

## SEQUENCE LISTING

<110> Danisco A/S  
 Danisco US Inc., Genencor Division

<120> A METHOD OF PREPARING FOOD PRODUCTS USING TS23 ALPHA-AMYLASE

<130> 17732PCT00

<160> 18

<170> PatentIn version 3.5

<210> 1  
 <211> 583  
 <212> PRT  
 <213> Bacillus sp. TS-23

<400> 1

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

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

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

Lys Gly Thr Ser Gln Ser Asp Val Gly Tyr Gly Val 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 Lys Thr Gln Tyr Ile Gln Ala Ile Gln Ala Ala Lys Ala 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 Phe Val Asp Ala Val Glu Val Asp Pro Ser Asn Arg Asn  
 115 120 125

Gln Glu Thr 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 Ser Thr Gly Lys Ala Trp Asp Trp Glu Val Asp Thr  
 180 185 190  
 Glu Asn Gly Asn Tyr Asp Tyr Leu Met Phe Ala Asp Leu Asp Met Asp  
 195 200 205  
 His Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Thr Trp Tyr Val  
 210 215 220  
 Asn 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 Thr Tyr Val Arg Asn Gln Thr  
 245 250 255  
 Gly Lys Asn Leu Phe Ala Val Gly Glu Phe Trp Ser Tyr Asp Val Asn  
 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 Thr Ala Ser Lys Ser Ser Gly  
 290 295 300  
 Tyr Phe Asp Met Arg Tyr Leu Leu Asn Asn Thr Leu Met Lys Asp Gln  
 305 310 315 320  
 Pro Ser Leu Ala Val Thr Leu Val Asp Asn His Asp Thr Gln 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 Gly Leu Lys Ser Lys  
 370 375 380  
 Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln  
 385 390 395 400  
 Arg Asp Tyr Ile Asp His Gln Asp Ile Ile Gly Trp Thr Arg Glu Gly  
 405 410 415  
 Ile Asp Thr Lys Pro 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 Lys His Ala Gly Lys  
 435 440 445  
 Val 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 Ala Lys Thr Ser Asn Val Thr Phe Thr Val Asn Asn Ala Thr  
 485 490 495  
 Thr Thr Ser Gly Gln Asn Val Tyr Val Val Ala Asn Ile Pro Glu Leu  
 500 505 510  
 Gly Asn Trp Asn Thr Ala Asn Ala Ile Lys Met Asn Pro Ser Ser Tyr  
 515 520 525  
 Pro Thr Trp Lys Ala Thr Ile Ala Leu Pro Gln Gly Lys Ala Ile Glu  
 530 535 540  
 Phe Lys Phe Ile Lys Lys Asp Gln Ala Gly Asn Val Ile Trp Glu Ser  
 545 550 555 560  
 Thr Ser Asn Arg Thr Tyr Thr Val Pro Phe Ser Ser Thr Gly Ser Tyr  
 565 570 575  
 Thr Ala Ser Trp Asn Val Pro  
 580  
 <210> 2  
 <211> 484  
 <212> PRT  
 <213> Bacillus sp. TS-23  
 <400> 2  
 Asn Thr Ala Pro Ile Asn Glu Thr Met Met Gln Tyr Phe Glu Trp Asp  
 1 5 10 15  
 Leu Pro Asn Asp Gly Thr Leu Trp Thr Lys Val Lys Asn Glu Ala Ala  
 20 25 30  
 Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr  
 35 40 45  
 Lys Gly Thr Ser Gln Ser Asp Val Gly Tyr Gly Val 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	Lys	Thr	Gln	Tyr	Ile	Gln	Ala	Ile	Gln	Ala	Ala	Lys	Ala	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	Phe	Val	Asp	Ala	Val	Glu	Val	Asp	Pro	Ser	Asn	Arg	Asn
		115					120					125			
Gln	Glu	Thr	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	Ser	Thr	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp	Thr
			180					185					190		
Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Phe	Ala	Asp	Leu	Asp	Met	Asp
		195					200					205			
His	Pro	Glu	Val	Val	Thr	Glu	Leu	Lys	Asn	Trp	Gly	Thr	Trp	Tyr	Val
	210					215					220				
Asn	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	Thr	Tyr	Val	Arg	Asn	Gln	Thr
			245					250						255	
Gly	Lys	Asn	Leu	Phe	Ala	Val	Gly	Glu	Phe	Trp	Ser	Tyr	Asp	Val	Asn
			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	Thr	Ala	Ser	Lys	Ser	Ser	Gly
	290					295					300				
Tyr	Phe	Asp	Met	Arg	Tyr	Leu	Leu	Asn	Asn	Thr	Leu	Met	Lys	Asp	Gln
305					310					315					320
Pro	Ser	Leu	Ala	Val	Thr	Leu	Val	Asp	Asn	His	Asp	Thr	Gln	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	Gly	Leu	Lys	Ser	Lys
		370				375				380					
Ile	Asp	Pro	Leu	Leu	Ile	Ala	Arg	Arg	Asp	Tyr	Ala	Tyr	Gly	Thr	Gln
385				390						395			400		
Arg	Asp	Tyr	Ile	Asp	His	Gln	Asp	Ile	Ile	Gly	Trp	Thr	Arg	Glu	Gly
			405						410			415			
Ile	Asp	Thr	Lys	Pro	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	Lys	His	Ala	Gly	Lys
		435					440						445		
Val	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	Ala	Lys												

```

<210> 3
<211> 1752
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> SEQUENCE OF OPTIMIZED AMYTS23 GENE

<400> 3
aatacggcgc cgatcaacga aacgatgatg cagtattttg aatgggatct gccgaatgat 60
ggaacgctgt ggacgaaagt caaaaacgaa gcggcgaatc ttagcagcct gggaatcaca 120
gcactttggc ttccgccggc atataaagga acgagccaaa gcgatgtcgg ctatggcgtc 180
tatgatctgt atgacctggg cgaatttaac caaaaaggca cgatccggac gaaatatggc 240
acgaaaacac agtatatcca agcgatccag gcagcaaaag cagcaggcat gcaagtctat 300
gccgacgtcg tctttaatca taaagcggga gcggatggca cagaattttg cgatgccgtc 360

```

```

gaagttgatc cgagcaacag aaaccaagaa acgagcggca cgtatcaa at ccaagcgtgg 420
acgaaatttg attttccggg cagaggcaat acgtatagca gctttaaatg gcgctggtat 480
cattttgacg gcacggattg ggatgaaagc agaaaactga accggatcta taaatttcgg 540
agcacgggca aagcatggga ttgggaagtc gatacggaaa acggcaacta tgactatctg 600
atgtttgccg atctggatat ggatcatccg gaagtcgtca cggaactgaa aaattggggc 660
acgtggtatg ttaatacgac gaacatcgat ggcttttagac tggatgccgt caaacatata 720
aaatatagct tttttccgga ctggctgacg tatgtcagaa accagacggg caaaaacctt 780
tttgccgtcg gcgaattttg gagctatgac gtcaacaaac ttcataacta tatcacgaaa 840
acgaacggca gcatgagcct ttttgatgcc ccgcttcata acaactttta tacggcgagc 900
aaaagctcag gctattttga tatgagatat ctgctgaaca acacgctgat gaaagatcaa 960
ccgagcctgg cagtcacact ggtcgataac catgatacac aaccgggcca aagccttcaa 1020
agctgggtcg aaccgtgggt taaaccgctg gcgtatgcct ttatcctgac gagacaagaa 1080
gggtatcctt gcgtctttta tggcgactat tatggcatcc cgaaatataa tatcccgggc 1140
ctgaaaagca aaatcgatcc gctgctgac gccagacggg attatgccta tggcacacag 1200
cgggattata tcgaccatca ggacatcatc ggctggacaa gagaaggcat cgatacga 1260
ccgaatagcg gactggcagc actgattaca gatggaccgg gcggaagcaa atggatgtat 1320
gtcggcaaaa aacatgccgg caaagtcttt tatgatctga cgggcaacag aagcgatacg 1380
gtcacgatca atgctgatgg ctggggagaa tttaaagtca atggcggcag cgtttcaatc 1440
tgggtcgcca aaacgagcaa tgtcacgttt acggtcaaca atgccacgac aacgagcggc 1500
caaaatgtct atgtcgtcgc caatatcccg gaactgggca attggaatac ggcgaaacga 1560
atcaaaatga acccgagcag ctatccgaca tggaaaagcga caatcgctct gccgcaagga 1620
aaagcgatcg aatttaaatt tatcaaaaaa gaccaggcgg gcaatgttat ttgggaaagc 1680
acgagcaata gaacgtatac ggtcccgttt agcagcacag gaagctatac agcgagctgg 1740
aatgttccgt ga 1752

```

```

<210> 4
<211> 1455
<212> DNA
<213> ARTIFICIAL SEQUENCE

```

```

<220>
<223> DNA SEQUENCE OF OPTIMIZED AMYTS23T GENE

```

```

<400> 4
aatacggcgc cgatcaacga aacgatgatg cagtattttg aatgggatct gccgaatgat 60
ggaacgctgt ggacgaaagt caaaaacgaa gcggcgaaatc ttagcagcct gggaatcaca 120
gcactttggc ttccgccggc atataaagga acgagccaaa gcgatgtcgg ctatggcgtc 180

```

tatgatctgt atgacctggg cgaatttaac caaaaaggca cgatccggac gaaatatggc	240
acgaaaacac agtatatcca agcgatccag gcagcaaaag cagcaggcat gcaagtctat	300
gccgacgtcg tctttaatca taaagcggga gcggatggca cagaatttgt cgatgccgtc	360
gaagttgate cgagcaacag aaaccaagaa acgagcggca cgtatcaaat ccaagcgtgg	420
acgaaatttg attttccggg cagaggcaat acgtatagca gctttaaatg gcgctggtat	480
cattttgacg gcacggattg ggatgaaagc agaaaactga accggatcta taaatttcgg	540
agcacgggca aagcatggga ttgggaagtc gatacggaaa acggcaacta tgactatctg	600
atgtttgccg atctggatat ggatcatccg gaagtcgtca cggaactgaa aaattggggc	660
acgtggtatg ttaatacgcg gaacatcgat ggcttttagac tggatgccgt caaacatatc	720
aaatatagct tttttccgga ctggctgacg tatgtcagaa accagacggg caaaaacctt	780
tttgccgtcg gcgaattttg gagctatgac gtcaacaaac ttcataacta tatcacgaaa	840
acgaacggca gcatgagcct ttttgatgcc ccgcttcata acaactttta tacggcgagc	900
aaaagctcag gctattttga tatgagatat ctgctgaaca acacgctgat gaaagatcaa	960
ccgagcctgg cagtcacact ggtcgataac catgatacac aaccggggcca aagccttcaa	1020
agctgggtcg aaccgtgggt taaaccgctg gcgtatgcct ttatcctgac gagacaagaa	1080
gggtatcctt gcgtctttta tggcgactat tatggcatcc cgaaatataa tatcccgggc	1140
ctgaaaagca aaatcgatcc gctgctgac gccagacggg attatgccta tggcacacag	1200
cgggattata tcgaccatca ggacatcatc ggctggacaa gagaaggcat cgatacgaaa	1260
ccgaatagcg gactggcagc actgattaca gatggaccgg gcggaagcaa atggatgtat	1320
gtcggcaaaa aacatgccgg caaagtcttt tatgatctga cgggcaacag aagcgatacg	1380
gtcacgatca atgctgatgg ctggggagaa tttaaagtca atggcggcag cgtttcaatc	1440
tgggtcgcca aatga	1455

<210> 5  
 <211> 87  
 <212> DNA  
 <213> Bacillus licheniformis

<400> 5	
atgaaacaac aaaaacggct ttacgcccga ttgctgacgc tgttatttgc gctcatcttc	60
ttgctgcctc attctgcagc ttcagca	87

<210> 6  
 <211> 29  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 6

Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe

```

1              5              10              15

Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ser Ala
20              25

<210> 7
<211> 430
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> variant PS4 amylase

<400> 7

Met Asp Gln Ala Gly Lys Ser Pro Ala Gly Val Arg Tyr His Gly Gly
1              5              10              15

Asp Glu Ile Ile Leu Gln Gly Phe His Trp Asn Val Val Arg Glu Ala
20              25              30

Pro Tyr Asn Trp Tyr Asn Ile Leu Arg Gln Gln Ala Ser Thr Ile Ala
35              40              45

Ala Asp Gly Phe Ser Ala Ile Trp Met Pro Val Pro Trp Arg Asp Phe
50              55              60

Ser Ser Trp Thr Asp Gly Asp Lys Ser Gly Gly Gly Glu Gly Tyr Phe
65              70              75              80

Trp His Asp Phe Asn Lys Asn Gly Arg Tyr Gly Ser Asp Ala Gln Leu
85              90              95

Arg Gln Ala Ala Gly Ala Leu Gly Gly Ala Gly Val Lys Val Leu Tyr
100             105             110

Asp Val Val Pro Asn His Met Asn Arg Phe Tyr Pro Asp Lys Glu Ile
115            120            125

Asn Leu Pro Ala Gly Gln Arg Phe Trp Arg Asn Asp Cys Pro Asp Pro
130            135            140

Gly Asn Gly Pro Asn Asp Cys Asp Asp Gly Asp Arg Phe Leu Gly Gly
145            150            155            160

Glu Ala Asp Leu Asn Thr Gly His Pro Gln Ile Tyr Gly Met Phe Arg
165            170            175

Asp Glu Phe Thr Asn Leu Arg Ser Gly Tyr Gly Ala Gly Gly Phe Arg
180            185            190

```



Phe Asp Phe Val Arg Gly Tyr Ala Pro Glu Arg Val Asp Ser Trp Met  
 195 200 205

Ser Asp Ser Ala Asp Ser Ser Phe Cys Val Gly Glu Leu Trp Lys Glu  
 210 215 220

Pro Ser Glu Tyr Pro Pro Trp Asp Trp Arg Asn Thr Ala Ser Trp Gln  
 225 230 235 240

Gln Ile Ile Lys Asp Trp Ser Asp Arg Ala Lys Cys Pro Val Phe Asp  
 245 250 255

Phe Ala Leu Lys Glu Arg Met Gln Asn Gly Ser Val Ala Asp Trp Lys  
 260 265 270

His Gly Leu Asn Gly Asn Pro Asp Pro Arg Trp Arg Glu Val Ala Val  
 275 280 285

Thr Phe Val Asp Asn His Asp Thr Gly Tyr Ser Pro Gly Gln Asn Gly  
 290 295 300

Gly Gln His Lys Trp Pro Leu Gln Asp Gly Leu Ile Arg Gln Ala Tyr  
 305 310 315 320

Ala Tyr Ile Leu Thr Ser Pro Gly Thr Pro Val Val Tyr Trp Pro His  
 325 330 335

Met Tyr Asp Trp Gly Tyr Gly Asp Phe Ile Arg Gln Leu Ile Gln Val  
 340 345 350

Arg Arg Thr Ala Gly Val Arg Ala Asp Ser Ala Ile Ser Phe His Ser  
 355 360 365

Gly Tyr Ser Gly Leu Val Ala Thr Val Ser Gly Ser Gln Gln Thr Leu  
 370 375 380

Val Val Ala Leu Asn Ser Asp Leu Ala Asn Pro Gly Gln Val Ala Ser  
 385 390 395 400

Gly Ser Phe Ser Glu Ala Val Asn Ala Ser Asn Gly Gln Val Arg Val  
 405 410 415

Trp Arg Ser Gly Ser Gly Asp Gly Gly Gly Asn Asp Gly Gly  
 420 425 430

<210> 8  
 <211> 429  
 <212> PRT

<213> Pseudomonas saccharophila

<400> 8

Asp Gln Ala Gly Lys Ser Pro Ala Gly Val Arg Tyr His Gly Gly Asp  
1 5 10 15

Glu Ile Ile Leu Gln Gly Phe His Trp Asn Val Val Arg Glu Ala Pro  
20 25 30

Asn Asp Trp Tyr Asn Ile Leu Arg Gln Gln Ala Ser Thr Ile Ala Ala  
35 40 45

Asp Gly Phe Ser Ala Ile Trp Met Pro Val Pro Trp Arg Asp Phe Ser  
50 55 60

Ser Trp Thr Asp Gly Gly Lys Ser Gly Gly Gly Glu Gly Tyr Phe Trp  
65 70 75 80

His Asp Phe Asn Lys Asn Gly Arg Tyr Gly Ser Asp Ala Gln Leu Arg  
85 90 95

Gln Ala Ala Gly Ala Leu Gly Gly Ala Gly Val Lys Val Leu Tyr Asp  
100 105 110

Val Val Pro Asn His Met Asn Arg Gly Tyr Pro Asp Lys Glu Ile Asn  
115 120 125

Leu Pro Ala Gly Gln Gly Phe Trp Arg Asn Asp Cys Ala Asp Pro Gly  
130 135 140

Asn Tyr Pro Asn Asp Cys Asp Asp Gly Asp Arg Phe Ile Gly Gly Glu  
145 150 155 160

Ser Asp Leu Asn Thr Gly His Pro Gln Ile Tyr Gly Met Phe Arg Asp  
165 170 175

Glu Leu Ala Asn Leu Arg Ser Gly Tyr Gly Ala Gly Gly Phe Arg Phe  
180 185 190

Asp Phe Val Arg Gly Tyr Ala Pro Glu Arg Val Asp Ser Trp Met Ser  
195 200 205

Asp Ser Ala Asp Ser Ser Phe Cys Val Gly Glu Leu Trp Lys Gly Pro  
210 215 220

Ser Glu Tyr Pro Ser Trp Asp Trp Arg Asn Thr Ala Ser Trp Gln Gln  
225 230 235 240

```

Ile Ile Lys Asp Trp Ser Asp Arg Ala Lys Cys Pro Val Phe Asp Phe
      245                      250                      255

Ala Leu Lys Glu Arg Met Gln Asn Gly Ser Val Ala Asp Trp Lys His
      260                      265                      270

Gly Leu Asn Gly Asn Pro Asp Pro Arg Trp Arg Glu Val Ala Val Thr
      275                      280                      285

Phe Val Asp Asn His Asp Thr Gly Tyr Ser Pro Gly Gln Asn Gly Gly
      290                      295                      300

Gln His His Trp Ala Leu Gln Asp Gly Leu Ile Arg Gln Ala Tyr Ala
305                      310                      315                      320

Tyr Ile Leu Thr Ser Pro Gly Thr Pro Val Val Tyr Trp Ser His Met
      325                      330                      335

Tyr Asp Trp Gly Tyr Gly Asp Phe Ile Arg Gln Leu Ile Gln Val Arg
      340                      345                      350

Arg Thr Ala Gly Val Arg Ala Asp Ser Ala Ile Ser Phe His Ser Gly
      355                      360                      365

Tyr Ser Gly Leu Val Ala Thr Val Ser Gly Ser Gln Gln Thr Leu Val
      370                      375                      380

Val Ala Leu Asn Ser Asp Leu Ala Asn Pro Gly Gln Val Ala Ser Gly
385                      390                      395                      400

Ser Phe Ser Glu Ala Val Asn Ala Ser Asn Gly Gln Val Arg Val Trp
      405                      410                      415

Arg Ser Gly Ser Gly Asp Gly Gly Gly Asn Asp Gly Gly
      420                      425

<210> 9
<211> 530
<212> PRT
<213> Pseudomonas saccharophila

<400> 9

Asp Gln Ala Gly Lys Ser Pro Ala Gly Val Arg Tyr His Gly Gly Asp
1      5      10      15

Glu Ile Ile Leu Gln Gly Phe His Trp Asn Val Val Arg Glu Ala Pro
      20      25      30

Asn Asp Trp Tyr Asn Ile Leu Arg Gln Gln Ala Ser Thr Ile Ala Ala

```

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

290

295

300

Gln His His Trp Ala Leu Gln Asp Gly Leu Ile Arg Gln Ala Tyr Ala  
 305 310 315 320

Tyr Ile Leu Thr Ser Pro Gly Thr Pro Val Val Tyr Trp Ser His Met  
 325 330 335

Tyr Asp Trp Gly Tyr Gly Asp Phe Ile Arg Gln Leu Ile Gln Val Arg  
 340 345 350

Arg Thr Ala Gly Val Arg Ala Asp Ser Ala Ile Ser Phe His Ser Gly  
 355 360 365

Tyr Ser Gly Leu Val Ala Thr Val Ser Gly Ser Gln Gln Thr Leu Val  
 370 375 380

Val Ala Leu Asn Ser Asp Leu Ala Asn Pro Gly Gln Val Ala Ser Gly  
 385 390 395 400

Ser Phe Ser Glu Ala Val Asn Ala Ser Asn Gly Gln Val Arg Val Trp  
 405 410 415

Arg Ser Gly Ser Gly Asp Gly Gly Gly Asn Asp Gly Gly Glu Gly Gly  
 420 425 430

Leu Val Asn Val Asn Phe Arg Cys Asp Asn Gly Val Thr Gln Met Gly  
 435 440 445

Asp Ser Val Tyr Ala Val Gly Asn Val Ser Gln Leu Gly Asn Trp Ser  
 450 455 460

Pro Ala Ser Ala Val Arg Leu Thr Asp Thr Ser Ser Tyr Pro Thr Trp  
 465 470 475 480

Lys Gly Ser Ile Ala Leu Pro Asp Gly Gln Asn Val Glu Trp Lys Cys  
 485 490 495

Leu Ile Arg Asn Glu Ala Asp Ala Thr Leu Val Arg Gln Trp Gln Ser  
 500 505 510

Gly Gly Asn Asn Gln Val Gln Ala Ala Ala Gly Ala Ser Thr Ser Gly  
 515 520 525

Ser Phe  
 530

<210> 10

<211> 686  
 <212> PRT  
 <213> ARTIFICIAL SEQUENCE

<220>  
 <223> Optimized sequence, Novamyl

<400> 10

Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile Ile  
 1 5 10 15

Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys Ser  
 20 25 30

Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp Gly  
 35 40 45

Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln Leu  
 50 55 60

Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp Thr  
 65 70 75 80

Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg Asp  
 85 90 95

Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp Thr  
 100 105 110

Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp Phe  
 115 120 125

Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe Ala  
 130 135 140

Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr Phe  
 145 150 155 160

Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser Asn  
 165 170 175

Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro Ala  
 180 185 190

Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala Gln  
 195 200 205

Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp Gly  
 210 215 220

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

Leu Ala Asp Lys Leu Tyr Gln Lys Lys Asp Ile Phe Leu Val Gly Glu  
 245 250 255

Trp Tyr Gly Asp Asp Pro Gly Thr Ala Asn His Leu Glu Lys Val Arg  
 260 265 270

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

Val Ile Arg Asn Val Phe Gly Thr Phe Thr Gln Thr Met Tyr Asp Leu  
 290 295 300

Asn Asn Met Val Asn Gln Thr Gly Asn Glu Tyr Lys Tyr Lys Glu Asn  
 305 310 315 320

Leu Ile Thr Phe Ile Asp Asn His Asp Met Ser Arg Phe Leu Ser Val  
 325 330 335

Asn Ser Asn Lys Ala Asn Leu His Gln Ala Leu Ala Phe Ile Leu Thr  
 340 345 350

Ser Arg Gly Thr Pro Ser Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Ala  
 355 360 365

Gly Gly Asn Asp Pro Tyr Asn Arg Gly Met Met Pro Ala Phe Asp Thr  
 370 375 380

Thr Thr Thr Ala Phe Lys Glu Val Ser Thr Leu Ala Gly Leu Arg Arg  
 385 390 395 400

Asn Asn Ala Ala Ile Gln Tyr Gly Thr Thr Thr Gln Arg Trp Ile Asn  
 405 410 415

Asn Asp Val Tyr Ile Tyr Glu Arg Lys Phe Phe Asn Asp Val Val Leu  
 420 425 430

Val Ala Ile Asn Arg Asn Thr Gln Ser Ser Tyr Ser Ile Ser Gly Leu  
 435 440 445

Gln Thr Ala Leu Pro Asn Gly Ser Tyr Ala Asp Tyr Leu Ser Gly Leu  
 450 455 460

Leu Gly Gly Asn Gly Ile Ser Val Ser Asn Gly Ser Val Ala Ser Phe  
 465 470 475 480

Thr Leu Ala Pro Gly Ala Val Ser Val Trp Gln Tyr Ser Thr Ser Ala  
                   485                                  490                                  495

Ser Ala Pro Gln Ile Gly Ser Val Ala Pro Asn Met Gly Ile Pro Gly  
                   500                                  505                                  510

Asn Val Val Thr Ile Asp Gly Lys Gly Phe Gly Thr Thr Gln Gly Thr  
                   515                                  520                                  525

Val Thr Phe Gly Gly Val Thr Ala Thr Val Lys Ser Trp Thr Ser Asn  
                   530                                  535                                  540

Arg Ile Glu Val Tyr Val Pro Asn Met Ala Ala Gly Leu Thr Asp Val  
  545                                  550                                  555                                  560

Lys Val Thr Ala Gly Gly Val Ser Ser Asn Leu Tyr Ser Tyr Asn Ile  
                   565                                  570                                  575

Leu Ser Gly Thr Gln Thr Ser Val Val Phe Thr Val Lys Ser Ala Pro  
                   580                                  585                                  590

Pro Thr Asn Leu Gly Asp Lys Ile Tyr Leu Thr Gly Asn Ile Pro Glu  
                   595                                  600                                  605

Leu Gly Asn Trp Ser Thr Asp Thr Ser Gly Ala Val Asn Asn Ala Gln  
                   610                                  615                                  620

Gly Pro Leu Leu Ala Pro Asn Tyr Pro Asp Trp Phe Tyr Val Phe Ser  
  625                                  630                                  635                                  640

Val Pro Ala Gly Lys Thr Ile Gln Phe Lys Phe Phe Ile Lys Arg Ala  
                   645                                  650                                  655

Asp Gly Thr Ile Gln Trp Glu Asn Gly Ser Asn His Val Ala Thr Thr  
                   660                                  665                                  670

Pro Thr Gly Ala Thr Gly Asn Ile Thr Val Thr Trp Gln Asn  
                   675                                  680                                  685

<210> 11

<211> 29

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DNA Primers

<400> 11

ctcattctgc agcttcagca aatacggcg

29



<210> 12  
 <211> 35  
 <212> DNA  
 <213> ARTIFICIAL SEQUENCE  
  
 <220>  
 <223> DNA Primers  
  
 <400> 12  
 ctctgttaac tcatttggcg acccagattg aaacg 35  
  
 <210> 13  
 <211> 31  
 <212> DNA  
 <213> ARTIFICIAL SEQUENCE  
  
 <220>  
 <223> DNA Primers  
  
 <400> 13  
 ctataaat t acgggcaaag catgggattg g 31  
  
 <210> 14  
 <211> 33  
 <212> DNA  
 <213> ARTIFICIAL SEQUENCE  
  
 <220>  
 <223> DNA Primers  
  
 <400> 14  
 tgctttgccc gttaaatttat agatccggtt cag 33  
  
 <210> 15  
 <211> 28  
 <212> DNA  
 <213> ARTIFICIAL SEQUENCE  
  
 <220>  
 <223> DNA Primers  
  
 <400> 15  
 ctatgactat ctgctgtttg ccgatctg 28  
  
 <210> 16  
 <211> 28  
 <212> DNA  
 <213> ARTIFICIAL SEQUENCE  
  
 <220>  
 <223> DNA Primers  
  
 <400> 16  
 cagatcgga aacagcagat agtcatag 28  
  
 <210> 17  
 <211> 58  
 <212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DNA Primers

<400> 17

gcatgggatt gggaagtcga tacggaaaac ggcaactatg actatctgct gtttgccg 58

<210> 18

<211> 52

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DNA Primers

<400> 18

cgtatcgact tcccaatccc atgctttgcc cgtaaattta tagatccggt tc 52