Ile	Pro	Leu	Cys	Ala	Gly	Leu	Ala	Thr	Val	His	Gly	Leu	Leu	
145					150					155					160	
Pro	Pro	His	Pro	Gly	Ser	Met	Gln	Cys	Val	Glu	Met	Leu	His	Ala	Asp	
			165					170						175		
Val	Gly	Lys	Thr	Ile	Leu	Tyr	Gly	Phe	Ile	Val	Gly	Phe	Pro	Ala	Ala	
			180					185					190			

PF59083SeqList PF59083.txt

Ile Leu Ala Gly Pro Leu Tyr Gly Asn Trp Ile Thr Pro Arg Ile Gln
195 200 205
Leu Pro Ala His Asn Pro Phe Ala Glu Ser Leu Glu Gly Ser Ser Asp
210 215 220
Gln Asp Lys Asn Leu Pro Gly Phe Trp Leu Thr Ile Phe Ser Ile Leu
225 230 235 240
Leu Pro Val Leu Leu Met Val Phe Ser Ser Gly Ala Asn Ile Phe Leu
245 250 255
Pro His Gly Asn Asn Ile Arg Ala Phe Met Asn Phe Met Gly Asp Pro
260 265 270
Val Val Ser Leu Leu Ile Ala Leu Val Ser Met Val Thr Leu Gly
275 280 285
Phe Trp Arg Gly Phe Ser Ser Ala Asp Leu Leu Lys Phe Thr Asn Asp
290 295 300
Cys Leu Gly Pro Thr Ala Gly Ile Leu Leu Ile Gly Ala Gly Gly
305 310 315 320
Gly Phe Ser Glu Ile Leu Tyr Arg Ala Gly Val Ser Asn Ala Met Ala
325 330 335
Asp Leu Ser His Val Met His Leu Ser Pro Ile Met Leu Gly Phe Ile
340 345 350
Ile Ala Ala Val Ile Arg Val Ala Thr Gly Ser Gln Thr Val Ala Met
355 360 365
Ser Met Ser Gly Gly Met Leu Ala Pro Ile Ile Phe Ser Thr Pro Gly
370 375 380
Phe His Ser Pro Glu Leu Leu Val Leu Ser Ile Gly Ala Gly Ser Ser
385 390 395 400
Ile Leu Ser His Val Asn Asp Gly Ala Phe Trp Leu Leu Lys Glu Tyr
405 410 415
Leu Asn Met Thr Val Ser Gln Thr Phe Lys Thr Trp Thr Val Ser Val
420 425 430
Thr Ile Ala Ser Ile Ala Ala Leu Ile Leu Thr Phe Gly Leu Gln Ala
435 440 445
Leu Gly Leu
450

<210> 10236
<211> 1317
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1317)
<223> transl_table=11

<400> 10236
atg cca tta gtc att gtt gct atc ggt gta atc ttg ttg ttg ctc ctg 48
Met Pro Leu Val Ile Val Ala Ile Gly Val Ile Leu Leu Leu Leu Leu
1 5 10 15
atg atc cgc ttc aaa atg aac ggc ttc atc gct ctc gtc ctc gtg gcg 96
Met Ile Arg Phe Lys Met Asn Gly Phe Ile Ala Leu Val Leu Val Ala
20 25 30
ctt gct gtt gga tta atg caa gga atg ccg ctg gat aaa gtt att ggc 144
Leu Ala Val Gly Leu Met Gln Gly Met Pro Leu Asp Lys Val Ile Gly
35 40 45
tcc atc aaa gcc ggt gtc ggc ggg acg ctc ggt agc ctt gcc ctg atc 192
Ser Ile Lys Ala Gly Val Gly Gly Thr Leu Gly Ser Leu Ala Leu Ile
50 55 60
atg ggt ttt ggc gca atg ctg ggc aaa atg ctg gca gac tgc ggt ggc 240
Met Gly Phe Gly Ala Met Leu Gly Lys Met Leu Ala Asp Cys Gly Gly
65 70 75 80
gca caa cgt atc gcc acc acg ctg att gcc aaa ttt ggt aaa aaa cac 288
Ala Gln Arg Ile Ala Thr Thr Leu Ile Ala Lys Phe Gly Lys Lys His
85 90 95
atc cag tgg gcg gtg gta ctg acc ggt ttt acc gtt ggt ttt gcc ctg 336
Ile Gln Trp Ala Val Val Leu Thr Gly Phe Thr Val Gly Phe Ala Leu
100 105 110
ttc tat gaa gtg ggc ttt gtg ctg atg ctg ccg ctg gtg ttt acc atc 384
Phe Tyr Glu Val Gly Phe Val Leu Met Leu Pro Leu Val Phe Thr Ile

PF59083SeqList PF59083.txt

gct	gct	tct	gct	aat	att	cca	ctg	ctg	tat	gtt	ggt	gta	cca	atg	gcg	432
Ala	Ala	Ser	Ala	Asn	Ile	Pro	Leu	Leu	Tyr	Val	Gly	Val	Pro	Met	Ala	
130						135					140					
gct	gca	ctg	tct	gtg	acc	cac	ggc	ttc	ctg	cca	ccg	cat	ccg	ggt	ccg	480
Ala	Ala	Leu	Ser	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
145					150					155					160	
act	gct	att	gcc	acc	att	ttc	aat	gcc	gat	atg	ggt	aaa	acc	ctg	ctg	528
Thr	Ala	Ile	Ala	Thr	Ile	Phe	Asn	Ala	Asp	Met	Gly	Lys	Thr	Leu	Leu	
				165					170					175		
tac	ggt	act	att	ctg	gca	atc	ccg	acc	gtg	att	ctc	gcc	ggt	ccg	gtt	576
Tyr	Gly	Thr	Ile	Leu	Ala	Ile	Pro	Thr	Val	Ile	Leu	Ala	Gly	Pro	Val	
				180					185					190		
tac	gct	cg	gtg	ttg	aaa	ggt	atc	gat	aag	cca	att	ccg	gaa	ggt	ctc	624
Tyr	Ala	Arg	Val	Leu	Lys	Gly	Ile	Asp	Lys	Pro	Ile	Pro	Glu	Gly	Leu	
		195							200					205		
tac	agc	gct	aaa	acc	ttc	agc	gaa	gaa	gag	atg	ccg	agc	ttt	ggc	gtc	672
Tyr	Ser	Ala	Lys	Thr	Phe	Ser	Glu	Glu	Glu	Met	Pro	Ser	Phe	Gly	Val	
	210				215						220					
agc	gtc	tgg	acc	tct	ctg	gtg	ccg	gta	gta	ctg	atg	gct	atg	cgt	gct	720
Ser	Val	Trp	Thr	Ser	Leu	Val	Pro	Val	Val	Leu	Met	Ala	Met	Arg	Ala	
225					230					235					240	
att	gcc	gaa	atg	atc	ctg	ccg	aaa	ggt	cac	gct	ttc	ctg	ccg	gta	gct	768
Ile	Ala	Glu	Met	Ile	Leu	Pro	Lys	Gly	His	Ala	Phe	Leu	Pro	Val	Ala	
				245					250					255		
gag	ttc	ctc	ggt	gac	ccg	gta	atg	gca	acg	ctg	att	gcc	gtg	ctg	att	816
Glu	Phe	Leu	Gly	Asp	Pro	Val	Met	Ala	Thr	Leu	Ile	Ala	Val	Leu	Ile	
			260					265						270		
gct	atg	ttc	acc	ttt	ggt	cta	aac	cgt	ggt	cgt	tca	atg	gat	cag	att	864
Ala	Met	Phe	Thr	Phe	Gly	Leu	Asn	Arg	Gly	Arg	Ser	Met	Asp	Gln	Ile	
		275				280							285			
aac	gac	acg	ctg	ggt	tct	tcc	atc	aaa	atc	att	gct	atg	atg	ctg	ttg	912
Asn	Asp	Thr	Leu	Val	Ser	Ser	Ile	Lys	Ile	Ile	Ala	Met	Met	Leu	Leu	
	290				295					300						
atc	atc	ggt	ggt	ggc	ggt	ctg	ttc	aag	cag	gtg	ctg	gta	gac	agc	ggc	960
Ile	Ile	Gly	Gly	Gly	Gly	Ala	Phe	Lys	Gln	Val	Leu	Val	Asp	Ser	Gly	
305					310					315					320	
gtg	gac	aaa	tac	att	gct	tcc	atg	atg	cac	gaa	acc	aac	att	tct	ccg	1008
Val	Asp	Lys	Tyr	Ile	Ala	Ser	Met	Met	His	Glu	Thr	Asn	Ile	Ser	Pro	
				325					330					335		
ctg	ctg	atg	gcc	tgg	tct	att	gct	gcc	gta	ctg	cgt	atc	gct	ctg	ggt	1056
Leu	Leu	Met	Ala	Trp	Ser	Ile	Ala	Ala	Val	Leu	Arg	Ile	Ala	Leu	Gly	
			340					345						350		
tcc	gca	acc	ggt	gct	gca	atc	act	gct	ggt	ggt	atc	gct	gca	ccg	ctg	1104
Ser	Ala	Thr	Val	Ala	Ala	Ile	Thr	Ala	Gly	Gly	Ile	Ala	Ala	Pro	Leu	
		355					360							365		
att	gca	acg	acg	ggt	ggt	agc	ccg	gag	ctg	atg	ggt	att	gct	ggt	ggt	1152
Ile	Ala	Thr	Thr	Gly	Val	Ser	Pro	Glu	Leu	Met	Val	Ile	Ala	Val	Gly	
	370				375					380						
tcc	ggt	agt	gtg	att	ttc	tct	cat	gtg	aac	gat	ccg	ggc	ttc	tgg	ctg	1200
Ser	Gly	Ser	Val	Ile	Phe	Ser	His	Val	Asn	Asp	Pro	Gly	Phe	Trp	Leu	
385					390					395				400		
ttc	aaa	gag	tac	ttt	aac	ctg	act	atc	ggc	gag	acc	atc	aaa	tcc	tgg	1248
Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Thr	Ile	Gly	Glu	Thr	Ile	Lys	Ser	Trp	
				405					410					415		
tcg	atg	ctg	gaa	acc	att	atc	tcg	gtg	tgc	ggt	ctg	gta	ggc	tgt	ctg	1296
Ser	Met	Leu	Glu	Thr	Ile	Ile	Ser	Val	Cys	Gly	Leu	Val	Gly	Cys	Leu	
			420					425					430			
ctg	ctg	aat	atg	gtg	att	tga										1317
Leu	Leu	Asn	Met	Val	Ile											
		435														

<210> 10237

<211> 438

<212> PRT

<213> Escherichia coli

<400> 10237

Met Pro Leu Val Ile Val Ala Ile Gly Val Ile Leu Leu Leu Leu Leu

PF59083SeqList PF59083.txt

```

1           5           10           15
Met Ile Arg Phe Lys Met Asn Gly Phe Ile Ala Leu Val Leu Val Ala
                20           25           30
Leu Ala Val Gly Leu Met Gln Gly Met Pro Leu Asp Lys Val Ile Gly
                35           40           45
Ser Ile Lys Ala Gly Val Gly Gly Thr Leu Gly Ser Leu Ala Leu Ile
                50           55           60
Met Gly Phe Gly Ala Met Leu Gly Lys Met Leu Ala Asp Cys Gly Gly
65                70           75           80
Ala Gln Arg Ile Ala Thr Thr Leu Ile Ala Lys Phe Gly Lys Lys His
                85           90           95
Ile Gln Trp Ala Val Val Leu Thr Gly Phe Thr Val Gly Phe Ala Leu
                100          105          110
Phe Tyr Glu Val Gly Phe Val Leu Met Leu Pro Leu Val Phe Thr Ile
                115          120          125
Ala Ala Ser Ala Asn Ile Pro Leu Leu Tyr Val Gly Val Pro Met Ala
130                135          140          145
Ala Ala Leu Ser Val Thr His Gly Phe Leu Pro Pro His Pro Gly Pro
145                150          155          160
Thr Ala Ile Ala Thr Ile Phe Asn Ala Asp Met Gly Lys Thr Leu Leu
                165          170          175
Tyr Gly Thr Ile Leu Ala Ile Pro Thr Val Ile Leu Ala Gly Pro Val
                180          185          190
Tyr Ala Arg Val Leu Lys Gly Ile Asp Lys Pro Ile Pro Glu Gly Leu
195                200          205          210
Tyr Ser Ala Lys Thr Phe Ser Glu Glu Met Pro Ser Phe Gly Val
210                215          220          225
Ser Val Trp Thr Ser Leu Val Pro Val Val Leu Met Ala Met Arg Ala
225                230          235          240
Ile Ala Glu Met Ile Leu Pro Lys Gly His Ala Phe Leu Pro Val Ala
                245          250          255
Glu Phe Leu Gly Asp Pro Val Met Ala Thr Leu Ile Ala Val Leu Ile
260                265          270          275
Ala Met Phe Thr Phe Gly Leu Asn Arg Gly Arg Ser Met Asp Gln Ile
275                280          285          290
Asn Asp Thr Leu Val Ser Ser Ile Lys Ile Ile Ala Met Met Leu Leu
290                295          300          305
Ile Ile Gly Gly Gly Gly Ala Phe Lys Gln Val Leu Val Asp Ser Gly
305                310          315          320
Val Asp Lys Tyr Ile Ala Ser Met Met His Glu Thr Asn Ile Ser Pro
                325          330          335
Leu Leu Met Ala Trp Ser Ile Ala Ala Val Leu Arg Ile Ala Leu Gly
340                345          350          355
Ser Ala Thr Val Ala Ala Ile Thr Ala Gly Gly Ile Ala Ala Pro Leu
355                360          365          370
Ile Ala Thr Thr Gly Val Ser Pro Glu Leu Met Val Ile Ala Val Gly
370                375          380          385
Ser Gly Ser Val Ile Phe Ser His Val Asn Asp Pro Gly Phe Trp Leu
385                390          395          400
Phe Lys Glu Tyr Phe Asn Leu Thr Ile Gly Glu Thr Ile Lys Ser Trp
                405          410          415
Ser Met Leu Glu Thr Ile Ile Ser Val Cys Gly Leu Val Gly Cys Leu
420                425          430          435
Leu Leu Asn Met Val Ile
435

```

<210> 10238
 <211> 1341
 <212> DNA
 <213> Escherichia coli 0157

<220>
 <221> CDS
 <222> (1)..(1341)
 <223> transl_table=11

<400> 10238
 gtg act aca tta acg ctt gtt tta aca gca gta ggg tct gtt tta ctg
 Met Thr Thr Leu Thr Leu Val Leu Thr Ala Val Gly Ser Val Leu Leu
 Seite 10843

Seite 10844

PF59083SeqList PF59083.txt

370	gcg ctg tcg att tgt atc gcc ggt ggt tcg att gtt gtc agc cac gtt	1200
Ala Leu Ser Ile Cys Ile Ala Gly Gly Ser Ile Val Val Ser His Val		
385	aac gac gct ggt ttc tgg ttg ttc ggt aaa ttt acc ggc gcg acc gaa	1248
Asn Asp Ala Gly Phe Trp Leu Phe Gly Lys Phe Thr Gly Ala Thr Glu		
405	gcc gaa acg ctg aaa acc tgg acc atg atg gaa acc atc ctc ggc act	1296
Ala Glu Thr Leu Lys Thr Trp Thr Met Met Glu Thr Ile Leu Gly Thr		
420	gtc ggt gcc atc gtt ggg atg att gcg ttc cag ctg ttg agt taa	1341
Val Gly Ala Ile Val Gly Met Ile Ala Phe Gln Leu Leu Ser		
435		
440		
445		

<210> 10239

<211> 446

<212> PRT

<213> Escherichia coli 0157

<400> 10239

Met Thr Thr Leu Thr Leu Val Leu Thr Ala Val Gly Ser Val Leu Leu	
1 5 10 15	
Leu Leu Phe Leu Val Met Lys Ala Arg Met His Ala Phe Leu Ala Leu	
20 25 30	
Met Val Val Ser Met Gly Ala Gly Leu Phe Ser Gly Met Pro Leu Asp	
35 40 45	
Lys Ile Ala Ala Thr Met Glu Lys Gly Met Gly Gly Thr Leu Gly Phe	
50 55 60	
Leu Ala Val Val Val Ala Leu Gly Ala Met Phe Gly Lys Ile Leu His	
65 70 75 80	
Glu Thr Gly Ala Val Asp Gln Ile Ala Val Lys Met Leu Lys Ser Phe	
85 90 95	
Gly His Ser Arg Ala His Tyr Ala Ile Gly Leu Ala Gly Leu Val Cys	
100 105 110	
Ala Leu Pro Leu Phe Phe Glu Val Ala Ile Val Leu Leu Ile Ser Val	
115 120 125	
Ala Phe Ser Met Ala Arg His Thr Gly Thr Asn Leu Val Lys Leu Val	
130 135 140	
Ile Pro Leu Phe Ala Gly Val Ala Ala Ala Ala Phe Leu Val Pro	
145 150 155 160	
Gly Pro Ala Pro Met Leu Leu Ala Ser Gln Met Asn Ala Asp Phe Gly	
165 170 175	
Trp Met Ile Leu Ile Gly Leu Cys Ala Ala Ile Pro Gly Met Ile Ile	
180 185 190	
Ala Gly Pro Leu Trp Gly Asn Phe Ile Ser Arg Tyr Val Glu Leu His	
195 200 205	
Ile Pro Asp Asp Ile Ser Glu Pro His Leu Gly Glu Gly Lys Met Pro	
210 215 220	
Ser Phe Gly Phe Ser Leu Ser Leu Ile Leu Leu Pro Leu Val Leu Val	
225 230 235 240	
Gly Leu Lys Thr Ile Ala Ala Arg Phe Val Pro Glu Gly Ser Thr Ala	
245 250 255	
Tyr Glu Trp Phe Glu Phe Ile Gly His Pro Phe Thr Ala Ile Leu Val	
260 265 270	
Ala Cys Leu Val Ala Ile Tyr Gly Leu Ala Met Arg Gln Gly Met Pro	
275 280 285	
Lys Asp Lys Val Met Glu Ile Cys Gly His Ala Leu Gln Pro Ala Gly	
290 295 300	
Ile Ile Leu Leu Val Ile Gly Ala Gly Gly Val Phe Lys Gln Val Leu	
305 310 315 320	
Val Asp Ser Gly Val Gly Pro Ala Leu Gly Glu Ala Leu Thr Gly Met	
325 330 335	
Gly Leu Pro Ile Ala Ile Thr Cys Phe Val Leu Ala Ala Val Arg	
340 345 350	
Ile Ile Gln Gly Ser Ala Thr Val Ala Cys Leu Thr Ala Val Gly Leu	
355 360 365	
Val Met Pro Val Ile Glu Gln Leu Asn Tyr Ser Gly Ala Gln Met Ala	
370 375 380	
Ala Leu Ser Ile Cys Ile Ala Gly Gly Ser Ile Val Val Ser His Val	

PF59083SeqList PF59083.txt

385 390 395 400
 Asn Asp Ala Gly Phe Trp Leu Phe Gly Lys Phe Thr Gly Ala Thr Glu
 405 410 415
 Ala Glu Thr Leu Lys Thr Trp Thr Met Met Glu Thr Ile Leu Gly Thr
 420 425 430
 Val Gly Ala Ile Val Gly Met Ile Ala Phe Gln Leu Leu Ser
 435 440 445

<210> 10240
 <211> 1353
 <212> DNA
 <213> Pseudomonas aeruginosa

<220>
 <221> CDS
 <222> (1)..(1353)
 <223> transl_table=11

<400> 10240
 atg ttc ggc atg tca cac gat gcc tac ctg ctc ctc gac gcc ctg gtg 48
 Met Phe Gly Met Ser His Asp Ala Tyr Leu Leu Leu Asp Ala Leu Val
 1 5 10 15
 acc atc atc ggc ctg atc gtg ctg atc acc cgc ttc aag gtg cat ccc 96
 Thr Ile Ile Gly Leu Ile Val Leu Ile Thr Arg Phe Lys Val His Pro
 20 25 30
 ttc atc gcc ctg atc atc gcc gcc ggc ttc ctc ggc ctg acc tcg ggg 144
 Phe Ile Ala Leu Ile Ile Ala Ala Gly Phe Leu Gly Leu Thr Ser Gly
 35 40 45
 atg ccg gtg gag aag atc gtc aaa tcc ttc cag gac ggc ttc ggc ggc 192
 Met Pro Val Glu Lys Ile Val Lys Ser Phe Gln Asp Gly Phe Gly Gly
 50 55 60
 gtg ctc ggc ttc gtc ggc gtg atc ctc gcc ctg ggc acc atg ctc ggc 240
 Val Leu Gly Phe Val Gly Val Ile Leu Ala Leu Gly Thr Met Leu Gly
 65 70 75 80
 aag ctg atg gcc gat tcc ggc ggc gcc gac cag atc gcc cgc acc ctg 288
 Lys Leu Met Ala Asp Ser Gly Gly Ala Asp Gln Ile Ala Arg Thr Leu
 85 90 95
 atc cgc gcc ttc ggc aag gag cgg gtg cac tgg tcg atg atg ctc gcc 336
 Ile Arg Ala Phe Gly Lys Glu Arg Val His Trp Ser Met Met Leu Ala
 100 105 110
 gcg ttc ctg gtg ggc atc ccg ctg ttc ttc gag atc ggc ttc atc ctg 384
 Ala Phe Leu Val Gly Ile Pro Leu Phe Phe Glu Ile Gly Phe Ile Leu
 115 120 125
 ctg atc ccg ctg gtg ttc atc gtc gcc cgg cgc agc ggc gtg tcc ctg 432
 Leu Ile Pro Leu Val Phe Ile Val Ala Arg Arg Ser Gly Val Ser Leu
 130 135 140
 atc aag atc ggc atc ccg ttg ctc gcc ggc ctt tcc gcg gtg cac ggt 480
 Ile Lys Ile Gly Ile Pro Leu Leu Ala Gly Leu Ser Ala Val His Gly
 145 150 155 160
 ctg gtg ccg ccg cat ccc ggc ccg ctg ctg gcg atc ggc gtg ttc ggc 528
 Leu Val Pro Pro His Pro Gly Pro Leu Leu Ala Ile Gly Val Phe Gly
 165 170 175
 gcc gac atc ggc aag acc atc ctc tac ggc ctg atc gtc gcc ctg ccc 576
 Ala Asp Ile Gly Lys Thr Ile Leu Tyr Gly Leu Ile Val Ala Leu Pro
 180 185 190
 acc gcc gcc atc gcc ggc ccg ctg ttc ggc gcg ctg gtc tcg cgc tac 624
 Thr Ala Ala Ile Ala Gly Pro Leu Phe Gly Ala Leu Val Ser Arg Tyr
 195 200 205
 ata ccc ggc acg cca tcg gcg gaa ctg gtc gag cag atc gcc cac gag 672
 Ile Pro Gly Thr Pro Ser Ala Glu Leu Val Glu Gln Ile Ala His Glu
 210 215 220
 ccc gag acc cag gac ctg ccc agc ttc ggc gtg acc ctg gcg acc gtg 720
 Pro Glu Thr Gln Asp Leu Pro Ser Phe Gly Val Thr Leu Ala Thr Val
 225 230 235 240
 ctg ctg ccg gtg ttc ctg atg ctg ctg aag acc ttc gcc gac gtc gcc 768
 Leu Leu Pro Val Phe Leu Met Leu Leu Lys Thr Phe Ala Asp Val Ala
 245 250 255
 ttc ccc gat ggc cac gcg ttc cgc gcc tgg atg gac atg atc ggc cat 816
 Phe Pro Asp Gly His Ala Phe Arg Ala Trp Met Asp Met Ile Gly His

PF59083SeqList PF59083.txt

[illegible]

<210> 10241
<211> 450
<212> PRT
<213> Pseudomonas aeruginosa

<400>	10241															
Met	Phe	Gly	Met	Ser ₅	His	Asp	Ala	Tyr	Leu ₁₀	Leu	Leu	Asp	Ala	Leu ₁₅	Val	
1	Thr	Ile	Ile	Gly ₂₀	Leu	Ile	Val	Leu	Ile ₂₅	Thr	Arg	Phe	Lys	Val ₃₀	His	Pro
	Phe	Ile	Ala ₃₅	Leu	Ile	Ile	Ala	Ala ₄₀	Gly	Phe	Leu	Gly	Leu ₄₅	Thr	Ser	Gly
	Met	Pro	Val ₅₀	Glu	Lys	Ile	Val ₅₅	Lys	Ser	Phe	Gln	Asp ₆₀	Gly	Phe	Gly	Gly
	Val	Leu	Gly	Phe	Val	Gly ₇₀	Val	Ile	Leu	Ala	Leu ₇₅	Gly	Thr	Met	Leu	Gly ₈₀
65	Lys	Leu	Met	Ala	Asp ₈₅	Ser	Gly	Gly	Ala	Asp ₉₀	Gln	Ile	Ala	Arg	Thr ₉₅	Leu
	Ile	Arg	Ala	Phe ₁₀₀	Gly	Lys	Glu	Arg	Val ₁₀₅	His	Trp	Ser	Met	Met ₁₁₀	Leu	Ala
	Ala	Phe	Leu ₁₁₅	Val	Gly	Ile	Pro	Leu ₁₂₀	Phe	Phe	Glu	Ile	Gly ₁₂₅	Phe	Ile	Leu
	Leu	Ile	Pro	Leu	Val	Phe	Ile ₁₃₅	Val	Ala	Arg	Arg	Ser ₁₄₀	Gly	Val	Ser	Leu
	Ile	Lys	Ile	Gly	Ile	Pro	Leu ₁₅₀	Leu	Ala	Gly	Leu ₁₅₅	Ser	Ala	Val	His	Gly ₁₆₀
145	Leu	Val	Pro	Pro	His ₁₆₅	Pro	Gly	Pro	Leu	Leu ₁₇₀	Ala	Ile	Gly	Val	Phe ₁₇₅	Gly
	Ala	Asp	Ile	Gly ₁₈₀	Lys	Thr	Ile	Leu	Tyr ₁₈₅	Gly	Leu	Ile	Val	Ala ₁₉₀	Leu	Pro
	Thr	Ala	Ala	Ile	Ala	Gly	Pro	Leu	Phe	Gly	Ala	Leu	Val	Ser	Arg	Tyr

Seite 10847

PF59083SeqList PF59083.txt

Ile	Pro	Gly	Thr	Pro	Ser	Ala	Glu	Leu	Val	Glu	Gln	Ile	Ala	His	Glu
	210					215					220				
Pro	Glu	Thr	Gln	Asp	Leu	Pro	Ser	Phe	Gly	Val	Thr	Leu	Ala	Thr	Val
225					230					235					240
Leu	Leu	Pro	Val	Phe	Leu	Met	Leu	Leu	Lys	Thr	Phe	Ala	Asp	Val	Ala
				245					250					255	
Phe	Pro	Asp	Gly	His	Ala	Phe	Arg	Ala	Trp	Met	Asp	Met	Ile	Gly	His
			260					265					270		
Pro	Ile	Ser	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Val	Ala	Leu	Tyr	Thr	Phe
			275				280					285			
Gly	Tyr	Ala	Arg	Gly	Phe	Asp	Ser	Lys	Lys	Ile	Leu	Arg	Leu	Leu	Asp
	290					295					300				
Gln	Ser	Leu	Ala	Pro	Thr	Ala	Ala	Ile	Val	Met	Ile	Ile	Gly	Ala	Gly
305					310					315					320
Gly	Gly	Phe	Lys	Gln	Met	Leu	Val	Ala	Ser	Gly	Val	Gly	Asp	Val	Ile
				325					330					335	
Gly	His	Leu	Ala	Val	Asn	Ala	Gln	Ile	Ser	Pro	Ile	Leu	Leu	Ala	Trp
			340				345						350		
Leu	Val	Ala	Ala	Val	Ile	Arg	Ile	Ala	Thr	Gly	Ser	Ala	Thr	Val	Ala
		355				360						365			
Thr	Ile	Thr	Gly	Ala	Gly	Ile	Val	Val	Pro	Val	Ile	Asp	Leu	Ile	Pro
	370					375					380				
Gly	Val	Asn	Arg	Glu	Leu	Leu	Val	Leu	Ala	Thr	Gly	Ala	Gly	Ser	Leu
385					390					395					400
Ile	Leu	Ser	His	Val	Asn	Asp	Ala	Gly	Phe	Trp	Leu	Val	Lys	Gln	Tyr
			405					410					415		
Phe	Asn	Met	Ser	Val	Ser	Glu	Thr	Phe	Lys	Thr	Trp	Thr	Ala	Met	Glu
			420					425					430		
Thr	Ile	Leu	Ser	Val	Val	Gly	Leu	Val	Phe	Ile	Leu	Leu	Leu	Ser	Leu
		435				440						445			
Val	Leu														
	450														

<210> 10242
 <211> 1320
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1320)
 <223> transl_table=11

<400> 10242	
atg cca tta atc att att gcg gca ggc gtc gcg ctg ctt ctt atc ctg	48
Met Pro Leu Ile Ile Ile Ala Ala Gly Val Ala Leu Leu Leu Ile Leu	
1 5 10 15	
atg atc ggc ttt aaa gtt aac ggc ttt att gcc ctc gtt ctg gta gct	96
Met Ile Gly Phe Lys Val Asn Gly Phe Ile Ala Leu Val Leu Val Ala	
20 25 30	
gcc gtc gtc gga ttt gcc gaa ggg atg gat gca cag gcc gtc ctg cac	144
Ala Val Val Gly Phe Ala Glu Gly Met Asp Ala Gln Ala Val Leu His	
35 40 45	
tct ata caa aat ggt atc ggc agc acg ctc ggc ggg ctg gca atg atc	192
Ser Ile Gln Asn Gly Ile Gly Ser Thr Leu Gly Gly Leu Ala Met Ile	
50 55 60	
ctc ggt ttc ggg gcc atg tta ggc aag ctg att tct gat acg ggt gcg	240
Leu Gly Phe Gly Ala Met Leu Gly Lys Leu Ile Ser Asp Thr Gly Ala	
65 70 75 80	
gca caa cgt atc gcc act acg ctg att gct act ttt ggt aaa aaa cgc	288
Ala Gln Arg Ile Ala Thr Thr Leu Ile Ala Thr Phe Gly Lys Lys Arg	
85 90 95	
gtg caa tgg gcg cta gtg atc acc ggt ctg gtt gtg ggc ctc gcc atg	336
Val Gln Trp Ala Leu Val Ile Thr Gly Leu Val Val Gly Leu Ala Met	
100 105 110	
ttt ttt gaa gtg ggt ttt gtc ctg ctg ttg ccg ttg gta ttt acc atc	384
Phe Phe Glu Val Gly Phe Val Leu Leu Leu Pro Leu Val Phe Thr Ile	
115 120 125	

PF59083SeqList PF59083.txt

gta	gca	tca	tca	gga	tta	ccc	ctg	ttg	tat	gtt	ggc	gta	cca	atg	gta	432
Val	Ala	Ser	Ser	Gly	Leu	Pro	Leu	Leu	Tyr	Val	Gly	Val	Pro	Met	Val	
	130					135					140					
gca	gcg	ctc	tct	gta	acc	cac	tgt	ttt	ctg	ccg	cca	cat	cca	ggg	cct	480
Ala	Ala	Leu	Ser	Val	Thr	His	Cys	Phe	Leu	Pro	Pro	His	Pro	Gly	Pro	
145					150					155					160	
act	gcc	atc	gcg	act	atc	ttt	gag	gct	aat	ctc	gga	acg	act	tta	ctg	528
Thr	Ala	Ile	Ala	Thr	Ile	Phe	Glu	Ala	Asn	Leu	Gly	Thr	Thr	Leu	Leu	
				165					170					175		
tat	gga	ttt	atc	att	acc	att	ccg	aca	gtt	att	gtc	gca	gga	ccg	ctg	576
Tyr	Gly	Phe	Ile	Ile	Thr	Ile	Pro	Thr	Val	Ile	Val	Ala	Gly	Pro	Leu	
			180					185					190			
ttt	tct	aaa	ctg	cta	act	cgc	ttt	gag	aaa	gca	cca	ccg	gaa	ggc	tta	624
Phe	Ser	Lys	Leu	Leu	Thr	Arg	Phe	Glu	Lys	Ala	Pro	Pro	Glu	Gly	Leu	
		195					200					205				
ttt	aat	cct	cat	ctg	ttt	agc	gaa	gag	gag	atg	ccc	tcc	ttc	tg	aac	672
Phe	Asn	Pro	His	Leu	Phe	Ser	Glu	Glu	Glu	Met	Pro	Ser	Phe	Trp	Asn	
	210					215					220					
agt	att	ttc	gct	gcc	gtg	atc	ccg	gtc	atc	ctg	atg	gct	atc	gcc	gcc	720
Ser	Ile	Phe	Ala	Ala	Val	Ile	Pro	Val	Ile	Leu	Met	Ala	Ile	Ala	Ala	
225					230					235					240	
gtt	tgt	gaa	att	acg	tta	ccg	aaa	act	aac	acc	gtg	cgc	ctc	ttc	ttt	768
Val	Cys	Glu	Ile	Thr	Leu	Pro	Lys	Thr	Asn	Thr	Val	Arg	Leu	Phe	Phe	
				245				250						255		
gaa	ttt	gtc	ggt	aac	cct	gcc	gtt	gcg	ctg	ttt	att	gcc	att	gtt	att	816
Glu	Phe	Val	Gly	Asn	Pro	Ala	Val	Ala	Leu	Phe	Ile	Ala	Ile	Val	Ile	
			260				265						270			
gcg	att	ttc	aca	ctg	ggc	cga	cgt	aat	gga	cgc	acc	atc	gag	caa	atc	864
Ala	Ile	Phe	Thr	Leu	Gly	Arg	Arg	Asn	Gly	Arg	Thr	Ile	Glu	Gln	Ile	
		275					280					285				
atg	gat	atc	att	ggg	gat	tct	ata	ggc	gct	atc	gcg	atg	att	gtg	ttt	912
Met	Asp	Ile	Ile	Gly	Asp	Ser	Ile	Gly	Ala	Ile	Ala	Met	Ile	Val	Phe	
	290					295					300					
att	atc	gct	ggc	ggc	ggc	gcg	ttt	aag	cag	gta	tta	gta	gat	agc	ggc	960
Ile	Ile	Ala	Gly	Gly	Gly	Ala	Phe	Lys	Gln	Val	Leu	Val	Asp	Ser	Gly	
305					310					315					320	
gtc	ggg	cac	tat	att	tca	cac	tta	atg	acc	gga	act	aca	ctt	tcg	ccg	1008
Val	Gly	His	Tyr	Ile	Ser	His	Leu	Met	Thr	Gly	Thr	Thr	Leu	Ser	Pro	
				325				330						335		
tta	ttg	atg	tgc	ttg	act	gtt	gcg	gcg	ctg	ttg	cgt	atc	gct	ctg	ggc	1056
Leu	Leu	Met	Cys	Trp	Thr	Val	Ala	Ala	Leu	Leu	Arg	Ile	Ala	Leu	Gly	
			340				345						350			
tct	gcc	acc	gtc	gcg	gcc	att	acc	acc	gcg	ggt	gtg	gtg	ttg	ccg	att	1104
Ser	Ala	Thr	Val	Ala	Ala	Ile	Thr	Thr	Ala	Gly	Val	Val	Leu	Pro	Ile	
		355					360					365				
atc	aac	gtt	acc	cat	gcc	gat	ccc	gct	tta	atg	gta	ctg	gca	acc	ggc	1152
Ile	Asn	Val	Thr	His	Ala	Asp	Pro	Ala	Leu	Met	Val	Leu	Ala	Thr	Gly	
	370					375					380					
gcg	ggc	agc	gtg	atc	gcg	tca	cac	gta	aac	gac	cct	ggc	ttc	tg	cta	1200
Ala	Gly	Ser	Val	Ile	Ala	Ser	His	Val	Asn	Asp	Pro	Gly	Phe	Trp	Leu	
385					390					395					400	
ttt	aaa	ggg	tat	ttt	aat	ctg	acg	gtt	ggc	gaa	acg	ttg	cgt	acc	tg	1248
Phe	Lys	Gly	Tyr	Phe	Asn	Leu	Thr	Val	Gly	Glu	Thr	Leu	Arg	Thr	Trp	
				405				410						415		
acg	gtg	atg	gaa	acc	ctt	att	tct	att	atg	ggt	ttg	ctg	ggc	gtg	tta	1296
Thr	Val	Met	Glu	Thr	Leu	Ile	Ser	Ile	Met	Gly	Leu	Leu	Gly	Val	Leu	
			420				425						430			
gcc	att	aac	gcc	gta	ttg	cac	tga									1320
Ala	Ile	Asn	Ala	Val	Leu	His										
		435														

<210> 10243

<211> 439

<212> PRT

<213> Escherichia coli

<400> 10243

Met Pro Leu Ile Ile Ile Ala Ala Gly Val Ala Leu Leu Leu Ile Leu
1 5 10 15

PF59083SeqList PF59083.txt

Met Ile Gly Phe Lys Val Asn Gly Phe Ile Ala Leu Val Leu Val Ala
 20 25 30
 Ala Val Val Gly Phe Ala Glu Gly Met Asp Ala Gln Ala Val Leu His
 35 40 45
 Ser Ile Gln Asn Gly Ile Gly Ser Thr Leu Gly Gly Leu Ala Met Ile
 50 55 60
 Leu Gly Phe Gly Ala Met Leu Gly Lys Leu Ile Ser Asp Thr Gly Ala
 65 70 75 80
 Ala Gln Arg Ile Ala Thr Thr Leu Ile Ala Thr Phe Gly Lys Lys Arg
 85 90 95
 Val Gln Trp Ala Leu Val Ile Thr Gly Leu Val Val Gly Leu Ala Met
 100 105 110
 Phe Phe Glu Val Gly Phe Val Leu Leu Leu Pro Leu Val Phe Thr Ile
 115 120 125
 Val Ala Ser Ser Gly Leu Pro Leu Leu Tyr Val Gly Val Pro Met Val
 130 135 140
 Ala Ala Leu Ser Val Thr His Cys Phe Leu Pro Pro His Pro Gly Pro
 145 150 155 160
 Thr Ala Ile Ala Thr Ile Phe Glu Ala Asn Leu Gly Thr Thr Leu Leu
 165 170 175
 Tyr Gly Phe Ile Ile Thr Ile Pro Thr Val Ile Val Ala Gly Pro Leu
 180 185 190
 Phe Ser Lys Leu Leu Thr Arg Phe Glu Lys Ala Pro Pro Glu Gly Leu
 195 200 205
 Phe Asn Pro His Leu Phe Ser Glu Glu Glu Met Pro Ser Phe Trp Asn
 210 215 220
 Ser Ile Phe Ala Ala Val Ile Pro Val Ile Leu Met Ala Ile Ala Ala
 225 230 235 240
 Val Cys Glu Ile Thr Leu Pro Lys Thr Asn Thr Val Arg Leu Phe Phe
 245 250 255
 Glu Phe Val Gly Asn Pro Ala Val Ala Leu Phe Ile Ala Ile Val Ile
 260 265 270
 Ala Ile Phe Thr Leu Gly Arg Arg Asn Gly Arg Thr Ile Glu Gln Ile
 275 280 285
 Met Asp Ile Ile Gly Asp Ser Ile Gly Ala Ile Ala Met Ile Val Phe
 290 295 300
 Ile Ile Ala Gly Gly Gly Ala Phe Lys Gln Val Leu Val Asp Ser Gly
 305 310 315 320
 Val Gly His Tyr Ile Ser His Leu Met Thr Gly Thr Thr Leu Ser Pro
 325 330 335
 Leu Leu Met Cys Trp Thr Val Ala Ala Leu Leu Arg Ile Ala Leu Gly
 340 345 350
 Ser Ala Thr Val Ala Ala Ile Thr Thr Ala Gly Val Val Leu Pro Ile
 355 360 365
 Ile Asn Val Thr His Ala Asp Pro Ala Leu Met Val Leu Ala Thr Gly
 370 375 380
 Ala Gly Ser Val Ile Ala Ser His Val Asn Asp Pro Gly Phe Trp Leu
 385 390 395 400
 Phe Lys Gly Tyr Phe Asn Leu Thr Val Gly Glu Thr Leu Arg Thr Trp
 405 410 415
 Thr Val Met Glu Thr Leu Ile Ser Ile Met Gly Leu Leu Gly Val Leu
 420 425 430
 Ala Ile Asn Ala Val Leu His
 435

<210> 10244
 <211> 1365
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1365)
 <223> transl_table=11

<400> 10244
 atg tcc aca att aca ttg tta tgc att gcg tta gct ggc gta atc atg
 Met Ser Thr Ile Thr Leu Leu Cys Ile Ala Leu Ala Gly Val Ile Met
 1 5 10 15

PF59083SeqList PF59083.txt																
ctg	ttg	ctg	ctg	gtc	atc	aag	gca	aag	gta	caa	cca	ttc	ggt	gct	ttg	96
Leu	Leu	Leu	Leu	Val	Ile	Lys	Ala	Lys	Val	Gln	Pro	Phe	Val	Ala	Leu	
			20					25				30				
ctc	ctc	gtc	agc	ctg	tta	gtc	gca	ctt	gcg	gca	ggt	ata	ccg	gcg	ggc	144
Leu	Leu	Val	Ser	Leu	Leu	Val	Ala	Leu	Ala	Ala	Gly	Ile	Pro	Ala	Gly	
		35					40					45				
gaa	gtg	ggt	aaa	gtg	atg	atc	gcc	ggg	atg	ggc	ggt	gtg	ctt	ggt	tcc	192
Glu	Val	Gly	Lys	Val	Met	Ile	Ala	Gly	Met	Gly	Gly	Val	Leu	Gly	Ser	
	50					55				60						
gtc	act	att	att	att	ggt	ctg	ggc	gct	atg	ctg	ggg	cgt	atg	atc	gaa	240
Val	Thr	Ile	Ile	Ile	Gly	Leu	Gly	Ala	Met	Leu	Gly	Arg	Met	Ile	Glu	
	65				70					75					80	
cac	tct	ggt	ggt	gca	gag	tca	ctg	gct	aat	tat	ttc	agt	cgc	aag	tta	288
His	Ser	Gly	Gly	Ala	Glu	Ser	Leu	Ala	Asn	Tyr	Phe	Ser	Arg	Lys	Leu	
				85					90					95		
ggt	gac	aaa	cga	act	atc	gct	gcg	ctg	act	ctg	gca	gcg	ttc	ttc	ctc	336
Gly	Asp	Lys	Arg	Thr	Ile	Ala	Ala	Leu	Thr	Leu	Ala	Ala	Phe	Phe	Leu	
			100					105					110			
ggt	att	ccc	gtc	ttc	ttt	gat	gtc	ggc	ttt	att	att	ctt	gcg	cca	atc	384
Gly	Ile	Pro	Val	Phe	Phe	Asp	Val	Gly	Phe	Ile	Ile	Ala	Pro	Ile		
		115					120					125				
att	tac	ggt	ttt	gcc	aag	gtt	gcc	aaa	ata	tcg	cca	ctc	aaa	ttt	ggc	432
Ile	Tyr	Gly	Phe	Ala	Lys	Val	Ala	Lys	Ile	Ser	Pro	Leu	Lys	Phe	Gly	
	130					135					140					
ctg	cct	gtc	gct	ggg	atc	ctc	act	gtt	cac	gtg	gcg	gta	ccg	ccg		480
Leu	Pro	Val	Ala	Gly	Ile	Met	Leu	Thr	Val	His	Val	Ala	Val	Pro	Pro	
	145				150				155						160	
cat	cca	ggc	cct	gtc	gcc	gca	gcg	ggg	tta	ctc	cac	gca	gac	atc	ggc	528
His	Pro	Gly	Pro	Val	Ala	Ala	Ala	Gly	Leu	Leu	His	Ala	Asp	Ile	Gly	
			165					170						175		
tgg	cta	acc	atc	atc	ggt	att	gcg	att	tct	att	ccc	gta	ggg	gtt	gtt	576
Trp	Leu	Thr	Ile	Ile	Gly	Ile	Ala	Ile	Ser	Ile	Pro	Val	Gly	Val	Val	
			180					185					190			
ggc	tac	ttt	gca	gcg	aaa	ata	atc	aat	aag	cgc	caa	tat	gcg	atg	tca	624
Gly	Tyr	Phe	Ala	Ala	Lys	Ile	Ile	Asn	Lys	Arg	Gln	Tyr	Ala	Met	Ser	
		195				200						205				
gta	gaa	gta	ctg	gaa	cag	atg	caa	ctg	gct	ccg	gcc	agt	gag	gaa	ggc	672
Val	Glu	Val	Leu	Glu	Gln	Met	Gln	Leu	Ala	Pro	Ala	Ser	Glu	Glu	Gly	
	210					215					220					
gcg	aca	aaa	tta	agc	gat	aaa	ata	aat	cca	ccg	ggc	gtc	gcg	ctg	gtc	720
Ala	Thr	Lys	Leu	Ser	Asp	Lys	Ile	Asn	Pro	Pro	Gly	Val	Ala	Leu	Val	
	225				230					235					240	
acc	tcg	cta	att	gtt	att	cct	atc	gcg	att	atc	atg	gcg	ggt	acg	gtt	768
Thr	Ser	Leu	Ile	Val	Ile	Pro	Ile	Ala	Ile	Ile	Met	Ala	Gly	Thr	Val	
			245						250					255		
tcc	gca	aca	ctg	atg	ccg	cct	tcg	cat	ccc	ctg	ctt	ggt	acg	cta	cag	816
Ser	Ala	Thr	Leu	Met	Pro	Pro	Ser	His	Pro	Leu	Leu	Gly	Thr	Leu	Gln	
			260					265					270			
ctg	atc	ggc	tca	cca	atg	gta	gct	cta	atg	att	gcg	ctg	gtg	ctg	gca	864
Leu	Ile	Gly	Ser	Pro	Met	Val	Ala	Leu	Met	Ile	Ala	Leu	Val	Leu	Ala	
		275				280						285				
ttc	tgg	tta	ttg	gct	tta	cgt	cgc	ggc	tgg	agc	tta	caa	cac	acc	agc	912
Phe	Trp	Leu	Leu	Ala	Leu	Arg	Arg	Gly	Trp	Ser	Leu	Gln	His	Thr	Ser	
	290					295					300					
gac	att	atg	ggc	tca	gcg	cct	act	gcg	gcg	gta	gtg	att	ttg	gtt		960
Asp	Ile	Met	Gly	Ser	Ala	Leu	Pro	Thr	Ala	Ala	Val	Val	Ile	Leu	Val	
	305				310					315					320	
act	ggt	gct	gga	ggg	gta	ttt	ggc	aaa	gtg	ctg	gtg	gaa	tcg	ggc	gtc	1008
Thr	Gly	Ala	Gly	Gly	Val	Phe	Gly	Lys	Val	Leu	Val	Glu	Ser	Gly	Val	
			325						330					335		
ggc	aaa	gcc	ctt	gcc	aac	atg	cta	caa	atg	att	gac	ctg	cct	ctg	tta	1056
Gly	Lys	Ala	Leu	Ala	Asn	Met	Leu	Gln	Met	Ile	Asp	Leu	Pro	Leu	Leu	
			340					345					350			
cca	gcc	gca	ttt	att	att	tca	ctg	gcg	ctg	cgt	gca	tcg	cag	ggg	tca	1104
Pro	Ala	Ala	Phe	Ile	Ile	Ser	Leu	Ala	Leu	Arg	Ala	Ser	Gln	Gly	Ser	
		355					360						365			
gca	acc	gta	gca	ata	ctg	aca	acc	ggc	ggg	tta	ctc	tca	gaa	gcg	gtg	1152
Ala	Thr	Val	Ala	Ile	Leu	Thr	Thr	Gly	Gly	Leu	Leu	Ser	Glu	Ala	Val	
	370					375					380					

PF59083SeqList PF59083.txt

atg gga ttg aat ccg att cag tgc gta ttg gtg acg ctg gca gcc tgc	1200
Met Gly Leu Asn Pro Ile Gln Cys Val Leu Val Thr Leu Ala Ala Cys	
385 390 395 400	
ttt ggt ggg ctt ggt gcg tca cat att aat gac tca ggg ttc tgg att	1248
Phe Gly Gly Leu Gly Ala Ser His Ile Asn Asp Ser Gly Phe Trp Ile	
405 410 415	
gtg acc aaa tat ctg ggg ttg tcg gta gca gac ggt ctg aaa acc tgg	1296
Val Thr Lys Tyr Leu Gly Leu Ser Val Ala Asp Gly Leu Lys Thr Trp	
420 425 430	
aca gtg tta acg acc att ctc ggt ttt acc gga ttc tta att acc tgg	1344
Thr Val Leu Thr Thr Ile Leu Gly Phe Thr Gly Phe Leu Ile Thr Trp	
435 440 445	
tgc gta tgg gcg gta att tga	1365
Cys Val Trp Ala Val Ile	
450	

<210> 10245

<211> 454

<212> PRT

<213> Escherichia coli

<400> 10245

Met Ser Thr Ile Thr Leu Leu Cys Ile Ala Leu Ala Gly Val Ile Met	
1 5 10 15	
Leu Leu Leu Val Ile Lys Ala Lys Val Gln Pro Phe Val Ala Leu	
20 25 30	
Leu Leu Val Ser Leu Leu Val Ala Leu Ala Ala Gly Ile Pro Ala Gly	
35 40 45	
Glu Val Gly Lys Val Met Ile Ala Gly Met Gly Val Leu Gly Ser	
50 55 60	
Val Thr Ile Ile Ile Gly Leu Gly Ala Met Leu Gly Arg Met Ile Glu	
65 70 75 80	
His Ser Gly Gly Ala Glu Ser Leu Ala Asn Tyr Phe Ser Arg Lys Leu	
85 90 95	
Gly Asp Lys Arg Thr Ile Ala Ala Leu Thr Leu Ala Ala Phe Phe Leu	
100 105 110	
Gly Ile Pro Val Phe Phe Asp Val Gly Phe Ile Ile Leu Ala Pro Ile	
115 120 125	
Ile Tyr Gly Phe Ala Lys Val Ala Lys Ile Ser Pro Leu Lys Phe Gly	
130 135 140	
Leu Pro Val Ala Gly Ile Met Leu Thr Val His Val Ala Val Pro Pro	
145 150 155 160	
His Pro Gly Pro Val Ala Ala Ala Gly Leu Leu His Ala Asp Ile Gly	
165 170 175	
Trp Leu Thr Ile Gly Ile Ala Ile Ser Ile Pro Val Gly Val Val	
180 185 190	
Gly Tyr Phe Ala Ala Lys Ile Ile Asn Lys Arg Gln Tyr Ala Met Ser	
195 200 205	
Val Glu Val Leu Glu Gln Met Gln Leu Ala Pro Ala Ser Glu Glu Gly	
210 215 220	
Ala Thr Lys Leu Ser Asp Lys Ile Asn Pro Pro Gly Val Ala Leu Val	
225 230 235 240	
Thr Ser Leu Ile Val Ile Pro Ile Ala Ile Ile Met Ala Gly Thr Val	
245 250 255	
Ser Ala Thr Leu Met Pro Pro Ser His Pro Leu Leu Gly Thr Leu Gln	
260 265 270	
Leu Ile Gly Ser Pro Met Val Ala Leu Met Ile Ala Leu Val Leu Ala	
275 280 285	
Phe Trp Leu Leu Ala Leu Arg Gly Trp Ser Leu Gln His Thr Ser	
290 295 300	
Asp Ile Met Gly Ser Ala Leu Pro Thr Ala Ala Val Val Ile Leu Val	
305 310 315 320	
Thr Gly Ala Gly Gly Val Phe Gly Lys Val Leu Val Glu Ser Gly Val	
325 330 335	
Gly Lys Ala Leu Ala Asn Met Leu Gln Met Ile Asp Leu Pro Leu Leu	
340 345 350	
Pro Ala Ala Phe Ile Ile Ser Leu Ala Leu Arg Ala Ser Gln Gly Ser	
355 360 365	
Ala Thr Val Ala Ile Leu Thr Thr Gly Gly Leu Leu Ser Glu Ala Val	

PF59083SeqList PF59083.txt

370 375 380
 Met Gly Leu Asn Pro Ile Gln Cys Val Leu Val Thr Leu Ala Ala Cys
 385 390 395 400
 Phe Gly Gly Leu Gly Ala Ser His Ile Asn Asp Ser Gly Phe Trp Ile
 405 410 415
 Val Thr Lys Tyr Leu Gly Leu Ser Val Ala Asp Gly Leu Lys Thr Trp
 420 425 430
 Thr Val Leu Thr Thr Ile Leu Gly Phe Thr Gly Phe Leu Ile Thr Trp
 435 440 445
 Cys Val Trp Ala Val Ile
 450

<210> 10246
 <211> 1350
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1350)
 <223> transl_table=11

<400> 10246
 atg cca cta att atc gtt gtg gca ggg att gct tta ctc ctg ctt tta 48
 Met Pro Leu Ile Ile Val Val Ala Gly Ile Ala Leu Leu Leu Leu
 1 5 10 15
 acc ata aaa att aag ctt aat acg ttt gtt tcg tta att att gtc tcg 96
 Thr Ile Lys Ile Lys Leu Asn Thr Phe Val Ser Leu Ile Ile Val Ser
 20 25 30
 att gct gtc gcc atc gcc agt ggt atg gat ttg agt aaa gtc gtc acc 144
 Ile Ala Val Ala Ile Ala Ser Gly Met Asp Leu Ser Lys Val Val Thr
 35 40 45
 tca gtc gaa tcc gga ctt ggc ggt acg ctg ggc cat att ggt ttg ata 192
 Ser Val Glu Ser Gly Leu Gly Gly Thr Leu Gly His Ile Gly Leu Ile
 50 55 60
 ttt ggc ttc ggt gtt atg ctc ggt cgc ttg ctg gcc gat gcg ggt ggt 240
 Phe Gly Phe Gly Val Met Leu Gly Arg Leu Leu Ala Asp Ala Gly Gly
 65 70 75 80
 gcg cag cga ata gcg ctg acc atg ctg aat tat ttc ggg aaa aat aaa 288
 Ala Gln Arg Ile Ala Leu Thr Met Leu Asn Tyr Phe Gly Lys Asn Lys
 85 90 95
 ctt gac tgg gca gtg gtc tgt tcg gcg ttt att gtc ggt atc gca ctt 336
 Leu Asp Trp Ala Val Val Cys Ser Ala Phe Ile Val Gly Ile Ala Leu
 100 105 110
 ttt ttc gaa gtc ggt tta att ctt ctg gta cct att tta ttc gct att 384
 Phe Phe Glu Val Gly Leu Ile Leu Leu Val Pro Ile Leu Phe Ala Ile
 115 120 125
 gcc cgt gaa gca aaa ata tca ccg atg ttt atg tgt gtg ccg atg ctt 432
 Ala Arg Glu Ala Lys Ile Ser Pro Met Phe Met Cys Val Pro Met Leu
 130 135 140
 tct ggt ttg ctg gtc gca cac ggt ttt ttg ccg ccg cac ccc ggc ccg 480
 Ser Gly Leu Leu Val Ala His Gly Phe Leu Pro Pro His Pro Gly Pro
 145 150 155 160
 act gtt atc gcc agg gaa tat ggc gct gat gta gga ttg gta ctg ata 528
 Thr Val Ile Ala Arg Glu Tyr Gly Ala Asp Val Gly Leu Val Leu Ile
 165 170 175
 tac ggt atc att gtc ggc att cca acc ttt att ctt tgc ggc ccg gta 576
 Tyr Gly Ile Ile Val Gly Ile Pro Thr Phe Ile Leu Cys Gly Pro Val
 180 185 190
 ttg aat aaa ttc tgc cag cgc att att ccg gac gcc ttt aaa gag 624
 Leu Asn Lys Phe Cys Gln Arg Ile Ile Pro Asp Ala Phe Lys Lys Glu
 195 200 205
 ggg aat ata gcc tct ctc ggc gcg acc cgc cga ttc agc gaa agc gaa 672
 Gly Asn Ile Ala Ser Leu Gly Ala Thr Arg Arg Phe Ser Glu Ser Glu
 210 215 220
 atg cca ggc ttt ggg atc agt ttt ctc acg gca atg ctg ccg gtg atc 720
 Met Pro Gly Phe Gly Ile Ser Phe Leu Thr Ala Met Leu Pro Val Ile
 225 230 235 240
 ctg atg gcg gtt gtc acc atc atc cag atg act cat gcc aaa agt gcc 768

PF59083SeqList PF59083.txt

Leu	Met	Ala	Val	Val	Thr	Ile	Ile	Gln	Met	Thr	His	Ala	Lys	Ser	Ala		
				245					250					255			
gcg	gat	tca	ggc	tta	ttt	tac	aac	gtg	ata	ctg	ttc	tta	ggt	aat	tca	816	
Ala	Asp	Ser	Gly	Leu	Phe	Tyr	Asn	Val	Ile	Leu	Phe	Leu	Gly	Asn	Ser		
			260					265					270				
acg	atc	gcc	atg	ctg	att	tca	ctg	cta	ttc	gcg	atc	tat	acc	atg	ggc	864	
Thr	Ile	Ala	Met	Leu	Ile	Ser	Leu	Leu	Phe	Ala	Ile	Tyr	Thr	Met	Gly		
			275					280					285				
ctg	ggg	cgc	ggg	aaa	aca	atc	cct	gac	ctg	atg	gat	tct	tgc	gga	aaa	912	
Leu	Gly	Arg	Gly	Lys	Thr	Ile	Pro	Asp	Leu	Met	Asp	Ser	Cys	Gly	Lys		
			290					295				300					
gct	atc	gcg	ggg	att	gcc	ggg	ctg	ctg	ctg	att	atc	ggg	ggg	ggg	ggg	960	
Ala	Ile	Ala	Gly	Ile	Ala	Gly	Leu	Leu	Leu	Ile	Ile	Gly	Gly	Gly	Gly		
					310					315					320		
gca	ttc	aag	caa	ggt	ctc	atc	gac	tct	ggc	ggt	ggg	cag	tat	att	tcc	1008	
Ala	Phe	Lys	Gln	Val	Leu	Ile	Asp	Ser	Gly	Val	Gly	Gln	Tyr	Ile	Ser		
					325				330					335			
acc	ctg	ggt	tgc	ggg	atg	gat	att	aac	ccg	atc	ctg	atg	gcc	tgg	ggc	1056	
Thr	Leu	Val	Ser	Gly	Met	Asp	Ile	Asn	Pro	Ile	Leu	Met	Ala	Trp	Gly		
					340			345					350				
gtg	gcc	gca	ttc	ctg	cgt	att	tgt	ctg	ggg	tca	gcc	acc	gtc	gcg	gcg	1104	
Val	Ala	Ala	Phe	Leu	Arg	Ile	Cys	Leu	Gly	Ser	Ala	Thr	Val	Ala	Ala		
			355				360					365					
atc	tct	acc	gcc	ggg	ctg	gtc	atc	cca	ttg	ttg	gca	gta	cat	ccc	aat	1152	
Ile	Ser	Thr	Ala	Gly	Leu	Val	Ile	Pro	Leu	Leu	Ala	Val	His	Pro	Asn		
			370			375					380						
acc	aac	ctg	gcc	ttg	att	acg	ctg	gct	acc	ggg	gcc	gga	tcc	tgt	att	1200	
Thr	Asn	Leu	Ala	Leu	Ile	Thr	Leu	Ala	Thr	Gly	Ala	Gly	Ser	Cys	Ile		
					390				395					400			
tgt	tct	cac	ggt	aac	gat	gcc	agt	ttc	tgg	att	aaa	gac	ttt	ttt	ttt	1248	
Cys	Ser	His	Val	Asn	Asp	Ala	Ser	Phe	Trp	Met	Ile	Lys	Asp	Phe	Phe		
				405					410					415			
ggc	ctg	acc	acc	aaa	gaa	acg	ctg	tta	tcc	tgg	acg	ctg	atg	tcc	aca	1296	
Gly	Leu	Thr	Thr	Lys	Glu	Thr	Leu	Leu	Ser	Trp	Thr	Leu	Met	Ser	Thr		
				420				425					430				
ctc	tta	tcc	atc	agt	ggg	ctg	att	ttt	att	ctg	ctc	gcc	agc	tta	gtt	1344	
Leu	Leu	Ser	Ile	Ser	Gly	Leu	Ile	Phe	Ile	Leu	Leu	Ala	Ser	Leu	Val		
				435			440					445					
tta	taa															1350	
Leu																	

<210> 10247
 <211> 449
 <212> PRT
 <213> Escherichia coli

<400> 10247
 Met Pro Leu Ile Ile Val Val Ala Gly Ile Ala Leu Leu Leu Leu Leu
 1 5 10 15
 Thr Ile Lys Ile Lys Leu Asn Thr Phe Val Ser Leu Ile Ile Val Ser
 20 25 30
 Ile Ala Val Ala Ile Ala Ser Gly Met Asp Leu Ser Lys Val Val Thr
 35 40 45
 Ser Val Glu Ser Gly Leu Gly Thr Leu Gly His Ile Gly Leu Ile
 50 55 60
 Phe Gly Phe Gly Val Met Leu Gly Arg Leu Leu Ala Asp Ala Gly Gly
 65 70 75 80
 Ala Gln Arg Ile Ala Leu Thr Met Leu Asn Tyr Phe Gly Lys Asn Lys
 85 90 95
 Leu Asp Trp Ala Val Val Cys Ser Ala Phe Ile Val Gly Ile Ala Leu
 100 105 110
 Phe Phe Glu Val Gly Leu Ile Leu Leu Val Pro Ile Leu Phe Ala Ile
 115 120 125
 Ala Arg Glu Ala Lys Ile Ser Pro Met Phe Met Cys Val Pro Met Leu
 130 135 140
 Ser Gly Leu Leu Val Ala His Gly Phe Leu Pro Pro His Pro Gly Pro
 145 150 155 160
 Thr Val Ile Ala Arg Glu Tyr Gly Ala Asp Val Gly Leu Val Leu Ile

PF59083SeqList PF59083.txt

Tyr Gly Ile Ile Val Gly Ile Pro Thr Phe Ile Leu Cys Gly Pro Val
 165 170 175
 180 185 190
 Leu Asn Lys Phe Cys Gln Arg Ile Ile Pro Asp Ala Phe Lys Lys Glu
 195 200 205
 Gly Asn Ile Ala Ser Leu Gly Ala Thr Arg Arg Phe Ser Glu Ser Glu
 210 215 220
 Met Pro Gly Phe Gly Ile Ser Phe Leu Thr Ala Met Leu Pro Val Ile
 225 230 235 240
 Leu Met Ala Val Val Thr Ile Ile Gln Met Thr His Ala Lys Ser Ala
 245 250 255
 Ala Asp Ser Gly Leu Phe Tyr Asn Val Ile Leu Phe Leu Gly Asn Ser
 260 265 270
 Thr Ile Ala Met Leu Ile Ser Leu Leu Phe Ala Ile Tyr Thr Met Gly
 275 280 285
 Leu Gly Arg Gly Lys Thr Ile Pro Asp Leu Met Asp Ser Cys Gly Lys
 290 295 300
 Ala Ile Ala Gly Ile Ala Gly Leu Leu Leu Ile Ile Gly Gly Gly Gly
 305 310 315 320
 Ala Phe Lys Gln Val Leu Ile Asp Ser Gly Val Gly Gln Tyr Ile Ser
 325 330 335
 Thr Leu Val Ser Gly Met Asp Ile Asn Pro Ile Leu Met Ala Trp Gly
 340 345 350
 Val Ala Ala Phe Leu Arg Ile Cys Leu Gly Ser Ala Thr Val Ala Ala
 355 360 365
 Ile Ser Thr Ala Gly Leu Val Ile Pro Leu Leu Ala Val His Pro Asn
 370 375 380
 Thr Asn Leu Ala Leu Ile Thr Leu Ala Thr Gly Ala Gly Ser Cys Ile
 385 390 395 400
 Cys Ser His Val Asn Asp Ala Ser Phe Trp Met Ile Lys Asp Phe Phe
 405 410 415
 Gly Leu Thr Thr Lys Glu Thr Leu Leu Ser Trp Thr Leu Met Ser Thr
 420 425 430
 Leu Leu Ser Ile Ser Gly Leu Ile Phe Ile Leu Leu Ala Ser Leu Val
 435 440 445
 Leu

<210> 10248
 <211> 1335
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1335)
 <223> transl_table=11

<400> 10248
 atg ccg att tta att gta gct gtc gga gtg ctg att ctg tta ttt ctc 48
 Met Pro Ile Leu Ile Val Ala Val Gly Val Leu Ile Leu Leu Phe Leu
 1 5 10 15
 att att aaa gta aaa tta aat acc ttt gtc tca ctg att gtc gtt tca 96
 Ile Ile Lys Val Lys Leu Asn Thr Phe Val Ser Leu Ile Val Val Ser
 20 25 30
 ttt tta gta gcc atc gga ctt gga atg gat atc aat aaa att gtt ctt 144
 Phe Leu Val Ala Ile Gly Leu Gly Met Asp Ile Asn Lys Ile Val Leu
 35 40 45
 tca att gag act gga att ggc ggg cag ctg ggg cat tta gct tta gtg 192
 Ser Ile Glu Thr Gly Ile Gly Gln Leu Gly His Leu Ala Leu Val
 50 55 60
 ttt gga ctt ggc gcg atg ctt ggg agg ctt gtc tca gat gct ggg ggc 240
 Phe Gly Leu Gly Ala Met Leu Gly Arg Leu Val Ser Asp Ala Gly Gly
 65 70 75 80
 ggc tac cgg atc gcc att acg ctg att gac aaa ttc ggg agg aaa cga 288
 Gly Tyr Arg Ile Ala Ile Thr Leu Ile Asp Lys Phe Gly Arg Lys Arg
 85 90 95
 ata cag gcg gcg gtt gtg gtt gcc tct ttt atc atc ggg att gcc cta 336
 Ile Gln Ala Ala Val Val Val Ala Ser Phe Ile Ile Gly Ile Ala Leu

PF59083SeqList PF59083.txt

										100											105											110																			
ttt	ttt	gaa	gtc	ggt	ctt	ggt	ctg	ttg	ata	ccg	att	ggt	tac	gcg	att		384																																		
Phe	Phe	Glu	Val	Gly	Leu	Val	Leu	Leu	Ile	Pro	Ile	Val	Tyr	Ala	Ile																																				
																115																	120																	125	
gct	aaa	gaa	tta	aaa	atg	cct	ttt	ctg	tat	ctg	gga	atc	ccg	atg	gcc		432																																		
Ala	Lys	Glu	Leu	Lys	Met	Pro	Phe	Leu	Tyr	Leu	Gly	Ile	Pro	Met	Ala																																				
																130																	135																	140	
gcc	gcc	tta	aat	ggt	act	cac	gga	ttt	ttg	ccc	ccg	cat	cct	gct	cca		480																																		
Ala	Ala	Leu	Asn	Val	Thr	His	Gly	Phe	Leu	Pro	Pro	His	Pro	Ala	Pro																																				
																145																	150																	155	
act	gct	atc	tca	ggt	gca	tat	ggt	gcc	cat	att	ggc	cag	gtg	ctg	ctt		528																																		
Thr	Ala	Ile	Ser	Val	Ala	Tyr	Gly	Ala	His	Ile	Gly	Gln	Val	Leu	Leu																																				
																165																	170																	175	
ttt	gga	atc	atc	atc	gct	ggt	ccg	aca	act	gtg	att	gcc	ggg	cct	tta		576																																		
Phe	Gly	Ile	Ile	Ile	Ala	Val	Pro	Thr	Thr	Val	Ile	Ala	Gly	Pro	Leu																																				
																180																	185																	190	
ttt	aat	aaa	ttt	gcg	atg	aaa	cgg	ttt	cct	ggt	gcg	tat	caa	aag	cat		624																																		
Phe	Asn	Lys	Phe	Ala	Met	Lys	Arg	Phe	Pro	Gly	Ala	Tyr	Gln	Lys	His																																				
																195																	200																	205	
gga	aac	cta	tcg	ggg	tta	gga	cca	agg	aaa	gaa	ttt	cag	ctg	gat	gaa		672																																		
Gly	Asn	Leu	Ser	Gly	Leu	Gly	Pro	Arg	Lys	Glu	Phe	Gln	Leu	Asp	Glu																																				
																210																	215																	220	
aca	ccg	ggc	ttt	gcg	atc	agt	gct	gtc	acg	tct	tta	ttc	ccg	ggt	atc		720																																		
Thr	Pro	Gly	Phe	Ala	Ile	Ser	Ala	Val	Thr	Ser	Leu	Phe	Pro	Val	Ile																																				
																225																	230																	235	
ttt	atg	gca	atg	gca	aca	att	ttt	tct	tta	tta	ttg	agt	gaa	cat	tca		768																																		
Phe	Met	Ala	Met	Ala	Thr	Ile	Phe	Ser	Leu	Leu	Leu	Ser	Glu	His	Ser																																				
																245																	250																	255	
aaa	gga	aaa	gac	att	ata	gaa	ttt	atc	ggc	act	ccg	gga	acg	gca	atg		816																																		
Lys	Gly	Lys	Asp	Ile	Ile	Glu	Phe	Ile	Gly	Thr	Pro	Gly	Thr	Ala	Met																																				
																260																	265																	270	
ctc	att	tcg	ctg	ttg	ctt	gca	ctc	tat	acg	atg	gga	tat	gcc	cg	aaa		864																																		
Leu	Ile	Ser	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Met	Gly	Tyr	Ala	Arg	Lys																																				
																275																	280																	285	
ata	tct	atg	cag	gaa	atc	ggc	aga	tct	att	tca	gaa	tca	att	tcg	caa		912																																		
Ile	Ser	Met	Gln	Glu	Ile	Gly	Arg	Ser	Ile	Ser	Glu	Ser	Ile	Ser	Gln																																				
																290																	295																	300	
att	gcg	atg	atg	ctg	ctc	atc	ata	gga	ggg	gga	gga	gcg	ttt	aaa	cag		960																																		
Ile	Ala	Met	Met	Leu	Leu	Ile	Ile	Gly	Gly	Gly	Gly	Ala	Phe	Lys	Gln																																				
																305																	310																	315	
gtg	ctg	att	gac	ggc	gga	gtc	ggc	gat	tat	gtc	gct	gat	ttt	ttc	cg		1008																																		
Val	Leu	Ile	Asp	Gly	Gly	Val	Gly	Asp	Tyr	Val	Ala	Asp	Phe	Phe	Arg																																				
																325																	330																	335	
caa	aca	aac	atg	tcg	ccg	cta	ttc	gtt	gca	tgg	acc	atc	gcc	gcg	gtt		1056																																		
Gln	Thr	Asn	Met	Ser	Pro	Leu	Phe	Val	Ala	Trp	Thr	Ile	Ala	Ala	Val																																				
																340																	345																	350	
ctg	cg	ctg	tgt	cta	ggc	tct	gct	acc	gtg	gct	gcg	ctt	acc	aca	gcg		1104																																		
Leu	Arg	Leu	Cys	Leu	Gly	Ser	Ala	Thr	Val	Ala	Ala	Leu	Thr	Thr	Ala																																				
																355																	360																	365	
gga	atg	gca	gct	ccg	ctt	atg	gag	gct	ggc	agt	gta	aac	cct	gcg	tta		1152																																		
Gly	Met	Ala	Ala	Pro	Leu	Met	Glu	Ala	Gly	Ser	Val	Asn	Pro	Ala	Leu																																				
																370																	375																	380	
atg	gtg	ctt	gca	aca	gga	gcc	ggc	agt	gtc	att	gcg	tgt	cat	gta	aat		1200																																		
Met	Val	Leu	Ala	Thr	Gly	Ala	Gly	Ser	Val	Ile	Ala	Cys	His	Val	Asn																																				
																385																	390																	395	
gat	gca	gga	ttt	tgg	atg	gta	aag	gaa	ttt	ttc	ggc	ttg	agc	atg	aaa		1248																																		
Asp	Ala	Gly	Phe	Trp	Met	Val	Lys	Glu	Phe	Phe	Gly	Leu	Ser	Met	Lys																																				
																405																	410																	415	
gaa	aca	ttt	caa	acc	tgg	acg	ctg	ctt	aca	aca	gtt	ctt	tcg	gtt	aca		1296																																		
Glu	Thr	Phe	Gln	Thr	Trp	Thr	Leu	Leu	Thr	Thr	Val	Leu	Ser	Val	Thr																																				
																420																	425																	430	
ggg	ctc	ggc	tgt	gtg	tta	ttg	gca	ggg	ctt	gtg	atg	taa					1335																																		
Gly	Leu	Gly	Cys	Val	Leu	Leu	Ala	Gly	Leu	Val	Met																																								
																435																	440																		

<210> 10249

<211> 444

<212> PRT

<213> Bacillus subtilis

PF59083SeqList PF59083.txt

```

<400> 10249
Met Pro Ile Leu Ile Val Ala Val Gly Val Leu Ile Leu Leu Phe Leu
1      5      10      15
Ile Ile Lys Val Lys Leu Asn Thr Phe Val Ser Leu Ile Val Val Ser
20      25      30
Phe Leu Val Ala Ile Gly Leu Gly Met Asp Ile Asn Lys Ile Val Leu
35      40      45
Ser Ile Glu Thr Gly Ile Gly Gly Gln Leu Gly His Leu Ala Leu Val
50      55      60
Phe Gly Leu Gly Ala Met Leu Gly Arg Leu Val Ser Asp Ala Gly Gly
65      70      75      80
Gly Tyr Arg Ile Ala Ile Thr Leu Ile Asp Lys Phe Gly Arg Lys Arg
85      90      95
Ile Gln Ala Ala Val Val Val Ala Ser Phe Ile Ile Gly Ile Ala Leu
100     105     110
Phe Phe Glu Val Gly Leu Val Leu Leu Ile Pro Ile Val Tyr Ala Ile
115     120     125
Ala Lys Glu Leu Lys Met Pro Phe Leu Tyr Leu Gly Ile Pro Met Ala
130     135     140
Ala Ala Leu Asn Val Thr His Gly Phe Leu Pro Pro His Pro Ala Pro
145     150     155     160
Thr Ala Ile Ser Val Ala Tyr Gly Ala His Ile Gly Gln Val Leu Leu
165     170     175
Phe Gly Ile Ile Ala Val Pro Thr Thr Val Ile Ala Gly Pro Leu
180     185     190
Phe Asn Lys Phe Ala Met Lys Arg Phe Pro Gly Ala Tyr Gln Lys His
195     200     205
Gly Asn Leu Ser Gly Leu Gly Pro Arg Lys Glu Phe Gln Leu Asp Glu
210     215     220
Thr Pro Gly Phe Ala Ile Ser Ala Val Thr Ser Leu Phe Pro Val Ile
225     230     235     240
Phe Met Ala Met Ala Thr Ile Phe Ser Leu Leu Leu Ser Glu His Ser
245     250     255
Lys Gly Lys Asp Ile Ile Glu Phe Ile Gly Thr Pro Gly Thr Ala Met
260     265     270
Leu Ile Ser Leu Leu Leu Ala Leu Tyr Thr Met Gly Tyr Ala Arg Lys
275     280     285
Ile Ser Met Gln Glu Ile Gly Arg Ser Ile Ser Glu Ser Ile Ser Gln
290     295     300
Ile Ala Met Met Leu Leu Ile Ile Gly Gly Gly Gly Ala Phe Lys Gln
305     310     315     320
Val Leu Ile Asp Gly Gly Val Gly Asp Tyr Val Ala Asp Phe Phe Arg
325     330     335
Gln Thr Asn Met Ser Pro Leu Phe Val Ala Trp Thr Ile Ala Ala Val
340     345     350
Leu Arg Leu Cys Leu Gly Ser Ala Thr Val Ala Ala Leu Thr Thr Ala
355     360     365
Gly Met Ala Ala Pro Leu Met Glu Ala Gly Ser Val Asn Pro Ala Leu
370     375     380
Met Val Leu Ala Thr Gly Ala Gly Ser Val Ile Ala Cys His Val Asn
385     390     395     400
Asp Ala Gly Phe Trp Met Val Lys Glu Phe Phe Gly Leu Ser Met Lys
405     410     415
Glu Thr Phe Gln Thr Trp Thr Leu Leu Thr Thr Val Leu Ser Val Thr
420     425     430
Gly Leu Gly Cys Val Leu Leu Ala Gly Leu Val Met
435     440

```

```

<210> 10250
<211> 24
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> primer

```

```

<400> 10250
atgcatgtgc ttaacattct ctgg

```

<210> 10251
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 10251
 ttacgctacc atgctaataa tcagc

25

<210> 10252
 <211> 481
 <212> PRT
 <213> Artificial sequence

<220>
 <223> consensus sequence

<220>
 <221> Variant
 <222> (2)..(5)
 <223> Xaa in position 2 to 5 is any amino acid

<220>
 <221> Variant
 <222> (7)..(9)
 <223> Xaa in position 7 to 9 is any amino acid

<220>
 <221> Variant
 <222> (11)..(12)
 <223> Xaa in position 11 to 12 is any amino acid

<220>
 <221> Variant
 <222> (14)..(24)
 <223> Xaa in position 14 to 24 is any amino acid

<220>
 <221> Variant
 <222> (26)..(37)
 <223> Xaa in position 26 to 37 is any amino acid

<220>
 <221> Variant
 <222> (38)..(46)
 <223> Xaa in position 38 to 46 is any or no amino acid

<220>
 <221> Variant
 <222> (48)..(48)
 <223> Xaa in position 48 is any amino acid

<220>
 <221> Variant
 <222> (50)..(51)
 <223> Xaa in position 50 to 51 is any amino acid

<220>
 <221> Variant
 <222> (54)..(61)
 <223> Xaa in position 54 to 61 is any amino acid

<220>
 <221> Variant
 <222> (63)..(63)

<223> Xaa in position 63 is any amino acid

<220>
<221> Variant
<222> (65)..(65)
<223> Xaa in position 65 is any amino acid

<220>
<221> Variant
<222> (67)..(72)
<223> Xaa in position 67 to 72 is any amino acid

<220>
<221> Variant
<222> (74)..(74)
<223> Xaa in position 74 is any amino acid

<220>
<221> Variant
<222> (76)..(78)
<223> Xaa in position 76 to 78 is any amino acid

<220>
<221> Variant
<222> (80)..(86)
<223> Xaa in position 80 to 86 is any amino acid

<220>
<221> Variant
<222> (88)..(93)
<223> Xaa in position 88 to 93 is any amino acid

<220>
<221> Variant
<222> (95)..(102)
<223> Xaa in position 95 to 102 is any amino acid

<220>
<221> Variant
<222> (104)..(106)
<223> Xaa in position 104 to 106 is any amino acid

<220>
<221> Variant
<222> (108)..(110)
<223> Xaa in position 108 to 110 is any amino acid

<220>
<221> Variant
<222> (112)..(116)
<223> Xaa in position 112 to 116 is any amino acid

<220>
<221> Variant
<222> (118)..(135)
<223> Xaa in position 118 to 135 is any amino acid

<220>
<221> Variant
<222> (136)..(142)
<223> Xaa in position 136 to 142 is any or no amino acid

<220>
<221> Variant
<222> (144)..(151)
<223> Xaa in position 144 to 151 is any amino acid

<220>
<221> Variant

<222> (153)..(155)
<223> Xaa in position 153 to 155 is any amino acid

<220>
<221> Variant
<222> (160)..(160)
<223> Xaa in position 160 is any amino acid

<220>
<221> Variant
<222> (162)..(169)
<223> Xaa in position 162 to 169 is any amino acid

<220>
<221> Variant
<222> (171)..(172)
<223> Xaa in position 171 to 172 is any amino acid

<220>
<221> Variant
<222> (173)..(174)
<223> Xaa in position 173 to 174 is any or no amino acid

<220>
<221> Variant
<222> (176)..(180)
<223> Xaa in position 176 to 180 is any amino acid

<220>
<221> Variant
<222> (182)..(186)
<223> Xaa in position 182 to 186 is any amino acid

<220>
<221> Variant
<222> (188)..(221)
<223> Xaa in position 188 to 221 is any amino acid

<220>
<221> Variant
<222> (222)..(249)
<223> Xaa in position 222 to 249 is any or no amino acid

<220>
<221> Variant
<222> (251)..(261)
<223> Xaa in position 251 to 261 is any amino acid

<220>
<221> Variant
<222> (263)..(264)
<223> Xaa in position 263 to 264 is any amino acid

<220>
<221> Variant
<222> (266)..(286)
<223> Xaa in position 266 to 286 is any amino acid

<220>
<221> Variant
<222> (287)..(317)
<223> Xaa in position 287 to 317 is any or no amino acid

<220>
<221> Variant
<222> (319)..(322)
<223> Xaa in position 319 to 322 is any amino acid

<220>

```

<221> Variant
<222> (324)..(359)
<223> Xaa in position 324 to 359 is any amino acid

<220>
<221> Variant
<222> (360)..(361)
<223> Xaa in position 360 to 361 is any or no amino acid

<220>
<221> Variant
<222> (363)..(364)
<223> Xaa in position 363 to 364 is any amino acid

<220>
<221> Variant
<222> (366)..(366)
<223> Xaa in position 366 is any amino acid

<220>
<221> Variant
<222> (369)..(369)
<223> Xaa in position 369 is any amino acid

<220>
<221> Variant
<222> (371)..(373)
<223> Xaa in position 371 to 373 is any amino acid

<220>
<221> Variant
<222> (375)..(377)
<223> Xaa in position 375 to 377 is any amino acid

<220>
<221> Variant
<222> (379)..(400)
<223> Xaa in position 379 to 400 is any amino acid

<220>
<221> Variant
<222> (401)..(401)
<223> Xaa in position 401 is any or no amino acid

<220>
<221> Variant
<222> (403)..(405)
<223> Xaa in position 403 to 405 is any amino acid

<220>
<221> Variant
<222> (407)..(409)
<223> Xaa in position 407 to 409 is any amino acid

<220>
<221> Variant
<222> (416)..(417)
<223> Xaa in position 416 to 417 is any amino acid

<220>
<221> Variant
<222> (419)..(424)
<223> Xaa in position 419 to 424 is any amino acid

<220>
<221> Variant
<222> (426)..(439)
<223> Xaa in position 426 to 439 is any amino acid

```

PF59083SeqList PF59083.txt

<220>
 <221> Variant
 <222> (440)..(445)
 <223> Xaa in position 440 to 445 is any or no amino acid

<220>
 <221> Variant
 <222> (447)..(449)
 <223> Xaa in position 447 to 449 is any amino acid

<220>
 <221> Variant
 <222> (451)..(454)
 <223> Xaa in position 451 to 454 is any amino acid

<220>
 <221> Variant
 <222> (457)..(457)
 <223> Xaa in position 457 is any amino acid

<220>
 <221> Variant
 <222> (460)..(461)
 <223> Xaa in position 460 to 461 is any amino acid

<220>
 <221> Variant
 <222> (464)..(479)
 <223> Xaa in position 464 to 479 is any amino acid

<220>
 <221> Variant
 <222> (480)..(480)
 <223> Xaa in position 480 is any or no amino acid

<400> 10252
 Leu Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Phe Xaa Xaa Leu Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa
 35 40 45
 Gly Xaa Xaa Leu Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Met
 50 55 60
 Xaa Gly Xaa Xaa Xaa Xaa Xaa Gly Xaa Ala Xaa Xaa Xaa Ala Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa
 85 90 95
 Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Phe Xaa Xaa Xaa Gly Xaa
 100 105 110
 Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa
 130 135 140
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Pro Pro His Pro Xaa
 145 150 155 160
 Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Gly Xaa
 165 170 175
 Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa
 180 185 190
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 210 215 220
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 225 230 235 240
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa
 245 250 255
 Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa

PF59083SeqList PF59083.txt

			260					265					270				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			275					280					285				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			290					295					300				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa
305						310					315						320
Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
					325					330							335
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			340							345				350			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Gly	Xaa	Gly	Gly	
			355					360					365				
Xaa	Phe	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	370					375							380				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
385					390						395						400
Xaa	Ala	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Xaa	Gly	Ser	Ala	Thr	Val	Ala	Xaa	Xaa	Xaa
					405				410					415			
Xaa	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			420					425						430			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Xaa	Xaa
			435					440					445				
Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Ser	His	Xaa	Asn	Asp	Xaa	Xaa	Xaa	Phe	Trp	Xaa	Xaa
	450					455					460						
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
465					470					475							480
Trp																	

<210> 10253
 <211> 20
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (2)..(2)
 <223> Xaa in position 2 is any amino acid

<220>
 <221> Variant
 <222> (5)..(5)
 <223> Xaa in position 5 is Ala, Gly, Pro, Ser or Thr

<220>
 <221> Variant
 <222> (6)..(6)
 <223> Xaa in position 6 is any amino acid

<220>
 <221> Variant
 <222> (9)..(9)
 <223> Xaa in position 9 is Ile, Leu, Met or Val

<220>
 <221> Variant
 <222> (10)..(10)
 <223> Xaa in position 10 is Phe, Ile, Leu or Val

<220>
 <221> Variant
 <222> (11)..(16)
 <223> Xaa in position 11 to 16 is any amino acid

```

<220>
<221> Variant
<222> (17)..(17)
<223> Xaa in position 17 is Asp, Asn, Ser or Thr

<220>
<221> Variant
<222> (18)..(19)
<223> Xaa in position 18 to 19 is any amino acid

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is Asp, Glu, Gln or Thr

<400> 10253
His Xaa Asn Asp Xaa Xaa Phe Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1      5      10      15
Xaa Xaa Xaa Xaa
      20

<210> 10254
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
<221> Variant
<222> (2)..(10)
<223> Xaa in position 2 to 10 is any amino acid

<220>
<221> Variant
<222> (12)..(12)
<223> Xaa in position 12 is Ala, Thr or Val

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is Ile, Met or Val

<220>
<221> Variant
<222> (14)..(14)
<223> Xaa in position 14 is Phe, Ile, Leu or Met

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is any amino acid

<220>
<221> Variant
<222> (17)..(17)
<223> Xaa in position 17 is Ile, Leu or Met

<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is Phe, Ile, Leu, Met or Val

<220>
<221> Variant
<222> (19)..(20)
<223> Xaa in position 19 to 20 is any amino acid

```


PF59083SeqList PF59083.txt

```

<220>
<221> Variant
<222> (21)..(21)
<223> Xaa in position 21 is Ala, Cys, Gly, Ser or Thr

<220>
<221> Variant
<222> (23)..(23)
<223> Xaa in position 23 is Ala or Gly

<220>
<221> Variant
<222> (25)..(26)
<223> Xaa in position 25 to 26 is any amino acid

<220>
<221> Variant
<222> (27)..(27)
<223> Xaa in position 27 is Ile, Leu, Met or Val

<220>
<221> Variant
<222> (28)..(28)
<223> Xaa in position 28 is Ala, Gly or Ser

<220>
<221> Variant
<222> (29)..(30)
<223> Xaa in position 29 to 30 is any amino acid

<220>
<221> Variant
<222> (31)..(31)
<223> Xaa in position 31 is Phe, Ile, Leu, Met or Val

<400> 10254
Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Gly Xaa
1      5      10      15
Xaa Xaa Xaa Xaa Xaa Gly Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa
      20      25      30

<210> 10255
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
<221> Variant
<222> (2)..(9)
<223> Xaa in position 2 to 9 is any amino acid

<220>
<221> Variant
<222> (10)..(13)
<223> Xaa in position 10 to 13 is any or no amino acid

<220>
<221> Variant
<222> (15)..(16)
<223> Xaa in position 15 to 16 is any amino acid

<220>
<221> Variant
<222> (17)..(17)

```

<223> Xaa in position 17 is Ile, Leu or Val

<220>

<221> Variant

<222> (22)..(22)

<223> Xaa in position 22 is Ala, Gly or Ser

<220>

<221> Variant

<222> (23)..(23)

<223> Xaa in position 23 is Ala, Pro or Ser

<400> 10255

Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	His	Xaa	Xaa
1				5			10						15	
Xaa	Pro	Pro	His	Pro	Xaa	Xaa								
			20											

<210> 10256

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (2)..(4)

<223> Xaa in position 2 to 4 is any amino acid

<220>

<221> Variant

<222> (5)..(8)

<223> Xaa in position 5 to 8 is any or no amino acid

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Ala, Ile, Leu or Val

<220>

<221> Variant

<222> (11)..(12)

<223> Xaa in position 11 to 12 is any amino acid

<220>

<221> Variant

<222> (15)..(15)

<223> Xaa in position 15 is Ala, Gly or Ser

<220>

<221> Variant

<222> (18)..(18)

<223> Xaa in position 18 is Ala or Ser

<220>

<221> Variant

<222> (19)..(20)

<223> Xaa in position 19 to 20 is any amino acid

<220>

<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is Ser or Thr

<220>

<221> Variant

<222> (22)..(22)
 <223> Xaa in position 22 is Ala, Gly, Ser or Thr
 <220>
 <221> Variant
 <222> (23)..(23)
 <223> Xaa in position 23 is Ala, Cys, Gly, Ser, Thr or Val
 <220>
 <221> Variant
 <222> (24)..(24)
 <223> Xaa in position 24 is Ala, Gly, Ser or Thr
 <220>
 <221> Variant
 <222> (25)..(25)
 <223> Xaa in position 25 is Ile, Leu, Met or Val
 <400> 10256
 Ala Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Gly Ser Xaa Thr
 1 5 10 15
 Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25

<210> 10257
 <211> 34
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (2)..(3)
 <223> Xaa in position 2 to 3 is any amino acid

<220>
 <221> Variant
 <222> (4)..(4)
 <223> Xaa in position 4 is any or no amino acid

<220>
 <221> Variant
 <222> (6)..(6)
 <223> Xaa in position 6 is any or no amino acid

<220>
 <221> Variant
 <222> (9)..(9)
 <223> Xaa in position 9 is any amino acid

<220>
 <221> Variant
 <222> (10)..(10)
 <223> Xaa in position 10 is Phe or Leu

<220>
 <221> Variant
 <222> (11)..(13)
 <223> Xaa in position 11 to 13 is any amino acid

<220>
 <221> Variant
 <222> (14)..(14)
 <223> Xaa in position 14 is Ile, Leu or Val

<220>

PF59083SeqList PF59083.txt

```

<221> Variant
<222> (15)..(16)
<223> Xaa in position 15 to 16 is any amino acid

<220>
<221> Variant
<222> (17)..(17)
<223> Xaa in position 17 is Ala, Gly, Ser or Thr

<220>
<221> Variant
<222> (19)..(19)
<223> Xaa in position 19 is Ala, Ile, Leu or Val

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is Ala, Asp, Glu, Gly or Ser

<220>
<221> Variant
<222> (21)..(22)
<223> Xaa in position 21 to 22 is any amino acid

<220>
<221> Variant
<222> (23)..(23)
<223> Xaa in position 23 is Ile, Leu, Met or Val

<220>
<221> Variant
<222> (24)..(33)
<223> Xaa in position 24 to 33 is any amino acid

<220>
<221> Variant
<222> (34)..(34)
<223> Xaa in position 34 is Ala, Gly, Ile, Leu, Pro or Val

<400> 10257
Leu Xaa Xaa Xaa Gly Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1      5      10      15
Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      20      25      30
Xaa Xaa

```