

SEQUENCE LISTING

<110> PURAC
 PURAC BIOCHEM BV

<120> Genetic modification of S-lactic acid producing thermophilic
 bacteria

<130> 22805

<150> EP 14178150.0
 <151> 2014-07-23

<160> 34

<170> PatentIn version 3.5

<210> 1
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic primer

<400> 1
 tcgccttctt ctgtgtcatc 20

<210> 2
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic primer

<400> 2
 ctggaggaga gcaatgaaac 20

<210> 3
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic primer

<400> 3
 gcgcgggtac ccagcaaacc gagcggaatc ag 32

<210> 4
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>

<223>	Synthetic primer	
<400>	4	
	gcgcggtcga cggatgggta ggcattccatt c	31
<210>	5	
<211>	33	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic primer	
<400>	5	
	gcgcggtcga cgtctccctt agttacataa cgc	33
<210>	6	
<211>	32	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic primer	
<400>	6	
	gcgcgaagct tgcttcgcag tccaatcgtc gc	32
<210>	7	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic primer	
<400>	7	
	gctaagatcg gccatacggtt aagc	24
<210>	8	
<211>	21	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic primer	
<400>	8	
	ggagacgagc ttggcgtcct g	21
<210>	9	
<211>	28	
<212>	DNA	
<213>	Artificial Sequence	

<220>
 <223> Synthetic primer

 <400> 9
 gccctcgaga gggctcgctt ttgggaag 28

<210> 10
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic primer

 <400> 10
 gctcggttata gtcgatcggt tc 22

<210> 11
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic primer

 <400> 11
 gcgcgggatc cgctttccgt ttgccatttg ccg 33

<210> 12
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic primer

 <400> 12
 gcgcgctgca gggcaagact gacagaagag cttgg 35

<210> 13
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic primer

 <400> 13
 cagcagtaac ggcacccgat tg 22

<210> 14
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>		
<223>	Synthetic primer	
<400>	14	
	gcggatatga ttgaatttgt gactgcc	27
<210>	15	
<211>	33	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic primer	
<400>	15	
	tatgcgacgg gcgcgtggag gaatattgtc cgc	33
<210>	16	
<211>	36	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic primer	
<400>	16	
	attcctccac gcgcccgtcg catacagttc atgttg	36
<210>	17	
<211>	33	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic primer	
<400>	17	
	gcgcggggtc ccccaaattg cattaccggt gtg	33
<210>	18	
<211>	34	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic primer	
<400>	18	
	tgttattgct ggcagtttcc ctcccatgca tctg	34
<210>	19	
<211>	35	
<212>	DNA	

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 19

ggaggggaaac tgccagcaat aacaccaaca ggctc

35

<210> 20

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 20

gcgcgctgca gcgaaagcga acgaaattgc caac

34

<210> 21

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 21

gccaagatgg atatgggcgt tagc

24

<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 22

ccggagatgg acggaattga ag

22

<210> 23

<211> 423

<212> DNA

<213> Geobacillus thermoglucosidans

<220>

<221> CDS

<222> (1)..(423)

<400> 23

gtg aga atc gcg ttg atc gcg cat gat aaa aag aaa gcg gat atg att
Val Arg Ile Ala Leu Ile Ala His Asp Lys Lys Lys Ala Asp Met Ile
1 5 10 15

48

gaa ttt gtg act gcc tat cag ccg att tta gaa caa cat gaa ctg tat Glu Phe Val Thr Ala Tyr Gln Pro Ile Leu Glu Gln His Glu Leu Tyr 20 25 30	96
gcg acg ggc acg acc ggc ttg cgc att cag gaa gcg aca gga ctg ccg Ala Thr Gly Thr Thr Gly Leu Arg Ile Gln Glu Ala Thr Gly Leu Pro 35 40 45	144
gtg cat cgc ttt caa tcg ggg cca tat ggc ggc gat caa gaa att ggt Val His Arg Phe Gln Ser Gly Pro Tyr Gly Gly Asp Gln Glu Ile Gly 50 55 60	192
gca atg att gcc cgc aat gaa atg gat atg gtg ata ttt ttc cgc gat Ala Met Ile Ala Arg Asn Glu Met Asp Met Val Ile Phe Phe Arg Asp 65 70 75 80	240
ccg ttg acg gca cag ccg cat gag ccg gat gtc agt gcg ctc att cgc Pro Leu Thr Ala Gln Pro His Glu Pro Asp Val Ser Ala Leu Ile Arg 85 90 95	288
tta tgt gat gtc tat tcc gtg ccg ctt gca acc aat atg ggg acg gcg Leu Cys Asp Val Tyr Ser Val Pro Leu Ala Thr Asn Met Gly Thr Ala 100 105 110	336
gaa att tta att aaa ggg ctg gag cgc ggc gat ttt gcg tgg agg aat Glu Ile Leu Ile Lys Gly Leu Glu Arg Gly Asp Phe Ala Trp Arg Asn 115 120 125	384
att gtc cgc ggc cga aaa ggt gag aca aat gga ata taa Ile Val Arg Gly Arg Lys Gly Glu Thr Asn Gly Ile 130 135 140	423
<210> 24 <211> 140 <212> PRT <213> <i>Geobacillus thermoglucosidans</i>	
<400> 24	
Val Arg Ile Ala Leu Ile Ala His Asp Lys Lys Lys Ala Asp Met Ile 1 5 10 15	
Glu Phe Val Thr Ala Tyr Gln Pro Ile Leu Glu Gln His Glu Leu Tyr 20 25 30	
Ala Thr Gly Thr Thr Gly Leu Arg Ile Gln Glu Ala Thr Gly Leu Pro 35 40 45	
Val His Arg Phe Gln Ser Gly Pro Tyr Gly Gly Asp Gln Glu Ile Gly 50 55 60	
Ala Met Ile Ala Arg Asn Glu Met Asp Met Val Ile Phe Phe Arg Asp 65 70 75 80	

Pro Leu Thr Ala Gln Pro His Glu Pro Asp Val Ser Ala Leu Ile Arg
85 90 95

Leu Cys Asp Val Tyr Ser Val Pro Leu Ala Thr Asn Met Gly Thr Ala
100 105 110

Glu Ile Leu Ile Lys Gly Leu Glu Arg Gly Asp Phe Ala Trp Arg Asn
115 120 125

Ile Val Arg Gly Arg Lys Gly Glu Thr Asn Gly Ile
130 135 140

<210> 25
<211> 2250
<212> DNA
<213> *Geobacillus thermoglucosidans*

<220>
<221> CDS
<222> (1)..(2250)

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

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

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

aaa cat acg cta tct att tta aca att acg tct aac gtt gta tac ggg 1824
Lys His Thr Leu Ser Ile Leu Thr Ile Thr Ser Asn Val Val Tyr Gly
595 600 605

aaa aag acc gga aat aca cca gat ggc cgc cgc gct ggc gaa cgc ttt 1872
Lys Lys Thr Gly Asn Thr Pro Asp Gly Arg Arg Ala Gly Glu Pro Phe
610 615 620

gcc cca gga gca aac ccg ttg cac ggc cgt gac acg aaa gga gcg ctc 1920
Ala Pro Gly Ala Asn Pro Leu His Gly Arg Asp Thr Lys Gly Ala Leu
625 630 635 640

gct tcg cta agc tct gtc gcg aaa tta cca tat gaa cat gca tta gat 1968
Ala Ser Leu Ser Ser Val Ala Lys Leu Pro Tyr Glu His Ala Leu Asp
645 650 655

ggc att tcg aat acg ttc tcg atc gtg ccg aaa gcg tta gga aaa gag 2016
Gly Ile Ser Asn Thr Phe Ser Ile Val Pro Lys Ala Leu Gly Lys Glu
660 665 670

gaa gga gac cgt gtc cgc aac ctt gtc gcc gtt tta gac gga tac atg 2064
Glu Gly Asp Arg Val Arg Asn Leu Val Ala Val Leu Asp Gly Tyr Met
675 680 685

gaa aaa ggc ggg cat cat ctc aac att aac gtg ttg aac cgc gaa aca 2112
Glu Lys Gly Gly His His Leu Asn Ile Asn Val Leu Asn Arg Glu Thr
690 695 700

t	t	g	a	t	t	a	g	a	a	c	a	a	a	a	a		2160
Leu	Leu	Asp	Ala	Met	Glu	His	Pro	Glu	Lys	Tyr	Pro	Gln	Leu	Thr	Ile		
705					710					715					720		

cgc gtt tct gga tat gcc gtc aac ttc ata aaa tta acg cgc gaa caa 2208
Arg Val Ser Gly Tyr Ala Val Asn Phe Ile Lys Leu Thr Arg Glu Gln
725 730 735

caa atc gat gtc att aac cgc acg ttc cac gaa acg atg taa 2250
Gln Ile Asp Val Ile Asn Arg Thr Phe His Glu Thr Met
740 745

$\langle 210 \rangle$ 26

<211> 749

<212> PRT

<213> Geobacillus thermoglucosidans

<400> 26

Met Lys Gln Ala Thr Val Val Leu Asp Pro Trp Arg Asn Phe Lys Gly
1 5 10 15

Ser Lys Trp Lys Lys Ser Ile Asp Val Arg Asp Phe Ile Leu Asn Asn
20 25 30

Val Thr Val Tyr Tyr Gly Asp Glu Ser Phe Leu Glu Gly Pro Thr Glu
35 40 45

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

Glu Gly Thr Leu Thr Glu Lys Glu Ala Gln Glu Leu Val Asp His Phe
 290 295 300

Val Met Lys Leu Arg Leu Val Lys Phe Ala Arg Thr Pro Glu Tyr Asn
 305 310 315 320

Glu Leu Phe Ser Gly Asp Pro Thr Trp Val Thr Glu Ser Ile Gly Gly
 325 330 335

Ile Ala Ile Asp Gly Arg Pro Leu Val Thr Lys Asn Ser Phe Arg Phe
 340 345 350

Leu His Thr Leu Asp Asn Leu Gly Pro Ala Pro Glu Pro Asn Leu Thr
 355 360 365

Val Leu Trp Ser Lys Gln Leu Pro Glu Ala Phe Lys Glu Tyr Cys Ala
 370 375 380

Lys Met Ser Ile Lys Thr Ser Ser Ile Gln Tyr Glu Asn Asp Asp Leu
 385 390 395 400

Met Arg Val Glu Phe Gly Asp Asp Tyr Gly Ile Ala Cys Cys Val Ser
 405 410 415

Ala Met Arg Ile Gly Lys Gln Met Gln Phe Phe Gly Ala Arg Ala Asn
 420 425 430

Leu Ala Lys Ala Leu Leu Tyr Ala Ile Asn Gly Gly Val Asp Glu Lys
 435 440 445

Leu Lys Ile Gln Val Gly Pro Glu Phe Ala Pro Ile Thr Ser Glu Tyr
 450 455 460

Leu Asn Tyr Asp Glu Val Met His Lys Phe Asp Gln Val Leu Glu Trp
 465 470 475 480

Leu Ala Glu Leu Tyr Ile Asn Thr Leu Asn Val Ile His Tyr Met His
 485 490 495

Asp Lys Tyr Cys Tyr Glu Arg Ile Glu Met Ala Leu His Asp Thr His
 500 505 510

Val Leu Arg Thr Met Ala Thr Gly Ile Ala Gly Leu Ser Val Val Val

515				520				525							
Asp	Ser	Leu	Ser	Ala	Ile	Lys	Tyr	Ala	Lys	Val	Lys	Pro	Ile	Arg	Asp
	530					535					540				
Glu	Asn	Gly	Ile	Ala	Val	Asp	Phe	Glu	Met	Glu	Gly	Asp	Phe	Pro	Lys
545					550					555					560
Tyr	Gly	Asn	Asn	Asp	Asp	Arg	Val	Asp	Gln	Ile	Ala	Val	Asp	Leu	Val
				565					570					575	
Glu	Arg	Phe	Met	Thr	Lys	Leu	Lys	Lys	His	Lys	Thr	Tyr	Arg	Asp	Ser
			580					585					590		
Lys	His	Thr	Leu	Ser	Ile	Leu	Thr	Ile	Thr	Ser	Asn	Val	Val	Tyr	Gly
		595					600					605			
Lys	Lys	Thr	Gly	Asn	Thr	Pro	Asp	Gly	Arg	Arg	Ala	Gly	Glu	Pro	Phe
	610					615					620				
Ala	Pro	Gly	Ala	Asn	Pro	Leu	His	Gly	Arg	Asp	Thr	Lys	Gly	Ala	Leu
625					630					635					640
Ala	Ser	Leu	Ser	Ser	Val	Ala	Lys	Leu	Pro	Tyr	Glu	His	Ala	Leu	Asp
				645					650					655	
Gly	Ile	Ser	Asn	Thr	Phe	Ser	Ile	Val	Pro	Lys	Ala	Leu	Gly	Lys	Glu
			660					665					670		
Glu	Gly	Asp	Arg	Val	Arg	Asn	Leu	Val	Ala	Val	Leu	Asp	Gly	Tyr	Met
		675					680					685			
Glu	Lys	Gly	Gly	His	His	Leu	Asn	Ile	Asn	Val	Leu	Asn	Arg	Glu	Thr
	690					695					700				
Leu	Leu	Asp	Ala	Met	Glu	His	Pro	Glu	Lys	Tyr	Pro	Gln	Leu	Thr	Ile
705					710					715					720
Arg	Val	Ser	Gly	Tyr	Ala	Val	Asn	Phe	Ile	Lys	Leu	Thr	Arg	Glu	Gln
				725					730					735	
Gln	Ile	Asp	Val	Ile	Asn	Arg	Thr	Phe	His	Glu	Thr	Met			
			740					745							

<210> 27
 <211> 750
 <212> DNA
 <213> *Geobacillus thermoglucosidans*

<220>
 <221> CDS
 <222> (1)..(750)

<400> 27
 atg aaa gga ttt att cat tcc atc gaa tca tgc ggc acc gtc gac ggg 48
 Met Lys Gly Phe Ile His Ser Ile Glu Ser Cys Gly Thr Val Asp Gly
 1 5 10 15

ccg ggc ctt cgc tat gtc atc ttt aca caa ggc tgt gtg ctg cgc tgc 96
 Pro Gly Leu Arg Tyr Val Ile Phe Thr Gln Gly Cys Val Leu Arg Cys
 20 25 30

caa tat tgc cat aac gcc gat acg tgg gaa att gga aaa gga aaa gaa 144
 Gln Tyr Cys His Asn Ala Asp Thr Trp Glu Ile Gly Lys Gly Lys Glu
 35 40 45

atg act gtg gaa gaa atc atc gat gac gtg aaa aca tac ttg ccg ttt 192
 Met Thr Val Glu Glu Ile Ile Asp Asp Val Lys Thr Tyr Leu Pro Phe
 50 55 60

atc aac gct tcc aat ggc gga att acc gtc agc ggc gga gag cct ttg 240
 Ile Asn Ala Ser Asn Gly Gly Ile Thr Val Ser Gly Gly Glu Pro Leu
 65 70 75 80

tta caa atc gat ttt tta att gaa tta ttt aaa gca tgc aaa aaa ctg 288
 Leu Gln Ile Asp Phe Leu Ile Glu Leu Phe Lys Ala Cys Lys Lys Leu
 85 90 95

ggc att cat acc gcg atc gat tca tcg gga gga tgc tac acg acg gaa 336
 Gly Ile His Thr Ala Ile Asp Ser Ser Gly Gly Cys Tyr Thr Thr Glu
 100 105 110

gca tcg ttc cag caa aaa tta aat gaa tta ctt tcc tat acc gat tta 384
 Ala Ser Phe Gln Gln Lys Leu Asn Glu Leu Leu Ser Tyr Thr Asp Leu
 115 120 125

att ttg ctt gat tta aaa cat atc gat gag aaa aaa cac cgg aaa ctg 432
 Ile Leu Leu Asp Leu Lys His Ile Asp Glu Lys Lys His Arg Lys Leu
 130 135 140

aca gga aaa acc aat aaa cat att tta caa ttt gct cag ttt tta tcc 480
 Thr Gly Lys Thr Asn Lys His Ile Leu Gln Phe Ala Gln Phe Leu Ser
 145 150 155 160

gaa aaa aac gtt cct gtt tgg atc cgg cat gtt ctc gtt cca acc atc 528
 Glu Lys Asn Val Pro Val Trp Ile Arg His Val Leu Val Pro Thr Ile
 165 170 175

aca gac gac ccg aat gac ttg cgc cgt ctc gcc gct ttt att cgc aca 576
 Thr Asp Asp Pro Asn Asp Leu Arg Arg Leu Ala Ala Phe Ile Arg Thr
 180 185 190

tta	aag	aat	gtg	aaa	aaa	att	gaa	att	ctc	cca	tac	cat	aaa	tta	gga	624
Leu	Lys	Asn	Val	Lys	Lys	Ile	Glu	Ile	Leu	Pro	Tyr	His	Lys	Leu	Gly	
		195					200					205				

gta tac aaa tgg aaa gcg ctt gga tta aaa tac cct ttg gaa gga atc 672
Val Tyr Lys Trp Lys Ala Leu Gly Leu Lys Tyr Pro Leu Glu Gly Ile
210 215 220

gag	cct	cct	tcg	gaa	gaa	agc	gta	caa	atg	gca	cag	cga	att	ctt	aac	720
Glu	Pro	Pro	Ser	Glu	Glu	Ser	Val	Gln	Met	Ala	Gln	Arg	Ile	Leu	Asn	
225					230					235					240	

gga aca gaa gat aca gta tct ctt gcg taa 750
Gly Thr Glu Asp Thr Val Ser Leu Ala
245

<210>	28
<211>	249
<212>	PRT
<213>	Geobacillus thermoglucosidans

<400> 28

Met Lys Gly Phe Ile His Ser Ile Glu Ser Cys Gly Thr Val Asp Gly
1 5 10 15

Pro Gly Leu Arg Tyr Val Ile Phe Thr Gln Gly Cys Val Leu Arg Cys
20 25 30

Gln Tyr Cys His Asn Ala Asp Thr Trp Glu Ile Gly Lys Gly Lys Glu
35 40 45

Met Thr Val Glu Glu Ile Ile Asp Asp Val Lys Thr Tyr Leu Pro Phe
50 55 60

Ile Asn Ala Ser Asn Gly Gly Ile Thr Val Ser Gly Gly Glu Pro Leu
65 70 75 80

Leu Gln Ile Asp Phe Leu Ile Glu Leu Phe Lys Ala Cys Lys Lys Leu
85 90 95

Gly Ile His Thr Ala Ile Asp Ser Ser Gly Gly Cys Tyr Thr Thr Glu
100 105 110

Ala Ser Phe Gln Gln Lys Leu Asn Glu Leu Leu Ser Tyr Thr Asp Leu
115 120 125

Ile Leu Leu Asp Leu Lys His Ile Asp Glu Lys Lys His Arg Lys Leu
130 135 140

Thr Gly Lys Thr Asn Lys His Ile Leu Gln Phe Ala Gln Phe Leu Ser
145 150 155 160

Glu Lys Asn Val Pro Val Trp Ile Arg His Val Leu Val Pro Thr Ile
165 170 175

Thr Asp Asp Pro Asn Asp Leu Arg Arg Leu Ala Ala Phe Ile Arg Thr
180 185 190

Leu Lys Asn Val Lys Lys Ile Glu Ile Leu Pro Tyr His Lys Leu Gly
195 200 205

Val Tyr Lys Trp Lys Ala Leu Gly Leu Lys Tyr Pro Leu Glu Gly Ile
210 215 220

Glu Pro Pro Ser Glu Glu Ser Val Gln Met Ala Gln Arg Ile Leu Asn
225 230 235 240

Gly Thr Glu Asp Thr Val Ser Leu Ala
245

<210> 29
<211> 2604
<212> DNA
<213> Geobacillus thermoglucosidans

<220>
<221> CDS
<222> (1)..(2604)

<400> 29
atg gct gtg gag gag aga gtc gtc gat aaa aaa atc gaa gta gca aaa 48
Met Ala Val Glu Glu Arg Val Val Asp Lys Lys Ile Glu Val Ala Lys
1 5 10 15

atg att gat gag ctt gtc gct aat gca cag aaa gcg ttg gaa caa att 96
Met Ile Asp Glu Leu Val Ala Asn Ala Gln Lys Ala Leu Glu Gln Ile
20 25 30

cgc gct tac gat caa gaa acg atc gat cat atc gtg aaa gaa atg gcg 144
Arg Ala Tyr Asp Gln Glu Thr Ile Asp His Ile Val Lys Glu Met Ala
35 40 45

tta gcc ggg ctc gac aag cat atg gca tta gcc aag ctt gca gta gaa 192
Leu Ala Gly Leu Asp Lys His Met Ala Leu Ala Lys Leu Ala Val Glu
50 55 60

gaa aca aaa cgc ggt gta tat gaa gat aaa atc ata aaa aac ctt ttt 240
Glu Thr Lys Arg Gly Val Tyr Glu Asp Lys Ile Ile Lys Asn Leu Phe
65 70 75 80

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

305	310	315	320	
atc gct gtg ccg gaa gac aca aaa att ctt gtt gct gag tta aaa ggg Ile Ala Val Pro Glu Asp Thr Lys Ile Leu Val Ala Glu Leu Lys Gly 325 330 335				1008
gtc ggg cca aaa tat ccg ttg tct cgg gaa aaa tta agc cct gtc ctt Val Gly Pro Lys Tyr Pro Leu Ser Arg Glu Lys Leu Ser Pro Val Leu 340 345 350				1056
gct tgc tat aaa gtt aac agc acg gaa gaa gga ttt aag cgc tgt gaa Ala Cys Tyr Lys Val Asn Ser Thr Glu Glu Gly Phe Lys Arg Cys Glu 355 360 365				1104
gaa atg ctg gaa ttt ggc ggc ttg gga cat tcg gct gtc atc cat tcc Glu Met Leu Glu Phe Gly Gly Leu Gly His Ser Ala Val Ile His Ser 370 375 380				1152
gat aat caa aac gtg gtt acc gaa ttt ggc aaa cgg atg aaa gcg gga Asp Asn Gln Asn Val Val Thr Glu Phe Gly Lys Arg Met Lys Ala Gly 385 390 395 400				1200
cgg att atc gtt aat gcg cca tct tcg caa gga gca atc ggc gat att Arg Ile Ile Val Asn Ala Pro Ser Ser Gln Gly Ala Ile Gly Asp Ile 405 410 415				1248
tac aat gcg tac att ccg tca tta acg ctg gga tgc ggc aca ttt ggc Tyr Asn Ala Tyr Ile Pro Ser Leu Thr Leu Gly Cys Gly Thr Phe Gly 420 425 430				1296
gga aac tct gtt tcg aca aac gtc agt gcg att cat ctt atc aat ata Gly Asn Ser Val Ser Thr Asn Val Ser Ala Ile His Leu Ile Asn Ile 435 440 445				1344
aaa aga atg gca aaa agg acg gta aat atg caa tgg ttt aaa gtg ccg Lys Arg Met Ala Lys Arg Thr Val Asn Met Gln Trp Phe Lys Val Pro 450 455 460				1392
ccg aaa att tat ttc gaa aaa aat gct gta caa tac tta gcg aaa atg Pro Lys Ile Tyr Phe Glu Lys Asn Ala Val Gln Tyr Leu Ala Lys Met 465 470 475 480				1440
ccg gat att tcc aga gct ttt atc gtc acc gac ccg gga atg gtc aag Pro Asp Ile Ser Arg Ala Phe Ile Val Thr Asp Pro Gly Met Val Lys 485 490 495				1488
ctc gga tat gtc gat aaa gtg ctg tat tac ttg cgc aga cgc ccg gat Leu Gly Tyr Val Asp Lys Val Leu Tyr Tyr Leu Arg Arg Arg Pro Asp 500 505 510				1536
tat gtg cat agt gaa att ttc tcc gaa gta gag cca gat cct tca att Tyr Val His Ser Glu Ile Phe Ser Glu Val Glu Pro Asp Pro Ser Ile 515 520 525				1584
gag acg gta atg aaa ggt gtc gat atg atg aga agt ttc gag ccg gat Glu Thr Val Met Lys Gly Val Asp Met Met Arg Ser Phe Glu Pro Asp 530 535 540				1632
gtg att atc gcg ctt gga ggc ggc tcg cca atg gat gcg gca aaa gcg				1680

Val 545	Ile	Ile	Ala	Leu	Gly 550	Gly	Gly	Ser	Pro	Met 555	Asp	Ala	Ala	Lys	Ala 560	
atg	tgg	ctc	ttt	tac	gag	cat	ccg	aca	gcg	gat	ttc	aac	gca	tta	aaa	1728
Met	Trp	Leu	Phe	Tyr	Glu	His	Pro	Thr	Ala	Asp	Phe	Asn	Ala	Leu	Lys	
				565					570					575		
caa	aaa	ttt	tta	gat	att	cga	aaa	cgc	gtt	tat	aaa	tat	cca	aaa	ctg	1776
Gln	Lys	Phe	Leu	Asp	Ile	Arg	Lys	Arg	Val	Tyr	Lys	Tyr	Pro	Lys	Leu	
			580					585					590			
ggc	caa	aaa	gcg	aaa	ttt	gtc	gcc	att	ccg	acg	aca	tca	gga	aca	gga	1824
Gly	Gln	Lys	Ala	Lys	Phe	Val	Ala	Ile	Pro	Thr	Thr	Ser	Gly	Thr	Gly	
		595					600					605				
tcg	gaa	gta	acg	tcc	ttt	gcc	gtc	att	acc	gat	aaa	aaa	acg	aat	ata	1872
Ser	Glu	Val	Thr	Ser	Phe	Ala	Val	Ile	Thr	Asp	Lys	Lys	Thr	Asn	Ile	
	610					615					620					
aaa	tat	ccg	ttg	gca	gat	tat	gaa	ttg	aca	ccg	gac	gtc	gcg	att	gtg	1920
Lys	Tyr	Pro	Leu	Ala	Asp	Tyr	Glu	Leu	Thr	Pro	Asp	Val	Ala	Ile	Val	
625					630					635					640	
gat	ccg	caa	ttt	gtc	atg	acc	gtg	cca	aaa	cat	gtc	acc	gcc	gat	acg	1968
Asp	Pro	Gln	Phe	Val	Met	Thr	Val	Pro	Lys	His	Val	Thr	Ala	Asp	Thr	
				645					650					655		
gga	atg	gat	gta	ttg	aca	cat	gcg	atc	gaa	gcg	tat	gtc	tcc	aat	atg	2016
Gly	Met	Asp	Val	Leu	Thr	His	Ala	Ile	Glu	Ala	Tyr	Val	Ser	Asn	Met	
			660					665					670			
gca	aat	gat	tat	acc	gat	ggt	ctt	gcc	atg	aaa	gca	atc	caa	ctc	gta	2064
Ala	Asn	Asp	Tyr	Thr	Asp	Gly	Leu	Ala	Met	Lys	Ala	Ile	Gln	Leu	Val	
		675					680					685				
ttt	gaa	tat	ttg	ccg	cgg	gca	tat	caa	aac	gga	gcg	gat	gag	ctt	gcc	2112
Phe	Glu	Tyr	Leu	Pro	Arg	Ala	Tyr	Gln	Asn	Gly	Ala	Asp	Glu	Leu	Ala	
	690					695					700					
cgg	gag	aaa	atg	cat	aac	gcc	tct	acg	att	gcg	gga	atg	gca	ttt	gcc	2160
Arg	Glu	Lys	Met	His	Asn	Ala	Ser	Thr	Ile	Ala	Gly	Met	Ala	Phe	Ala	
705					710					715					720	
aac	gcg	ttt	tta	ggc	att	aac	cat	agt	ttg	gct	cat	aaa	ctt	ggc	gcg	2208
Asn	Ala	Phe	Leu	Gly	Ile	Asn	His	Ser	Leu	Ala	His	Lys	Leu	Gly	Ala	
			725						730					735		
gaa	ttc	cat	att	ccg	cat	ggg	cgc	gcg	aat	acc	att	ttg	atg	ccg	cat	2256
Glu	Phe	His	Ile	Pro	His	Gly	Arg	Ala	Asn	Thr	Ile	Leu	Met	Pro	His	
			740					745					750			
gtc	att	cgc	tat	aac	gca	gcg	aaa	ccg	aaa	aaa	ttt	acc	gca	ttt	ccg	2304
Val	Ile	Arg	Tyr	Asn	Ala	Ala	Lys	Pro	Lys	Lys	Phe	Thr	Ala	Phe	Pro	
		755					760					765				
aaa	tac	gaa	tat	ttc	aaa	gcg	gac	cag	cgc	tat	gca	gaa	att	gcg	aga	2352
Lys	Tyr	Glu	Tyr	Phe	Lys	Ala	Asp	Gln	Arg	Tyr	Ala	Glu	Ile	Ala	Arg	
	770					775					780					

```

atg ctc ggc ttg ccg gcc cgc aca acg gaa gaa ggg gtc gaa agc ctc      2400
Met Leu Gly Leu Pro Ala Arg Thr Thr Glu Glu Gly Val Glu Ser Leu
785                      790                      795                      800

gtt cag gcg atc att aag ctg gca aaa cag ttg gat atg ccg ctg agc      2448
Val Gln Ala Ile Ile Lys Leu Ala Lys Gln Leu Asp Met Pro Leu Ser
                        805                      810                      815

att gaa gca tgc ggc gtc agc aaa caa gaa ttt gaa agc aaa gtt gaa      2496
Ile Glu Ala Cys Gly Val Ser Lys Gln Glu Phe Glu Ser Lys Val Glu
                        820                      825                      830

aaa tta gcc gaa ttg gct ttc gaa gac caa tgt act act gct aac ccg      2544
Lys Leu Ala Glu Leu Ala Phe Glu Asp Gln Cys Thr Thr Ala Asn Pro
                        835                      840                      845

aaa ctc ccg ctt gtt agc gat tta gtt cat att tat cgc caa gcg ttt      2592
Lys Leu Pro Leu Val Ser Asp Leu Val His Ile Tyr Arg Gln Ala Phe
                        850                      855                      860

aaa gga gtt taa                                                    2604
Lys Gly Val
865

<210>  30
<211>  867
<212>  PRT
<213>  Geobacillus thermoglucosidans

<400>  30

Met Ala Val Glu Glu Arg Val Val Asp Lys Lys Ile Glu Val Ala Lys
1                      5                      10                      15

Met Ile Asp Glu Leu Val Ala Asn Ala Gln Lys Ala Leu Glu Gln Ile
20                      25                      30

Arg Ala Tyr Asp Gln Glu Thr Ile Asp His Ile Val Lys Glu Met Ala
35                      40                      45

Leu Ala Gly Leu Asp Lys His Met Ala Leu Ala Lys Leu Ala Val Glu
50                      55                      60

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

Ala Thr Glu Tyr Ile Tyr His Asn Ile Lys Tyr Asp Lys Thr Val Gly
85                      90                      95

Ile Ile His Glu Asn Pro His Glu Glu Ile Ile Glu Ile Ala Glu Pro
100                     105                     110

```

Val	Gly	Val	Ile	Ala	Gly	Ile	Thr	Pro	Val	Thr	Asn	Pro	Thr	Ser	Thr	115	120	125	
Thr	Met	Phe	Lys	Ala	Leu	Ile	Ser	Ile	Lys	Thr	Arg	Asn	Pro	Ile	Ile	130	135	140	
Phe	Ala	Phe	His	Pro	Ser	Ala	Gln	Arg	Cys	Ser	Ser	Glu	Ala	Ala	Arg	145	150	155	160
Val	Leu	Arg	Asp	Ala	Ala	Val	Arg	Ala	Gly	Ala	Pro	Glu	His	Cys	Ile	165	170	175	
Gln	Trp	Ile	Glu	Thr	Pro	Ser	Leu	Asp	Ala	Thr	Asn	Gln	Leu	Met	His	180	185	190	
His	Pro	Gly	Val	Ser	Leu	Ile	Leu	Ala	Thr	Gly	Gly	Ala	Gly	Met	Val	195	200	205	
Lys	Ala	Ala	Tyr	Ser	Ser	Gly	Lys	Pro	Ala	Leu	Gly	Val	Gly	Pro	Gly	210	215	220	
Asn	Val	Pro	Cys	Tyr	Ile	Glu	Lys	Thr	Ala	Asn	Ile	Lys	Arg	Ala	Val	225	230	235	240
Asn	Asp	Leu	Ile	Leu	Ser	Lys	Thr	Phe	Asp	Asn	Gly	Met	Ile	Cys	Ala	245	250	255	
Ser	Glu	Gln	Ala	Val	Ile	Ile	Asp	Lys	Glu	Ile	Tyr	Glu	Gln	Val	Lys	260	265	270	
Lys	Glu	Met	Ile	Glu	Asn	His	Cys	Tyr	Phe	Leu	Asn	Glu	Glu	Glu	Lys	275	280	285	
Lys	Lys	Val	Glu	Lys	Leu	Val	Ile	Asn	Glu	Asn	Thr	Cys	Ala	Val	Asn	290	295	300	
Pro	Asp	Ile	Val	Gly	Lys	Pro	Ala	Tyr	Glu	Ile	Ala	Lys	Met	Ala	Gly	305	310	315	320
Ile	Ala	Val	Pro	Glu	Asp	Thr	Lys	Ile	Leu	Val	Ala	Glu	Leu	Lys	Gly	325	330	335	
Val	Gly	Pro	Lys	Tyr	Pro	Leu	Ser	Arg	Glu	Lys	Leu	Ser	Pro	Val	Leu	340	345	350	

Ala Cys Tyr Lys Val Asn Ser Thr Glu Glu Gly Phe Lys Arg Cys Glu
355 360 365

Glu Met Leu Glu Phe Gly Gly Leu Gly His Ser Ala Val Ile His Ser
370 375 380

Asp Asn Gln Asn Val Val Thr Glu Phe Gly Lys Arg Met Lys Ala Gly
385 390 395 400

Arg Ile Ile Val Asn Ala Pro Ser Ser Gln Gly Ala Ile Gly Asp Ile
405 410 415

Tyr Asn Ala Tyr Ile Pro Ser Leu Thr Leu Gly Cys Gly Thr Phe Gly
420 425 430

Gly Asn Ser Val Ser Thr Asn Val Ser Ala Ile His Leu Ile Asn Ile
435 440 445

Lys Arg Met Ala Lys Arg Thr Val Asn Met Gln Trp Phe Lys Val Pro
450 455 460

Pro Lys Ile Tyr Phe Glu Lys Asn Ala Val Gln Tyr Leu Ala Lys Met
465 470 475 480

Pro Asp Ile Ser Arg Ala Phe Ile Val Thr Asp Pro Gly Met Val Lys
485 490 495

Leu Gly Tyr Val Asp Lys Val Leu Tyr Tyr Leu Arg Arg Arg Pro Asp
500 505 510

Tyr Val His Ser Glu Ile Phe Ser Glu Val Glu Pro Asp Pro Ser Ile
515 520 525

Glu Thr Val Met Lys Gly Val Asp Met Met Arg Ser Phe Glu Pro Asp
530 535 540

Val Ile Ile Ala Leu Gly Gly Gly Ser Pro Met Asp Ala Ala Lys Ala
545 550 555 560

Met Trp Leu Phe Tyr Glu His Pro Thr Ala Asp Phe Asn Ala Leu Lys
565 570 575

Gln Lys Phe Leu Asp Ile Arg Lys Arg Val Tyr Lys Tyr Pro Lys Leu

				580						585							590
Gly	Gln	Lys	Ala	Lys	Phe	Val	Ala	Ile	Pro	Thr	Thr	Ser	Gly	Thr	Gly		
		595					600					605					
Ser	Glu	Val	Thr	Ser	Phe	Ala	Val	Ile	Thr	Asp	Lys	Lys	Thr	Asn	Ile		
	610					615					620						
Lys	Tyr	Pro	Leu	Ala	Asp	Tyr	Glu	Leu	Thr	Pro	Asp	Val	Ala	Ile	Val		
625					630					635					640		
Asp	Pro	Gln	Phe	Val	Met	Thr	Val	Pro	Lys	His	Val	Thr	Ala	Asp	Thr		
				645					650					655			
Gly	Met	Asp	Val	Leu	Thr	His	Ala	Ile	Glu	Ala	Tyr	Val	Ser	Asn	Met		
			660					665						670			
Ala	Asn	Asp	Tyr	Thr	Asp	Gly	Leu	Ala	Met	Lys	Ala	Ile	Gln	Leu	Val		
		675					680					685					
Phe	Glu	Tyr	Leu	Pro	Arg	Ala	Tyr	Gln	Asn	Gly	Ala	Asp	Glu	Leu	Ala		
	690					695					700						
Arg	Glu	Lys	Met	His	Asn	Ala	Ser	Thr	Ile	Ala	Gly	Met	Ala	Phe	Ala		
705					710					715					720		
Asn	Ala	Phe	Leu	Gly	Ile	Asn	His	Ser	Leu	Ala	His	Lys	Leu	Gly	Ala		
				725					730					735			
Glu	Phe	His	Ile	Pro	His	Gly	Arg	Ala	Asn	Thr	Ile	Leu	Met	Pro	His		
			740					745					750				
Val	Ile	Arg	Tyr	Asn	Ala	Ala	Lys	Pro	Lys	Lys	Phe	Thr	Ala	Phe	Pro		
		755					760					765					
Lys	Tyr	Glu	Tyr	Phe	Lys	Ala	Asp	Gln	Arg	Tyr	Ala	Glu	Ile	Ala	Arg		
	770					775					780						
Met	Leu	Gly	Leu	Pro	Ala	Arg	Thr	Thr	Glu	Glu	Gly	Val	Glu	Ser	Leu		
785					790					795					800		
Val	Gln	Ala	Ile	Ile	Lys	Leu	Ala	Lys	Gln	Leu	Asp	Met	Pro	Leu	Ser		
				805					810						815		

Ile Glu Ala Cys Gly Val Ser Lys Gln Glu Phe Glu Ser Lys Val Glu
820 825 830

Lys Leu Ala Glu Leu Ala Phe Glu Asp Gln Cys Thr Thr Ala Asn Pro
835 840 845

Lys Leu Pro Leu Val Ser Asp Leu Val His Ile Tyr Arg Gln Ala Phe
850 855 860

Lys Gly Val
865

<210> 31
<211> 975
<212> DNA
<213> Geobacillus thermoglucosidans

<220>
<221> CDS
<222> (1)..(975)

<400> 31
gtg agc agt gat tta ttt tcg aca tta aaa gaa aaa ata gcg gga aaa 48
Val Ser Ser Asp Leu Phe Ser Thr Leu Lys Glu Lys Ile Ala Gly Lys
1 5 10 15
caa cgg aaa atc gtg ttt ccg gaa ggg ctt gat gag cgt att tta aca 96
Gln Arg Lys Ile Val Phe Pro Glu Gly Leu Asp Glu Arg Ile Leu Thr
20 25 30
gcg gta agc cgt ctg gcg aac gag caa atc gtc acg ccg att gtc att 144
Ala Val Ser Arg Leu Ala Asn Glu Gln Ile Val Thr Pro Ile Val Ile
35 40 45
ggc aat gaa gaa gcg gtt aag caa aaa gca agc gag ctt ggg ctg acg 192
Gly Asn Glu Glu Ala Val Lys Gln Lys Ala Ser Glu Leu Gly Leu Thr
50 55 60
ctt ccg aat gtc gaa atc att gat ccg cat cag tac ggg gaa atg gac 240
Leu Pro Asn Val Glu Ile Ile Asp Pro His Gln Tyr Gly Glu Met Asp
65 70 75 80
aag ctt gtt gcg gca ttt gtc gaa cgc cgc aaa ggg aaa gtg acg gaa 288
Lys Leu Val Ala Ala Phe Val Glu Arg Arg Lys Gly Lys Val Thr Glu
85 90 95
gaa gcg gcg cgg aag ctg ctt ctt gac gaa aat tat ttt ggc acc atg 336
Glu Ala Ala Lys Leu Leu Leu Asp Glu Asn Tyr Phe Gly Thr Met
100 105 110
ctt gtg tac atg gat aag gcg cat ggg ctt gtc agc ggc gcg gcg cat 384
Leu Val Tyr Met Asp Lys Ala His Gly Leu Val Ser Gly Ala Ala His
115 120 125

tcg acg gct gat acg gtg cgg cct gcg ttg caa att ata aaa acg aaa Ser Thr Ala Asp Thr Val Arg Pro Ala Leu Gln Ile Ile Lys Thr Lys 130 135 140	432
caa ggc gtc cgc aaa acg tca gga gta ttc att atg gtg cgc ggt gat Gln Gly Val Arg Lys Thr Ser Gly Val Phe Ile Met Val Arg Gly Asp 145 150 155 160	480
gaa aag tac gtg ttt gcc gat tgc gcg atc aac att gcc ccg gac agc Glu Lys Tyr Val Phe Ala Asp Cys Ala Ile Asn Ile Ala Pro Asp Ser 165 170 175	528
caa gat ttg gcg gaa atc gct gtc gaa agc gcc aac acg gca aaa atg Gln Asp Leu Ala Glu Ile Ala Val Glu Ser Ala Asn Thr Ala Lys Met 180 185 190	576
ttc gac att gag ccg cgc gtg gcg atg ttg agc ttt tcg aca aaa gga Phe Asp Ile Glu Pro Arg Val Ala Met Leu Ser Phe Ser Thr Lys Gly 195 200 205	624
tca gcg aaa tcg cca gaa acg gaa aaa gtc gtc gaa gcg gtg cgg ctt Ser Ala Lys Ser Pro Glu Thr Glu Lys Val Val Glu Ala Val Arg Leu 210 215 220	672
gcg aaa gaa atg gcg cct gac tta gtg ctg gac ggt gag ttt cag ttc Ala Lys Glu Met Ala Pro Asp Leu Val Leu Asp Gly Glu Phe Gln Phe 225 230 235 240	720
gac gcg gcg ttt gtt ccg tct gtc gcg aaa aag aaa gcg cca gat tcc Asp Ala Ala Phe Val Pro Ser Val Ala Lys Lys Lys Ala Pro Asp Ser 245 250 255	768
gtc att caa gga gac gcg aac gta ttt att ttc cca agc ctt gaa gcg Val Ile Gln Gly Asp Ala Asn Val Phe Ile Phe Pro Ser Leu Glu Ala 260 265 270	816
gga aat atc ggc tat aaa atc gcc cag cgt ctc ggc aac ttt gaa gcg Gly Asn Ile Gly Tyr Lys Ile Ala Gln Arg Leu Gly Asn Phe Glu Ala 275 280 285	864
gtc ggc ccg att ttg caa gga ctc aat aag cct gtg aac gac ctg tca Val Gly Pro Ile Leu Gln Gly Leu Asn Lys Pro Val Asn Asp Leu Ser 290 295 300	912
cgc ggt tgc aat gcg gaa gat gtg tac aag ctg acg ctt ata act gcg Arg Gly Cys Asn Ala Glu Asp Val Tyr Lys Leu Thr Leu Ile Thr Ala 305 310 315 320	960
gcg caa tcg cta taa Ala Gln Ser Leu	975

<210> 32
 <211> 324
 <212> PRT
 <213> Geobacillus thermoglucosidans
 <400> 32

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

Asp Ala Ala Phe Val Pro Ser Val Ala Lys Lys Lys Ala Pro Asp Ser
245 250 255

Val Ile Gln Gly Asp Ala Asn Val Phe Ile Phe Pro Ser Leu Glu Ala
260 265 270

Gly Asn Ile Gly Tyr Lys Ile Ala Gln Arg Leu Gly Asn Phe Glu Ala
275 280 285

Val Gly Pro Ile Leu Gln Gly Leu Asn Lys Pro Val Asn Asp Leu Ser
290 295 300

Arg Gly Cys Asn Ala Glu Asp Val Tyr Lys Leu Thr Leu Ile Thr Ala
305 310 315 320

Ala Gln Ser Leu

<210> 33
<211> 750
<212> DNA
<213> Geobacillus thermoglucosidans

<220>
<221> CDS
<222> (1)..(750)

<400> 33
atg gat gtc gat gtc aag cga gat cag acg ctg tta aaa gat cat gag 48
Met Asp Val Asp Val Lys Arg Asp Gln Thr Leu Leu Lys Asp His Glu
1 5 10 15

atg aaa aag ctt att cgc cgc agc caa gag ggg gac caa cag gcg cgc 96
Met Lys Lys Leu Ile Arg Arg Ser Gln Glu Gly Asp Gln Gln Ala Arg
20 25 30

aat gaa att atc caa aaa aac atg cgc ctc gtt tgg tcg gtc gtc cag 144
Asn Glu Ile Ile Gln Lys Asn Met Arg Leu Val Trp Ser Val Val Gln
35 40 45

cgc ttt ttg aac cgc gga tac gag ccg gac gat tta ttt caa att ggc 192
Arg Phe Leu Asn Arg Gly Tyr Glu Pro Asp Asp Leu Phe Gln Ile Gly
50 55 60

tgc atc ggc ttg ctt aaa tct gtt gat aag ttt gat ttg tcg tat gac 240
Cys Ile Gly Leu Leu Lys Ser Val Asp Lys Phe Asp Leu Ser Tyr Asp
65 70 75 80

gtg aag ttt tcc aca tat gcg gtg ccg atg atc atc ggc gaa att cag 288
Val Lys Phe Ser Thr Tyr Ala Val Pro Met Ile Ile Gly Glu Ile Gln

	85	90	95	
cgg ttt atc cgc gat gac ggg acg gtg aaa gtg agc cgt tcc tta aaa				336
Arg Phe Ile Arg Asp Asp Gly Thr Val Lys Val Ser Arg Ser Leu Lys				
	100	105	110	
gaa acg ggc aat aaa atc cgg aaa gca aga gac gag ctt tcg aaa aaa				384
Glu Thr Gly Asn Lys Ile Arg Lys Ala Arg Asp Glu Leu Ser Lys Lys				
	115	120	125	
cat gga cgg gcg cca acg gtg aca gaa atc gcc gat tat tta gaa att				432
His Gly Arg Ala Pro Thr Val Thr Glu Ile Ala Asp Tyr Leu Glu Ile				
	130	135	140	
tct cca gaa gaa gtg gtg ctt gcc cag gaa gcc gtt cgt tcc ccg gct				480
Ser Pro Glu Glu Val Val Leu Ala Gln Glu Ala Val Arg Ser Pro Ala				
	145	150	155	160
tcc att cac gaa aca gtg tat gaa aac gac ggc gac ccg atc acg ctc				528
Ser Ile His Glu Thr Val Tyr Glu Asn Asp Gly Asp Pro Ile Thr Leu				
	165	170	175	
ctc gat caa att gct gat gcc gac gaa gca tca tgg ttt gat aaa atc				576
Leu Asp Gln Ile Ala Asp Ala Asp Glu Ala Ser Trp Phe Asp Lys Ile				
	180	185	190	
gcg ttg aaa aaa gcg att gag gag ctg gat gaa cgg gaa cgt ctc atc				624
Ala Leu Lys Lys Ala Ile Glu Glu Leu Asp Glu Arg Glu Arg Leu Ile				
	195	200	205	
gtc tat ttg cgt tat tac aaa gat caa acc cag tcg gaa gtg gca tca				672
Val Tyr Leu Arg Tyr Tyr Lys Asp Gln Thr Gln Ser Glu Val Ala Ser				
	210	215	220	
aga tta ggc atc tct caa gtt caa gta tcc cgt ctt gaa aaa aaa att				720
Arg Leu Gly Ile Ser Gln Val Gln Val Ser Arg Leu Glu Lys Lys Ile				
	225	230	235	240
tta cag caa ata aag gag aga atg gat ggg				750
Leu Gln Gln Ile Lys Glu Arg Met Asp Gly				
	245	250		

<210> 34

<211> 250

<212> PRT

<213> Geobacillus thermoglucosidans

<400> 34

Met	Asp	Val	Asp	Val	Lys	Arg	Asp	Gln	Thr	Leu	Leu	Lys	Asp	His	Glu
1				5					10					15	

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

Asn	Glu	Ile	Ile	Gln	Lys	Asn	Met	Arg	Leu	Val	Trp	Ser	Val	Val	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Arg Phe Leu Asn Arg Gly Tyr Glu Pro Asp Asp Leu Phe Gln Ile Gly		
50	55	60
Cys Ile Gly Leu Leu Lys Ser Val Asp Lys Phe Asp Leu Ser Tyr Asp		
65	70	75
Val Lys Phe Ser Thr Tyr Ala Val Pro Met Ile Ile Gly Glu Ile Gln		
	85	90
Arg Phe Ile Arg Asp Asp Gly Thr Val Lys Val Ser Arg Ser Leu Lys		
	100	105
Glu Thr Gly Asn Lys Ile Arg Lys Ala Arg Asp Glu Leu Ser Lys Lys		
	115	120
His Gly Arg Ala Pro Thr Val Thr Glu Ile Ala Asp Tyr Leu Glu Ile		
	130	135
Ser Pro Glu Glu Val Val Leu Ala Gln Glu Ala Val Arg Ser Pro Ala		
145	150	155
Ser Ile His Glu Thr Val Tyr Glu Asn Asp Gly Asp Pro Ile Thr Leu		
	165	170
Leu Asp Gln Ile Ala Asp Ala Asp Glu Ala Ser Trp Phe Asp Lys Ile		
	180	185
Ala Leu Lys Lys Ala Ile Glu Glu Leu Asp Glu Arg Glu Arg Leu Ile		
	195	200
Val Tyr Leu Arg Tyr Tyr Lys Asp Gln Thr Gln Ser Glu Val Ala Ser		
	210	215
Arg Leu Gly Ile Ser Gln Val Gln Val Ser Arg Leu Glu Lys Lys Ile		
225	230	235
Leu Gln Gln Ile Lys Glu Arg Met Asp Gly		
	245	250