

SEQUENCE LISTING

<110> Novozymes A/S

<120> VARIANTS AND COMPOSITIONS COMPRISING VARIANTS WITH HIGH STABILITY
IN PRESENCE OF A CHELATING AGENT

<130> 11605-WO-PCT

<160> 26

<170> PatentIn version 3.4

<210> 1

<211> 1440

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1)..(1440)

<400> 1

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

Gly 145	Arg	Asn	Asn	Ala	Tyr 150	Ser	Asp	Phe	Lys	Trp 155	Arg	Trp	Phe	His	Phe 160	
aat	ggt	gtt	gac	tgg	gat	cag	cgc	tat	caa	gaa	aat	cat	att	ttc	cgc	528
Asn	Gly	Val	Asp	Trp 165	Asp	Gln	Arg	Tyr	Gln 170	Glu	Asn	His	Ile	Phe 175	Arg	
ttt	gca	aat	acg	aac	tgg	aac	tgg	cga	gtg	gat	gaa	gag	aac	ggt	aat	576
Phe	Ala	Asn	Thr 180	Asn	Trp	Asn	Trp	Arg 185	Val	Asp	Glu	Glu	Asn 190	Gly	Asn	
tat	gat	tac	ctg	tta	gga	tcg	aat	atc	gac	ttt	agt	cat	cca	gaa	gta	624
Tyr	Asp	Tyr 195	Leu	Leu	Gly	Ser	Asn 200	Ile	Asp	Phe	Ser	His 205	Pro	Glu	Val	
caa	gat	gag	ttg	aag	gat	tgg	ggt	agc	tgg	ttt	acc	gat	gag	tta	gat	672
Gln	Asp	Glu	Leu	Lys	Asp	Trp 215	Gly	Ser	Trp	Phe	Thr 220	Asp	Glu	Leu	Asp	
210																
ttg	gat	ggt	tat	cgt	tta	gat	gct	att	aaa	cat	att	cca	ttc	tgg	tat	720
Leu	Asp	Gly	Tyr	Arg	Leu 230	Asp	Ala	Ile	Lys	His 235	Ile	Pro	Phe	Trp	Tyr 240	
225																
aca	tct	gat	tgg	gtt	cgg	cat	cag	cgc	aac	gaa	gca	gat	caa	gat	tta	768
Thr	Ser	Asp	Trp	Val 245	Arg	His	Gln	Arg	Asn 250	Glu	Ala	Asp	Gln 255	Asp	Leu	
ttt	gtc	gta	ggg	gaa	tat	tgg	aag	gat	gac	gta	ggt	gct	ctc	gaa	ttt	816
Phe	Val	Val 260	Gly	Glu	Tyr	Trp	Lys	Asp 265	Asp	Val	Gly	Ala 270	Leu	Glu	Phe	
tat	tta	gat	gaa	atg	aat	tgg	gag	atg	tct	cta	ttc	gat	gtt	cca	ctt	864
Tyr	Leu	Asp 275	Glu	Met	Asn	Trp	Glu	Met 280	Ser	Leu	Phe	Asp 285	Val	Pro	Leu	
aat	tat	aat	ttt	tac	cgg	gct	tca	caa	caa	ggt	gga	agc	tat	gat	atg	912
Asn	Tyr	Asn	Phe	Tyr	Arg	Ala 295	Ser	Gln	Gln	Gly	Gly 300	Ser	Tyr	Asp	Met	
290																
cgt	aat	att	tta	cga	gga	tct	tta	gta	gaa	gcg	cat	ccg	atg	cat	gca	960
Arg	Asn	Ile	Leu	Arg	Gly 310	Ser	Leu	Val	Glu	Ala 315	His	Pro	Met	His	Ala 320	
305																
gtt	acg	ttt	gtt	gat	aat	cat	gat	act	cag	cca	ggg	gag	tca	tta	gag	1008
Val	Thr	Phe	Val 325	Asp	Asn	His	Asp	Thr	Gln 330	Pro	Gly	Glu	Ser 335	Leu	Glu	
tca	tgg	gtt	gct	gat	tgg	ttt	aag	cca	ctt	gct	tat	gcg	aca	att	ttg	1056
Ser	Trp	Val 340	Ala	Asp	Trp	Phe	Lys	Pro 345	Leu	Ala	Tyr	Ala 350	Thr	Ile	Leu	
acg	cgt	gaa	ggt	ggt	tat	cca	aat	gta	ttt	tac	ggt	gat	tac	tat	ggg	1104
Thr	Arg	Glu	Gly	Gly	Tyr	Pro	Asn 360	Val	Phe	Tyr	Gly	Asp 365	Tyr	Tyr	Gly	
355																
att	cct	aac	gat	aac	att	tca	gct	aaa	aaa	gat	atg	att	gat	gag	ctg	1152
Ile	Pro	Asn	Asp	Asn	Ile	Ser 375	Ala	Lys	Lys	Asp	Met 380	Ile	Asp	Glu	Leu	
370																
ctt	gat	gca	cgt	caa	aat	tac	gca	tat	ggc	acg	cag	cat	gac	tat	ttt	1200
Leu	Asp	Ala	Arg	Gln	Asn	Tyr	Ala	Tyr	Gly	Thr	Gln	His	Asp	Tyr	Phe	

385		390		395		400	
gat cat tgg gat gtt gta gga tgg act agg gaa gga tct tcc tcc aga							1248
Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg							
		405		410		415	
cct aat tca ggc ctt gcg act att atg tcg aat gga cct ggt ggt tcc							1296
Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser							
		420		425		430	
aag tgg atg tat gta gga cgt cag aat gca gga caa aca tgg aca gat							1344
Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp							
		435		440		445	
tta act ggt aat aac gga gcg tcc gtt aca att aat ggc gat gga tgg							1392
Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp							
		450		455		460	
ggc gaa ttc ttt acg aat gga gga tct gta tcc gtg tac gtg aac caa							1440
Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln							
		465		470		480	

<210> 2
 <211> 480
 <212> PRT
 <213> Bacillus sp.

<400> 2

Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
1 5 10 15

Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
20 25 30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
85 90 95

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

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
130 135 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145 150 155 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
165 170 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
195 200 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
210 215 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225 230 235 240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
245 250 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
260 265 270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
275 280 285

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
290 295 300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
325 330 335

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
340 345 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
355 360 365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
 370 375 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
 385 390 395 400

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
 405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
 420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
 435 440 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
 450 455 460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
 465 470 475 480

<210> 3
 <211> 1476
 <212> DNA
 <213> Bacillus circulans

<220>
 <221> CDS
 <222> (1)..(1476)

<400> 3
 aag aga aat cat acc atg atg cag ttt ttt gaa tgg cac ctg gct gca 48
 Lys Arg Asn His Thr Met Met Gln Phe Phe Glu Trp His Leu Ala Ala
 1 5 10 15
 gac gga gat cat tgg aag cga ctg gct gaa atg gcc ccg gaa ttg aaa 96
 Asp Gly Asp His Trp Lys Arg Leu Ala Glu Met Ala Pro Glu Leu Lys
 20 25 30
 gcc aaa ggc att gat acg gta tgg gtg cct cct gtg acc aaa gcc gta 144
 Ala Lys Gly Ile Asp Thr Val Trp Val Pro Pro Val Thr Lys Ala Val
 35 40 45
 tca gct gag gat aca ggt tat ggt gta tat gat ctg tat gat ttg ggt 192
 Ser Ala Glu Asp Thr Gly Tyr Gly Val Tyr Asp Leu Tyr Asp Leu Gly
 50 55 60
 gaa ttt gac caa aag ggt acc gtg cgt acc aaa tac ggc acc aag cag 240
 Glu Phe Asp Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gln
 65 70 75 80
 gaa ctg ata gag gcc att gct gag tgt cag aag aac gga atc gcc gtc 288
 Glu Leu Ile Glu Ala Ile Ala Glu Cys Gln Lys Asn Gly Ile Ala Val

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

gaa tca tgg att ggt gat tgg ttt aag ccg agc gct tat gcg ttg acg	1056
Glu Ser Trp Ile Gly Asp Trp Phe Lys Pro Ser Ala Tyr Ala Leu Thr	
340 345 350	

cta tta cgt cgt gat ggc tat ccg gtt gta ttt tac ggc gat tat tat	1104
Leu Leu Arg Arg Asp Gly Tyr Pro Val Val Phe Tyr Gly Asp Tyr Tyr	
355 360 365	

ggc att ggt ggt cct gaa cct gtg gat ggc aaa aaa gaa att ctg gac	1152
Gly Ile Gly Gly Pro Glu Pro Val Asp Gly Lys Lys Glu Ile Leu Asp	
370 375 380	

att ctg ctg tct gcc cgt tgc aac aaa gcg tat gga gag cag gaa gat	1200
Ile Leu Leu Ser Ala Arg Cys Asn Lys Ala Tyr Gly Glu Gln Glu Asp	
385 390 395 400	

tac ttc gat cac gcc aat acg att ggc tgg gta cgt cgt ggc gta gag	1248
Tyr Phe Asp His Ala Asn Thr Ile Gly Trp Val Arg Arg Gly Val Glu	
405 410 415	

gaa atc gaa ggt tcc ggt tgt gca gtg gtc atc tcc aac ggg gat gac	1296
Glu Ile Glu Gly Ser Gly Cys Ala Val Val Ile Ser Asn Gly Asp Asp	
420 425 430	

ggt gag aag aga atg ttc atc gga gag cat cgt gct ggt gaa gtc tgg	1344
Gly Glu Lys Arg Met Phe Ile Gly Glu His Arg Ala Gly Glu Val Trp	
435 440 445	

gtg gat ctg acg aag agc tgt gat gat cag att acc att gag gaa gac	1392
Val Asp Leu Thr Lys Ser Cys Asp Asp Gln Ile Thr Ile Glu Glu Asp	
450 455 460	

ggc tgg gcc acc ttc cat gtg tgc ggt gga ggt gtc tcg gta tgg gct	1440
Gly Trp Ala Thr Phe His Val Cys Gly Gly Gly Val Ser Val Trp Ala	
465 470 475 480	

ctt cct gaa cag aat gag gac tgc gct gac gct gag	1476
Leu Pro Glu Gln Asn Glu Asp Cys Ala Asp Ala Glu	
485 490	

<210> 4
 <211> 492
 <212> PRT
 <213> Bacillus circulans

<400> 4

Lys Arg Asn His Thr Met Met Gln Phe Phe Glu Trp His Leu Ala Ala	
1 5 10 15	

Asp Gly Asp His Trp Lys Arg Leu Ala Glu Met Ala Pro Glu Leu Lys	
20 25 30	

Ala Lys Gly Ile Asp Thr Val Trp Val Pro Pro Val Thr Lys Ala Val	
35 40 45	

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

Glu Phe Asp Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gln
65 70 75 80

Glu Leu Ile Glu Ala Ile Ala Glu Cys Gln Lys Asn Gly Ile Ala Val
85 90 95

Tyr Val Asp Leu Val Met Asn His Lys Ala Gly Ala Asp Glu Thr Glu
100 105 110

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

Ser Glu Pro Phe Glu Ile Glu Gly Trp Thr Lys Phe Thr Phe Pro Gly
130 135 140

Arg Gly Asp Gln Tyr Ser Ser Phe Lys Trp Asn Ser Glu His Phe Asn
145 150 155 160

Gly Thr Asp Phe Asp Ala Arg Glu Glu Arg Thr Gly Val Phe Arg Ile
165 170 175

Ala Gly Glu Asn Lys Lys Trp Asn Glu Asn Val Asp Asp Glu Phe Gly
180 185 190

Asn Tyr Asp Tyr Leu Met Phe Ala Asn Ile Asp Tyr Asn His Pro Asp
195 200 205

Val Arg Arg Glu Met Ile Asp Trp Gly Lys Trp Leu Ile Asp Thr Leu
210 215 220

Gln Cys Gly Gly Phe Arg Leu Asp Ala Ile Lys His Ile Asn His Glu
225 230 235 240

Phe Ile Lys Glu Phe Ala Ala Glu Met Ile Arg Lys Arg Gly Gln Asp
245 250 255

Phe Tyr Ile Val Gly Glu Phe Trp Asn Ser Asn Leu Asp Ala Cys Arg
260 265 270

Glu Phe Leu Asp Thr Val Asp Tyr Gln Ile Asp Leu Phe Asp Val Ser
275 280 285

Leu His Tyr Lys Leu His Glu Ala Ser Leu Lys Gly Arg Asp Phe Asp

290

295

300

Leu Ser Lys Ile Phe Asp Asp Thr Leu Val Gln Thr His Pro Thr His
 305 310 315 320

Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro His Glu Ala Leu
 325 330 335

Glu Ser Trp Ile Gly Asp Trp Phe Lys Pro Ser Ala Tyr Ala Leu Thr
 340 345 350

Leu Leu Arg Arg Asp Gly Tyr Pro Val Val Phe Tyr Gly Asp Tyr Tyr
 355 360 365

Gly Ile Gly Gly Pro Glu Pro Val Asp Gly Lys Lys Glu Ile Leu Asp
 370 375 380

Ile Leu Leu Ser Ala Arg Cys Asn Lys Ala Tyr Gly Glu Gln Glu Asp
 385 390 395 400

Tyr Phe Asp His Ala Asn Thr Ile Gly Trp Val Arg Arg Gly Val Glu
 405 410 415

Glu Ile Glu Gly Ser Gly Cys Ala Val Val Ile Ser Asn Gly Asp Asp
 420 425 430

Gly Glu Lys Arg Met Phe Ile Gly Glu His Arg Ala Gly Glu Val Trp
 435 440 445

Val Asp Leu Thr Lys Ser Cys Asp Asp Gln Ile Thr Ile Glu Glu Asp
 450 455 460

Gly Trp Ala Thr Phe His Val Cys Gly Gly Gly Val Ser Val Trp Ala
 465 470 475 480

Leu Pro Glu Gln Asn Glu Asp Cys Ala Asp Ala Glu
 485 490

<210> 5
 <211> 1455
 <212> DNA
 <213> bacillus sp.

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

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

att aaa tat agc ttt aca cgt gat tgg ttg acc cat gta aga aac gca	768
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala	
245 250 255	
acg gga aaa gaa atg ttt gct gtt gct gaa ttt tgg aaa aat gat tta	816
Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu	
260 265 270	
ggc gcc ttg gag aac tat tta aat aaa aca aac tgg aat cat tct gtc	864
Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val	
275 280 285	
ttt gat gtc ccc ctt cat tat aat ctt tat aac gcg tca aat agt gga	912
Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly	
290 295 300	
ggc aac tat gac atg gca aaa ctt ctt aat gga acg gtt gtt caa aag	960
Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys	
305 310 315 320	
cat cca atg cat gcc gta act ttt gtg gat aat cac gat tct caa cct	1008
His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro	
325 330 335	
ggg gaa tca tta gaa tca ttt gta caa gaa tgg ttt aag cca ctt gct	1056
Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala	
340 345 350	
tat gcg ctt att tta aca aga gaa caa ggc tat ccc tct gtc ttc tat	1104
Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr	
355 360 365	
ggc gac tac tat gga att cca aca cat agt gtc cca gca atg aaa gcc	1152
Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala	
370 375 380	
aag att gat cca atc tta gag gcg cgt caa aat ttt gca tat gga aca	1200
Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr	
385 390 395 400	
caa cat gat tat ttt gac cat cat aat ata atc gga tgg aca cgt gaa	1248
Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu	
405 410 415	
gga aat acc acg cat ccc aat tca gga ctt gcg act atc atg tcg gat	1296
Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp	
420 425 430	
ggg cca ggg gga gag aaa tgg atg tac gta ggg caa aat aaa gca ggt	1344
Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly	
435 440 445	
caa gtt tgg cat gac ata act gga aat aaa cca gga aca gtt acg atc	1392
Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile	
450 455 460	
aat gca gat gga tgg gct aat ttt tca gta aat gga gga tct gtt tcc	1440
Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser	
465 470 475 480	
att tgg gtg aaa cga	1455

Ile Trp Val Lys Arg
485

<210> 6
<211> 485
<212> PRT
<213> bacillus sp.

<400> 6

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
20 25 30

Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
85 90 95

Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
245 250 255

Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300

Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
435 440 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
 450 455 460

Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
 465 470 475 480

Ile Trp Val Lys Arg
 485

<210> 7
 <211> 1455
 <212> DNA
 <213> Bacillus sp.

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

<400> 7
 cat cat aac ggt acg aac ggg aca atg atg caa tac ttt gaa tgg tat 48
 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
 1 5 10 15
 cta cct aat gac gga aat cat tgg aat cga tta aac tct gat gcg agt 96
 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Asn Ser Asp Ala Ser
 20 25 30
 aac ctt aaa agc aaa ggg att aca gcg gtg tgg att cct cca gca tgg 144
 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
 35 40 45
 aag ggc gct tct caa aat gac gta gga tac gga gcc tat gac ctg tat 192
 Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60
 gat ctg gga gaa ttt aat caa aaa ggt acc gtc cgt aca aaa tat gga 240
 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 65 70 75 80
 aca cgt agt cag tta caa gct gcg gta acc tcc tta aaa aat aat gga 288
 Thr Arg Ser Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
 85 90 95
 att caa gta tat ggt gac gtt gtt atg aat cac aaa ggt ggc gca gac 336
 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110
 gct act gaa atg gta agg gcc gtt gaa gtg aat ccc aat aac cgt aac 384
 Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
 115 120 125
 caa gaa gtg act ggt gaa tat acc att gaa gct tgg act aga ttt gat 432
 Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp
 130 135 140
 ttt cca ggg cga gga aat act cat tct agc ttt aaa tgg aga tgg tat 480

Phe 145	Pro	Gly	Arg	Gly	Asn 150	Thr	His	Ser	Ser	Phe 155	Lys	Trp	Arg	Trp	Tyr 160	
cat	ttt	gat	ggg	gtg	gat	tgg	gat	cag	tca	cgt	aga	ctg	aac	aat	cgc	528
His	Phe	Asp	Gly	Val	Asp	Trp	Asp	Gln	Ser	Arg	Arg	Leu	Asn	Asn	Arg	
				165					170						175	
atc	tat	aaa	ttt	aga	ggg	cat	ggc	aaa	gct	tgg	gat	tgg	gaa	gtt	gat	576
Ile	Tyr	Lys	Phe	Arg	Gly	His	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp	
			180					185					190			
acg	gaa	aat	ggg	aat	tat	gat	tat	tta	atg	tac	gct	gat	att	gat	atg	624
Thr	Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Met	
		195					200					205				
gat	cac	cca	gaa	gta	gta	aat	gaa	tta	aga	aat	tgg	ggg	gtt	tgg	tac	672
Asp	His	Pro	Glu	Val	Val	Asn	Glu	Leu	Arg	Asn	Trp	Gly	Val	Trp	Tyr	
	210					215					220					
aca	aac	aca	tta	gga	ctc	gat	gga	ttt	aga	ata	gat	gcg	gtt	aaa	cat	720
Thr	Asn	Thr	Leu	Gly	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Val	Lys	His	
225				230				235						240		
ata	aag	tat	agc	ttt	acg	cgc	gat	tgg	att	aat	cac	gtt	aga	agt	gca	768
Ile	Lys	Tyr	Ser	Phe	Thr	Arg	Asp	Trp	Ile	Asn	His	Val	Arg	Ser	Ala	
			245					250					255			
aca	ggg	aaa	aat	atg	ttt	gcg	gtt	gct	gag	ttt	tgg	aag	aat	gat	tta	816
Thr	Gly	Lys	Asn	Met	Phe	Ala	Val	Ala	Glu	Phe	Trp	Lys	Asn	Asp	Leu	
		260					265					270				
ggg	gca	att	gaa	aac	tat	ctg	cag	aaa	aca	aac	tgg	aac	cat	tca	gtc	864
Gly	Ala	Ile	Glu	Asn	Tyr	Leu	Gln	Lys	Thr	Asn	Trp	Asn	His	Ser	Val	
	275					280						285				
ttt	gat	gtg	ccg	tta	cat	tat	aat	ctt	tat	aat	gca	tca	aaa	agc	gga	912
Phe	Asp	Val	Pro	Leu	His	Tyr	Asn	Leu	Tyr	Asn	Ala	Ser	Lys	Ser	Gly	
	290					295				300						
ggg	aac	tat	gat	atg	cga	aac	ata	ttt	aat	gga	acg	gtt	gtt	caa	cga	960
Gly	Asn	Tyr	Asp	Met	Arg	Asn	Ile	Phe	Asn	Gly	Thr	Val	Val	Gln	Arg	
305				310				315						320		
cat	cca	agt	cat	gct	gta	aca	ttt	gtt	gat	aat	cat	gat	tcg	cag	cct	1008
His	Pro	Ser	His	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Ser	Gln	Pro	
			325					330					335			
gaa	gaa	gca	tta	gaa	tct	ttt	gtt	gaa	gaa	tgg	ttt	aaa	cca	tta	gcg	1056
Glu	Glu	Ala	Leu	Glu	Ser	Phe	Val	Glu	Glu	Trp	Phe	Lys	Pro	Leu	Ala	
			340				345					350				
tat	gcg	ctt	aca	tta	acg	cgt	gaa	caa	gga	tac	cct	tct	gta	ttt	tac	1104
Tyr	Ala	Leu	Thr	Leu	Thr	Arg	Glu	Gln	Gly	Tyr	Pro	Ser	Val	Phe	Tyr	
	355					360					365					
gga	gat	tat	tat	ggg	att	cca	aca	cat	gga	gtg	cca	gca	atg	aga	tca	1152
Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	Thr	His	Gly	Val	Pro	Ala	Met	Arg	Ser	
	370				375					380						
aaa	atc	gat	ccg	att	tta	gaa	gca	cgt	caa	aag	tat	gca	tac	gga	aaa	1200
Lys	Ile	Asp	Pro	Ile	Leu	Glu	Ala	Arg	Gln	Lys	Tyr	Ala	Tyr	Gly	Lys	

385	390	395	400	
caa aat gat tac tta gac cat cat aat atc att ggt tgg acg cgt gaa				1248
Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu				
	405	410	415	
ggg aat aca gca cac ccc aat tca ggt cta gct acc atc atg tct gat				1296
Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp				
	420	425	430	
gga gcg ggt gga agt aag tgg atg ttt gtt ggg cgt aat aag gct ggt				1344
Gly Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly				
	435	440	445	
caa gta tgg agt gat att aca gga aac cgt aca ggt acg gtt aca atc				1392
Gln Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile				
	450	455	460	
aat gca gac ggt tgg ggc aat ttc tct gtg aat gga ggg tca gtt tct				1440
Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser				
	465	470	475	480
att tgg gtc aac aaa				1455
Ile Trp Val Asn Lys				
	485			

<210> 8
 <211> 485
 <212> PRT
 <213> Bacillus sp.

<400> 8

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

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Arg Leu Asn Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly His Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

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

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Gln Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
290 295 300

Gly Asn Tyr Asp Met Arg Asn Ile Phe Asn Gly Thr Val Val Gln Arg
305 310 315 320

His Pro Ser His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys
385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
435 440 445

Gln Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Asn Lys
485

<210> 9
<211> 1458
<212> DNA
<213> Bacillus sp.

<220>
<221> CDS
<222> (1)..(1458)

<400> 9
cac cat aat ggt acg aac ggc aca atg atg cag tac ttt gaa tgg tat 48
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15
cta cca aat gac gga aac cat tgg aat aga tta agg tct gat gca agt 96
Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
20 25 30
aac cta aaa gat aaa ggg atc tca gcg gtt tgg att cct cct gca tgg 144
Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp
35 40 45
aag ggt gcc tct caa aat gat gtg ggg tat ggt gct tat gat ctg tat 192
Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr

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

ggg aat tat gat atg agg caa ata ttt aat ggt aca gtc gtg caa aga	960
Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg	
305 310 315 320	

cat cca atg cat gct gtt aca ttt gtt gat aat cat gat tcg caa cct	1008
His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro	
325 330 335	

gaa gaa gct tta gag tct ttt gtt gaa gaa tgg ttc aaa cca tta gcg	1056
Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala	
340 345 350	

tat gct ttg aca tta aca cgt gaa caa ggc tac cct tct gta ttt tat	1104
Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr	
355 360 365	

gga gat tat tat ggc att cca acg cat ggt gta cca gcg atg aaa tcg	1152
Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser	
370 375 380	

aaa att gac ccg att cta gaa gcg cgt caa aag tat gca tat gga aga	1200
Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg	
385 390 395 400	

caa aat gac tac tta gac cat cat aat atc att ggt tgg aca cgt gaa	1248
Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu	
405 410 415	

ggg aat aca gca cac ccc aac tct ggt tta gct act atc atg tcc gat	1296
Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp	
420 425 430	

gga gca gga gga aat aag tgg atg ttt gtt ggg cgt aat aaa gct ggt	1344
Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly	
435 440 445	

caa gtt tgg acc gat atc act gga aat cgt gca ggt act gtt acg att	1392
Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile	
450 455 460	

aat gct gat gga tgg ggt aat ttt tct gta aat gga gga tca gtt tct	1440
Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser	
465 470 475 480	

att tgg gta aac aaa taa	1458
Ile Trp Val Asn Lys	
485	

<210> 10
 <211> 485
 <212> PRT
 <213> Bacillus sp.

<400> 10

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
20 25 30

Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

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

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

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp
180 185 190

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

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu

260

265

270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
 275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
 290 295 300

Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg
 305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
 340 345 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
 370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg
 385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
 405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430

Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
 435 440 445

Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile
 450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
 465 470 475 480

Ile Trp Val Asn Lys
 485

<210> 11

<211> 1455

<212> DNA
<213> Bacillus Sp

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

<400> 11
cat cat aat gga aca aat ggt act atg atg caa tat ttc gaa tgg tat 48
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

ttg cca aat gac ggg aat cat tgg aac agg ttg agg gat gac gca gct 96
Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
20 25 30

aac tta aag agt aaa ggg ata aca gct gta tgg att cca cct gca tgg 144
Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

aag ggg act tcc cag aat gat gta ggt tat gga gcc tat gat tta tat 192
Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

gat ctt gga gag ttt aac cag aag ggg acg gtt cgt aca aaa tat gga 240
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

aca cgc aac cag ctg cag gct gcc gtg aca tct tta aaa aat aac ggc 288
Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
85 90 95

att cag gta tat ggt gat gtc gtc atg aat cat aaa ggt gga gca gat 336
Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

ggt acg gaa att gta aat gcg gta gaa gtg aat cgg agc aac cga aac 384
Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
115 120 125

cag gaa acc tca gga gag tat gca ata gaa gcg tgg aca aag ttt gat 432
Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

ttt cct gga aga gga aat aac cat tcc agc ttt aag tgg cgc tgg tat 480
Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160

cat ttt gat ggg aca gat tgg gat cag tca cgc cag ctt caa aac aaa 528
His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
165 170 175

ata tat aaa ttc agg gga aca ggc aag gcc tgg gac tgg gaa gtc gat 576
Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

aca gag aat ggc aac tat gac tat ctt atg tat gca gac gtg gat atg 624
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
195 200 205

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

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
 450 455 460

aat gca gac gga tgg ggt aat ttc tct gtt aat gga ggg tcc gtt tcg 1440
 Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
 465 470 475 480

gtt tgg gtg aag caa 1455
 Val Trp Val Lys Gln
 485

<210> 12
 <211> 485
 <212> PRT
 <213> Bacillus Sp

<400> 12

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
 1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
 20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
 35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 65 70 75 80

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

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
 115 120 125

Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
 130 135 140

Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
 145 150 155 160

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

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
195 200 205

Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
245 250 255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300

Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305 310 315 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Val Trp Val Lys Gln
485

<210> 13
<211> 1452
<212> DNA
<213> Bacillus amyloliquefaciens

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

<400> 13
gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac 48
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
1 5 10 15
ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat 96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
20 25 30
atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc 144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
35 40 45
caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa 192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60
ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag 240
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65 70 75 80
ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac 288
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
85 90 95
gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat 336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
100 105 110
gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg 384

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

355	360	365	
aca aaa ggg aca tcg cca aag gaa att ccc tca ctg aaa gat aat ata			1152
Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile			
370	375	380	
gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc cag cac			1200
Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His			
385	390	395	400
gat tat att gac cac ccg gat gtg atc gga tgg acg agg gaa ggt gac			1248
Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp			
	405	410	415
agc tcc gcc gcc aaa tca ggt ttg gcc gct tta atc acg gac gga ccc			1296
Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro			
	420	425	430
ggc gga tca aag cgg atg tat gcc ggc ctg aaa aat gcc ggc gag aca			1344
Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr			
	435	440	445
tgg tat gac ata acg ggc aac cgt tca gat act gta aaa atc gga tct			1392
Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser			
	450	455	460
gac ggc tgg gga gag ttt cat gta aac gat ggg tcc gtc tcc att tat			1440
Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr			
465	470	475	480
gtt cag aaa taa			1452
Val Gln Lys			

<210> 14
 <211> 483
 <212> PRT
 <213> Bacillus amyloliquefaciens

 <400> 14

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

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

Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
 385 390 395 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
 405 410 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
 435 440 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
 450 455 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
 465 470 475 480

Val Gln Lys

<210> 15
 <211> 1548
 <212> DNA
 <213> Bacillus stearothermophilus

<220>
 <221> CDS
 <222> (1)..(1548)

<400> 15
 gcc gca ccg ttt aac ggc acc atg atg cag tat ttt gaa tgg tac ttg 48
 Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu
 1 5 10 15

ccg gat gat ggc acg tta tgg acc aaa gtg gcc aat gaa gcc aac aac 96
 Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn

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

ttg cac aat tac att acg aaa aca gac gga acg atg tct ttg ttt gat	864
Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp	
275 280 285	
gcc ccg tta cac aac aaa ttt tat acc gct tcc aaa tca ggg ggc gca	912
Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala	
290 295 300	
ttt gat atg cgc acg tta atg acc aat act ctc atg aaa gat caa ccg	960
Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro	
305 310 315 320	
aca ttg gcc gtc acc ttc gtt gat aat cat gac acc gaa ccc ggc caa	1008
Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln	
325 330 335	
gcg ctg cag tca tgg gtc gac cca tgg ttc aaa ccg ttg gct tac gcc	1056
Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala	
340 345 350	
ttt att cta act cgg cag gaa gga tac ccg tgc gtc ttt tat ggt gac	1104
Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp	
355 360 365	
tat tat ggc att cca caa tat aac att cct tcg ctg aaa agc aaa atc	1152
Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile	
370 375 380	
gat ccg ctc ctc atc gcg cgc agg gat tat gct tac gga acg caa cat	1200
Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His	
385 390 395 400	
gat tat ctt gat cac tcc gac atc atc ggg tgg aca agg gaa ggg ggc	1248
Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly	
405 410 415	
act gaa aaa cca gga tcc gga ctg gcc gca ctg atc acc gat ggg ccg	1296
Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro	
420 425 430	
gga gga agc aaa tgg atg tac gtt ggc aaa caa cac gct gga aaa gtg	1344
Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Lys Gln His Ala Gly Lys Val	
435 440 445	
ttc tat gac ctt acc ggc aac cgg agt gac acc gtc acc atc aac agt	1392
Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser	
450 455 460	
gat gga tgg ggg gaa ttc aaa gtc aat ggc ggt tcg gtt tcg gtt tgg	1440
Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp	
465 470 475 480	
gtt cct aga aaa acg acc gtt tct acc atc gct cgg ccg atc aca acc	1488
Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr	
485 490 495	
cga ccg tgg act ggt gaa ttc gtc cgt tgg acc gaa cca cgg ttg gtg	1536
Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val	
500 505 510	

gca tgg cct tga
Ala Trp Pro
515

1548

<210> 16
<211> 515
<212> PRT
<213> Bacillus stearothermophilus

<400> 16

Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu
1 5 10 15

Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
20 25 30

Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
35 40 45

Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
50 55 60

Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr
65 70 75 80

Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
85 90 95

Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
100 105 110

Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln
115 120 125

Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
130 135 140

Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
145 150 155 160

Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
165 170 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
180 185 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His

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

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
 450 455 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
 465 470 475 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr
 485 490 495

Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
 500 505 510

Ala Trp Pro
 515

<210> 17
 <211> 1455
 <212> DNA
 <213> bacillus sp.

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

<400> 17
 cat cat aat ggg acg aat ggg acc atg atg cag tat ttt gaa tgg cat 48
 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
 1 5 10 15
 ttg cca aat gac ggg aac cac tgg aac agg tta cga gat gac gca gct 96
 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
 20 25 30
 aac tta aag agt aaa ggg att acc gct gtt tgg att cct cct gca tgg 144
 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
 35 40 45
 aag ggg act tcg caa aat gat gtt ggg tat ggt gcc tat gat ttg tac 192
 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60
 gat ctt ggt gag ttt aac caa aag gga acc gtc cgt aca aaa tat ggc 240
 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 65 70 75 80
 aca agg agt cag ttg caa ggt gcc gtg aca tct ttg aaa aat aac ggg 288
 Thr Arg Ser Gln Leu Gln Gly Ala Val Thr Ser Leu Lys Asn Asn Gly
 85 90 95
 att caa gtt tat ggg gat gtc gtg atg aat cat aaa ggt gga gca gac 336
 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110

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

Tyr	Ala	Leu	Ile	Leu	Thr	Arg	Glu	Gln	Gly	Tyr	Pro	Ser	Val	Phe	Tyr		
		355					360					365					
ggg	gat	tac	tac	ggg	ata	cca	act	cat	ggg	gtt	cct	tcg	atg	aaa	tct	1152	
Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	Thr	His	Gly	Val	Pro	Ser	Met	Lys	Ser		
		370				375					380						
aaa	att	gat	cca	ctt	ctg	cag	gca	cgt	caa	acg	tat	gcc	tac	gga	acc	1200	
Lys	Ile	Asp	Pro	Leu	Leu	Gln	Ala	Arg	Gln	Thr	Tyr	Ala	Tyr	Gly	Thr		
		385			390					395					400		
caa	cat	gat	tat	ttt	gat	cat	cat	gat	att	atc	ggc	tgg	acg	aga	gaa	1248	
Gln	His	Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Ile	Gly	Trp	Thr	Arg	Glu		
				405					410					415			
ggg	gac	agc	tcc	cac	cca	aat	tca	gga	ctt	gca	act	att	atg	tcc	gat	1296	
Gly	Asp	Ser	Ser	His	Pro	Asn	Ser	Gly	Leu	Ala	Thr	Ile	Met	Ser	Asp		
			420					425					430				
ggg	cca	ggg	ggg	aat	aaa	tgg	atg	tat	gtc	ggg	aaa	cat	aaa	gct	ggc	1344	
Gly	Pro	Gly	Gly	Asn	Lys	Trp	Met	Tyr	Val	Gly	Lys	His	Lys	Ala	Gly		
		435				440						445					
caa	gta	tgg	aga	gat	atc	acc	gga	aat	agg	tct	ggg	acc	gtc	acc	att	1392	
Gln	Val	Trp	Arg	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Gly	Thr	Val	Thr	Ile		
		450				455					460						
aat	gca	gat	ggg	tgg	ggg	aat	ttc	act	gta	aac	gga	ggg	gca	gtt	tcg	1440	
Asn	Ala	Asp	Gly	Trp	Gly	Asn	Phe	Thr	Val	Asn	Gly	Gly	Ala	Val	Ser		
		465			470					475					480		
gtt	tgg	gtg	aag	caa												1455	
Val	Trp	Val	Lys	Gln													
				485													
<210> 18																	
<211> 485																	
<212> PRT																	
<213> bacillus sp.																	
<400> 18																	
His	His	Asn	Gly	Thr	Asn	Gly	Thr	Met	Met	Gln	Tyr	Phe	Glu	Trp	His		
1				5					10					15			
Leu	Pro	Asn	Asp	Gly	Asn	His	Trp	Asn	Arg	Leu	Arg	Asp	Asp	Ala	Ala		
			20					25					30				
Asn	Leu	Lys	Ser	Lys	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Trp		
		35					40					45					
Lys	Gly	Thr	Ser	Gln	Asn	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr		
		50				55					60						
Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly		
					70					75					80		

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

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Gly Thr Glu Met Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
115 120 125

Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
145 150 155 160

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

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
195 200 205

Asp His Pro Glu Val Ile Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
245 250 255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300

Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305 310 315 320

His Pro Ile His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Ser Trp Phe Lys Pro Leu Ala
 340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ser Met Lys Ser
 370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Tyr Ala Tyr Gly Thr
 385 390 395 400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
 405 410 415

Gly Asp Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys His Lys Ala Gly
 435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile
 450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Thr Val Asn Gly Gly Ala Val Ser
 465 470 475 480

Val Trp Val Lys Gln
 485

<210> 19
 <211> 1452
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (1)..(1452)

<400> 19
 gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc 48
 Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15

aat gac ggc caa cat tgg agg cgt ttg caa aac gac tcg gca tat ttg 96

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

260	265	270	
tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu 275 280 285			864
cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met 290 295 300			912
agg aaa ttg ctg aac ggt acg gtc gtt tcc aag cat ccg ttg aaa tcg Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser 305 310 315 320			960
ggt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu 325 330 335			1008
tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu 340 345 350			1056
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly 355 360 365			1104
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile 370 375 380			1152
gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His 385 390 395 400			1200
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp 405 410 415			1248
agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro 420 425 430			1296
ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr 435 440 445			1344
tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser 450 455 460			1392
gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr 465 470 475 480			1440
ggt caa aga tag Val Gln Arg			1452

<210> 20
<211> 483

<212> PRT
<213> Bacillus licheniformis

<400> 20

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1 5 10 15

Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
20 25 30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
100 105 110

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
115 120 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
130 135 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145 150 155 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
290 295 300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
355 360 365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr

465

470

475

480

Val Gln Arg

<210> 21

<211> 1455

<212> DNA

<213> bacillus sp.

<220>

<221> CDS

<222> (1)..(1455)

<400> 21

cac	cat	aat	ggc	aca	aat	gga	aca	atg	atg	caa	tat	ttt	gaa	tgg	tat	48
His	His	Asn	Gly	Thr	Asn	Gly	Thr	Met	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	
1				5					10					15		

ttg	cca	aat	gac	ggt	aat	cat	tgg	aat	aga	tta	aga	tca	gat	gca	agt	96
Leu	Pro	Asn	Asp	Gly	Asn	His	Trp	Asn	Arg	Leu	Arg	Ser	Asp	Ala	Ser	
			20					25					30			

aat	ctt	aaa	gat	aaa	ggg	att	aca	gcg	gtt	tgg	att	cca	cct	gct	tgg	144
Asn	Leu	Lys	Asp	Lys	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Trp	
		35					40					45				

aaa	ggg	gct	tct	caa	aat	gat	gta	ggg	tat	gga	gcc	tat	gat	ctg	tat	192
Lys	Gly	Ala	Ser	Gln	Asn	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr	
	50					55					60					

gat	tta	gga	gaa	ttc	aat	caa	aaa	gga	acc	gta	cgt	aca	aag	tac	gga	240
Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	
65					70					75					80	

acc	cgt	aat	caa	tta	caa	gct	gca	gta	acc	gcc	tta	aaa	agt	aat	ggt	288
Thr	Arg	Asn	Gln	Leu	Gln	Ala	Ala	Val	Thr	Ala	Leu	Lys	Ser	Asn	Gly	
			85						90					95		

att	caa	gta	tac	gga	gat	gtc	gta	atg	aat	cat	aag	ggt	gga	gcg	gat	336
Ile	Gln	Val	Tyr	Gly	Asp	Val	Val	Met	Asn	His	Lys	Gly	Gly	Ala	Asp	
		100						105					110			

gcc	act	gag	tgg	gtt	cga	gcg	gtt	gaa	gtg	aac	cca	agt	aat	cgt	aat	384
Ala	Thr	Glu	Trp	Val	Arg	Ala	Val	Glu	Val	Asn	Pro	Ser	Asn	Arg	Asn	
		115					120					125				

caa	gaa	gtc	tct	ggt	gat	tat	acg	att	gag	gct	tgg	act	aag	ttt	gat	432
Gln	Glu	Val	Ser	Gly	Asp	Tyr	Thr	Ile	Glu	Ala	Trp	Thr	Lys	Phe	Asp	
	130					135					140					

ttt	cct	ggt	cga	ggt	aat	acc	cac	tct	aac	ttt	aaa	tgg	aga	tgg	tat	480
Phe	Pro	Gly	Arg	Gly	Asn	Thr	His	Ser	Asn	Phe	Lys	Trp	Arg	Trp	Tyr	
145					150					155					160	

cat	ttc	gat	ggt	gta	gat	tgg	gat	cag	tca	cgt	caa	ttg	cag	aat	cga	528
His	Phe	Asp	Gly	Val	Asp	Trp	Asp	Gln	Ser	Arg	Gln	Leu	Gln	Asn	Arg	
				165					170					175		

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

ggt aat aca gca cat ccc aac tca gga cta gca act att atg tcg gat	1296
Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp	
420 425 430	

ggc cca gga gga aat aaa tgg atg tat gtt ggg cgt aat aag gct gga	1344
Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Arg Asn Lys Ala Gly	
435 440 445	

caa gtt tgg aga gat att aca gga aat cgc tca ggt acg gtg acg att	1392
Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile	
450 455 460	

aac gca gat ggg tgg ggt aat ttt tct gta aat ggt ggg tct gta tct	1440
Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser	
465 470 475 480	

ata tgg gta aat aat	1455
Ile Trp Val Asn Asn	
485	

<210> 22
 <211> 485
 <212> PRT
 <213> bacillus sp.

<400> 22

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
20 25 30

Asn Leu Lys Asp Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

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

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Trp Val Arg Ala Val Glu Val Asn Pro Ser Asn Arg Asn
115 120 125

Gln Glu Val Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp

130

135

140

Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
 145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Arg
 165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp
 180 185 190

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

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
 210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
 225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
 245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Ile
 260 265 270

Gly Ala Ile Glu Asn Tyr Leu Ser Lys Thr Asn Trp Asn His Ser Val
 275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Arg Ser Gly
 290 295 300

Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg
 305 310 315 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
 340 345 350

Tyr Ala Leu Thr Leu Thr Arg Asp Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
 370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys
385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Met Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Arg Asn Lys Ala Gly
435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Asn Asn
485

<210> 23
<211> 1452
<212> DNA
<213> bacillus sp

<220>
<221> CDS
<222> (1)..(1452)

<400> 23
gga agt gtg ccg gta aat ggc aca atg atg caa tat ttc gaa tgg tac 48
Gly Ser Val Pro Val Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15
ctt cca gac gat gga aca cta tgg acg aaa gta gca aat aac gct caa 96
Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Asn Ala Gln
20 25 30
tct tta gcg aat ctt ggc att act gcc ctt tgg ctt ccc cct gcc tat 144
Ser Leu Ala Asn Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr
35 40 45
aaa gga aca agc agc agt gac gtt gga tat ggc gtt tat gat tta tat 192
Lys Gly Thr Ser Ser Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr
50 55 60
gac ctt gga gag ttt aat caa aaa gga act gtc cga aca aaa tac ggg 240
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

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

Pro	Thr	Leu	Ala	Val	Thr	Leu	Val	Asp	Asn	His	Asp	Thr	Glu	Pro	Gly		
				325					330					335			
caa	tct	ctg	cag	tca	tgg	gtc	gag	cca	tgg	ttt	aaa	ccg	tta	gct	tac	1056	
Gln	Ser	Leu	Gln	Ser	Trp	Val	Glu	Pro	Trp	Phe	Lys	Pro	Leu	Ala	Tyr		
			340					345					350				
gca	ttt	atc	ttg	acc	cgc	caa	gaa	ggg	tat	cct	tgc	gtc	ttt	tat	gga	1104	
Ala	Phe	Ile	Leu	Thr	Arg	Gln	Glu	Gly	Tyr	Pro	Cys	Val	Phe	Tyr	Gly		
		355					360					365					
gat	tac	tat	ggg	att	cca	aaa	tac	aac	att	cct	gcg	ctg	aaa	agc	aaa	1152	
Asp	Tyr	Tyr	Gly	Ile	Pro	Lys	Tyr	Asn	Ile	Pro	Ala	Leu	Lys	Ser	Lys		
	370					375					380						
ctt	gat	ccg	ctg	tta	att	gcc	aga	aga	gat	tat	gcc	tat	gga	aca	cag	1200	
Leu	Asp	Pro	Leu	Leu	Ile	Ala	Arg	Arg	Asp	Tyr	Ala	Tyr	Gly	Thr	Gln		
385					390					395					400		
cac	gac	tat	att	gac	agt	gcg	gat	att	atc	ggg	tgg	acg	cgg	gaa	gga	1248	
His	Asp	Tyr	Ile	Asp	Ser	Ala	Asp	Ile	Ile	Gly	Trp	Thr	Arg	Glu	Gly		
			405					410						415			
gtg	gct	gaa	aaa	gca	aat	tca	gga	ctg	gct	gca	ctc	att	acc	gac	ggg	1296	
Val	Ala	Glu	Lys	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly		
			420					425					430				
cct	ggc	gga	agc	aaa	tgg	atg	tat	gtt	gga	aaa	caa	cac	gct	ggc	aaa	1344	
Pro	Gly	Gly	Ser	Lys	Trp	Met	Tyr	Val	Gly	Lys	Gln	His	Ala	Gly	Lys		
			435				440					445					
acg	ttt	tat	gat	tta	acc	ggc	aat	cga	agt	gat	aca	gtg	aca	atc	aat	1392	
Thr	Phe	Tyr	Asp	Leu	Thr	Gly	Asn	Arg	Ser	Asp	Thr	Val	Thr	Ile	Asn		
	450					455					460						
gct	gat	gga	tgg	gga	gaa	ttt	aaa	gtc	aat	gga	ggg	tct	gta	tcc	ata	1440	
Ala	Asp	Gly	Trp	Gly	Glu	Phe	Lys	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile		
465					470					475					480		
tg	g	t	c	a	a	a										1452	
Trp	Val	Pro	Lys														

<210> 24
 <211> 484
 <212> PRT
 <213> bacillus sp

<400> 24

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

Lys Gly Thr Ser Ser Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Lys Thr Gln Tyr Ile Gln Ala Ile Gln Ala Ala His Thr Ala Gly
85 90 95

Met Gln Val Tyr Ala Asp Val Val Phe Asn His Lys Ala Gly Ala Asp
100 105 110

Gly Thr Glu Leu Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn
115 120 125

Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160

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

Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp Thr
180 185 190

Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp
195 200 205

His Pro Glu Val Val Ser Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val
210 215 220

Thr Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile
225 230 235 240

Lys Tyr Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Thr Gln Thr
245 250 255

Gln Lys Pro Leu Phe Ala Val Gly Glu Phe Trp Ser Tyr Asp Ile Ser
260 265 270

Lys Leu His Asn Tyr Ile Thr Lys Thr Asn Gly Ser Met Ser Leu Phe
275 280 285

Asp Ala Pro Leu His Asn Asn Phe Tyr Ile Ala Ser Lys Ser Gly Gly
290 295 300

Tyr Phe Asp Met Arg Thr Leu Leu Asn Asn Thr Leu Met Lys Asp Gln
305 310 315 320

Pro Thr Leu Ala Val Thr Leu Val Asp Asn His Asp Thr Glu Pro Gly
325 330 335

Gln Ser Leu Gln Ser Trp Val Glu Pro Trp Phe Lys Pro Leu Ala Tyr
340 345 350

Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly
355 360 365

Asp Tyr Tyr Gly Ile Pro Lys Tyr Asn Ile Pro Ala Leu Lys Ser Lys
370 375 380

Leu Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln
385 390 395 400

His Asp Tyr Ile Asp Ser Ala Asp Ile Ile Gly Trp Thr Arg Glu Gly
405 410 415

Val Ala Glu Lys Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly
420 425 430

Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys
435 440 445

Thr Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn
450 455 460

Ala Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Ile
465 470 475 480

Trp Val Pro Lys

<210> 25
<211> 1455
<212> DNA
<213> Bacillus sp.

<220>
<221> CDS

<222> (1) .. (1455)

<400> 25

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

225	230	235	240	
att aaa tac agc ttt ttc cct gac tgg cta aca tat gta cgt aat caa				768
Ile Lys Tyr Ser Phe Phe Pro Asp Trp Leu Thr Tyr Val Arg Asn Gln	245	250	255	
aca gga aaa aat tta ttt gcc gtt ggg gaa ttt tgg agc tat gac gtc				816
Thr Gly Lys Asn Leu Phe Ala Val Gly Glu Phe Trp Ser Tyr Asp Val	260	265	270	
aat aag ctg cat aat tac att aca aaa aca aat gga tgc atg tca tta				864
Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asn Gly Ser Met Ser Leu	275	280	285	
ttt gat gca cct ttg cat aac aac ttt tat acc gct tcc aaa tgc agt				912
Phe Asp Ala Pro Leu His Asn Asn Phe Tyr Thr Ala Ser Lys Ser Ser	290	295	300	
gga tat ttt gac atg cgt tat tta ttg aat aat aca tta atg aaa gat				960
Gly Tyr Phe Asp Met Arg Tyr Leu Leu Asn Asn Thr Leu Met Lys Asp	305	310	315	320
caa cct tca ctc gct gtg aca ctt gtc gat aac cac gac acg caa cca				1008
Gln Pro Ser Leu Ala Val Thr Leu Val Asp Asn His Asp Thr Gln Pro	325	330	335	
ggg caa tct tta cag tca tgg gtc gaa cct tgg ttt aaa cca ctt gct				1056
Gly Gln Ser Leu Gln Ser Trp Val Glu Pro Trp Phe Lys Pro Leu Ala	340	345	350	
tac gcc ttt att tta acg aga caa gag gga tat cct tgc gta ttt tac				1104
Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr	355	360	365	
ggt gac tat tat gga atc ccg aaa tac aat att cca gga tta aaa agc				1152
Gly Asp Tyr Tyr Gly Ile Pro Lys Tyr Asn Ile Pro Gly Leu Lys Ser	370	375	380	
aaa atc gac ccg ctt tta att gct cgt cgg gac tat gcc tat gga aca				1200
Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr	385	390	395	400
caa cgt gat tac att gac cat caa gac att att gga tgg aca cgc gaa				1248
Gln Arg Asp Tyr Ile Asp His Gln Asp Ile Ile Gly Trp Thr Arg Glu	405	410	415	
ggc att gat aca aaa cca aac tct gga ctg gcg gct tta att acc gac				1296
Gly Ile Asp Thr Lys Pro Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp	420	425	430	
ggc cct ggc gga agc aaa tgg atg tat gtc ggt aaa aaa cat gct gga				1344
Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Lys His Ala Gly	435	440	445	
aaa gta ttt tat gat tta acc gga aac cga agt gac aca gta acg att				1392
Lys Val Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile	450	455	460	
aat gcg gat ggt tgg gga gaa ttt aaa gta aac gga ggc tcc gtt tgc				1440
Asn Ala Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser	465	470	475	480

att tgg gtg gct aaa
Ile Trp Val Ala Lys
485

1455

<210> 26
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 26

Ala Asn Thr Ala Pro Ile Asn Glu Thr Met Met Gln Tyr Phe Glu Trp
1 5 10 15

Asp Leu Pro Asn Asp Gly Thr Leu Trp Thr Lys Val Lys Asn Glu Ala
20 25 30

Ala Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala
35 40 45

Tyr Lys Gly Thr Ser Gln Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu
50 55 60

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

Gly Thr Lys Thr Gln Tyr Ile Gln Ala Ile Gln Ala Ala Lys Ala Ala
85 90 95

Gly Met Gln Val Tyr Ala Asp Val Val Phe Asn His Lys Ala Gly Ala
100 105 110

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

Asn Gln Glu Thr Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe
130 135 140

Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp
145 150 155 160

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

Ile Tyr Lys Phe Arg Ser Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Phe Ala Asp Leu Asp Met
195 200 205

Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Thr Trp Tyr
210 215 220

Val Asn Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Phe Pro Asp Trp Leu Thr Tyr Val Arg Asn Gln
245 250 255

Thr Gly Lys Asn Leu Phe Ala Val Gly Glu Phe Trp Ser Tyr Asp Val
260 265 270

Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asn Gly Ser Met Ser Leu
275 280 285

Phe Asp Ala Pro Leu His Asn Asn Phe Tyr Thr Ala Ser Lys Ser Ser
290 295 300

Gly Tyr Phe Asp Met Arg Tyr Leu Leu Asn Asn Thr Leu Met Lys Asp
305 310 315 320

Gln Pro Ser Leu Ala Val Thr Leu Val Asp Asn His Asp Thr Gln Pro
325 330 335

Gly Gln Ser Leu Gln Ser Trp Val Glu Pro Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Lys Tyr Asn Ile Pro Gly Leu Lys Ser
370 375 380

Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr
385 390 395 400

Gln Arg Asp Tyr Ile Asp His Gln Asp Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Ile Asp Thr Lys Pro Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp
420 425 430

Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Lys His Ala Gly

435

440

445

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

Asn Ala Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Ala Lys
485