

H 3831WO - SeqL_ST25
SEQUENCE LISTING

<110> Universität Hohenheim

<120> Paenibacillus wynnii beta-galactosidase for the production of lactose-depleted dairy products

<130> H 3831WO

<150> EP 19 152 027.9

<151> 16.01.2019

<160> 2

<170> PatentIn version 3.5

<210> 1

<211> 1042

<212> PRT

<213> Paenibacillus wynnii

<400> 1

Met Arg Lys Lys Leu Val Tyr Ser Pro Pro Thr Asn Gly Tyr Pro Glu
1 5 10 15

Trp Asn Asn Asn Pro Glu Cys Phe Gln Ile Asn Arg Met Asp Ala His
20 25 30

Ala Thr Trp Ile Pro Phe Asn Thr Thr Glu Asp Ala Leu Leu Gly Asp
35 40 45

Pro Gln Ser Ser Pro Asn Tyr Leu Ser Leu Asn Gly Met Trp Lys Phe
50 55 60

Ala Tyr Ala Glu Thr Pro Asp Gln Arg Ile Arg Asn Phe Phe Glu Lys
65 70 75 80

Asn Tyr Asp Cys Ser Ser Trp Ala Glu Leu Asn Val Pro Ser His Trp
85 90 95

Gln Met His Gly Tyr Asp Tyr Pro Gln Tyr Thr Asn Val Arg Tyr Pro
100 105 110

Trp Ser Glu Arg Glu Pro Glu Leu Lys Pro Pro Phe Ala Pro Thr Gln

H 3831W0 - SeqL_ST25

115

120

125

Tyr Asn Pro Val Gly Ser Tyr Val Arg Thr Phe Ser Val Pro Glu Asp
130 135 140

Trp Ser Gly Lys Pro Val Phe Ile Ser Phe Gln Gly Val Glu Ser Ala
145 150 155 160

Phe Tyr Val Trp Leu Asn Gly Glu Leu Val Gly Tyr Ser Glu Asp Thr
165 170 175

Phe Thr Pro Ala Glu Phe Asp Leu Thr Pro Tyr Leu Ile Pro Gly Asp
180 185 190

Asn Lys Leu Ala Val Glu Val Tyr Arg Trp Cys Asp Ala Ser Trp Leu
195 200 205

Glu Asp Gln Asp Phe Trp Arg Leu Ser Gly Ile Phe Arg Asp Val Tyr
210 215 220

Leu Tyr Thr Thr Pro Glu Ala His Ile Tyr Asp Phe Phe Val Arg Thr
225 230 235 240

Glu Leu Asp Glu Gln Tyr Arg His Ala Glu Leu Gln Leu Asp Val Lys
245 250 255

Leu Met Asp Tyr Phe Glu Arg Thr Ala Glu Ala Val Ile Val His Ala
260 265 270

Gln Leu Tyr Asp His Asp Gln Asn Ala Ile Phe Asp Gln Pro Leu Ser
275 280 285

Gln Thr Val Tyr Phe Asn Ser Ala Ser Thr Gln Thr Leu Gln Phe Ser
290 295 300

Ser Ser Ile Ile Asp Pro Leu Lys Trp Ser Ala Glu His Pro Asn Leu
305 310 315 320

Tyr Thr Leu Val Leu Ser Leu His His Val Asp Gly Glu Leu Met Glu

H 3831W0 - SeqL_ST25

325

330

335

Ala Val Ser Cys Arg Val Gly Phe Arg Thr Phe Glu Leu Lys Asp Gly
340 345 350

Leu Met Lys Ile Asn Gly Lys Arg Ile Val Phe Lys Gly Val Asn Arg
355 360 365

His Glu Phe Ser Cys Asp Thr Gly Arg Ser Ile Asp Val Asp Asp Met
370 375 380

Val Arg Asp Ile Leu Leu Met Lys Ala His Asn Ile Asn Ala Val Arg
385 390 395 400

Thr Ser His Tyr Pro Asn Gln Thr Ile Trp Tyr Asp Leu Cys Asp Gln
405 410 415

Tyr Gly Leu Tyr Val Ile Asp Glu Thr Asn Leu Glu Thr His Gly Ser
420 425 430

Trp Ser Tyr Gly Gln Thr Asp Leu Gly Gly Asn Thr Val Pro Gly Ser
435 440 445

Arg Pro Glu Trp Arg Ala Asn Val Leu Asp Arg Cys Asn Ser Met Leu
450 455 460

Gln Arg Asp Lys Asn His Pro Ser Ile Val Ile Trp Ser Leu Gly Asn
465 470 475 480

Glu Ser Phe Gly Gly Asp Asn Phe Val Ala Met His Asp Phe Leu Lys
485 490 495

Lys Glu Asp Pro Ser Arg Leu Val His Tyr Glu Gly Leu Phe His Tyr
500 505 510

Arg Glu Ser Asp Val Ala Ser Asp Ile Glu Ser Thr Met Tyr Ile Ser
515 520 525

Pro Ala Asp Val Glu Gln Tyr Ala Leu Asn Asp Pro Lys Lys Pro Tyr

H 3831W0 - SeqL_ST25

530

535

540

Ile Leu Cys Glu Tyr Ser His Ala Met Gly Asn Ser Cys Gly Gly Leu
545 550 555 560

His Leu Tyr Trp Glu Val Phe Glu Lys Tyr Asp Ile Leu Gln Gly Ala
565 570 575

Phe Ile Trp Asp Trp Ile Asp Gln Ala Ile Arg Leu Lys Gln Ala Asp
580 585 590

Gly Ser Met His Met Ala Tyr Gly Gly Asp Phe Gly Glu Ser Pro His
595 600 605

Asp Gly Asn Phe Cys Gly Asn Gly Leu Ile Phe Ala Asp Arg Ser Val
610 615 620

Ser Pro Lys Leu Tyr Glu Val Lys Lys Cys Tyr Gln Asn Val Lys Phe
625 630 635 640

Glu Ala Val Asp Leu Glu Arg Gly Ile Tyr Arg Val Thr Asn Gln Asn
645 650 655

Leu Phe Thr Asp Leu Ala Glu Tyr Ala Leu Ala Trp Glu Val Ser Cys
660 665 670

Asn Gly Asn Pro Val Leu Lys Gly Thr Val Asp Leu Ala Val Pro Ala
675 680 685

Gly Glu Ser Ala Glu Ile Ser Val Pro Val Val Asp Glu Pro Asn Leu
690 695 700

Gln Ser Glu Gly Glu His Val Leu Thr Phe Ser Leu Gln Leu Lys Lys
705 710 715 720

Ser Thr Leu Trp Ala Asp Ala Gly His Glu Val Ala Trp Glu Gln Phe
725 730 735

Leu Leu Pro Thr Pro Gln Phe Met Ala Gly Gln Asp Gln Asp Ser Val

H 3831W0 - SeqL_ST25

740

745

750

Leu Thr Ser Asp Arg Gly Val Ile Val Glu Glu Gln Ala Gly Arg Leu
755 760 765

Thr Val Gln Ala Ala Asp Val Ser Leu Gln Phe Ser Thr Ser Ser Gly
770 775 780

Tyr Leu Ile Ser Met Gln Asn Lys Gly Lys Glu Leu Leu Leu Glu Pro
785 790 795 800

Val Arg Pro Asn Phe Trp Arg Ala Val Thr Asp Asn Asp Leu Gly Asn
805 810 815

Lys His His Glu Arg Cys Ala Val Trp Asn Thr Ala Gly Ala Gly Cys
820 825 830

Thr Leu Ala Ser Phe Glu Ser His Lys Asn Val Asp Gly Val Thr Val
835 840 845

Arg Ala Lys Tyr Thr Val Pro Thr Val Pro Ile Ser Ser Leu Ile Leu
850 855 860

Glu Tyr Arg Ile Gln Glu Asn Gly Ser Ile Glu Val Phe Glu Glu Leu
865 870 875 880

Ser Pro Gly Met Gly Leu Pro Glu Ile Pro Glu Ile Gly Leu Met Phe
885 890 895

Ile Val Glu Asp Arg Leu Asp Thr Val Ser Trp Tyr Gly Arg Gly Pro
900 905 910

His Glu Asn Tyr Trp Asp Arg Lys Thr Gly Ala Arg Leu Gly Tyr Phe
915 920 925

Ser Gly Ser Val Gln Asp Gln Phe Val Pro Tyr Ile Arg Pro Gln Glu
930 935 940

Cys Gly Asn Lys Thr Asp Val Arg Phe Ala Ser Ile Thr Gly Gly Ile

H 3831W0 - SeqL_ST25

945		950		955		960
Asn Gly Ser Gly Phe Arg Val Asp Gly Asp Pro Val Leu Glu Leu Asn						
	965			970		975
Ala Leu Pro Trp Thr Pro Ala Glu Leu Glu Ala Asn Asp His Ile Tyr						
	980			985		990
Lys Leu Pro Ala Ser Asn Lys Thr Val Val Arg Val Asn Tyr Lys Gln						
	995			1000		1005
Met Gly Val Gly Gly Asp Asn Ser Trp Gly Ala Thr Thr His Pro						
	1010			1015		1020
Glu Phe Thr Leu Pro Ala Asp Gln Thr Tyr Gly Phe Arg Phe Thr						
	1025			1030		1035
Ile Arg Met Val						
	1040					

<210> 2
 <211> 3129
 <212> DNA
 <213> Paenibacillus wynnii

<400> 2	
atgcgtaaaa aacttgctta ttcacccccct accaacgggt acccggaatg gaataataat	60
cccgaatggtt ttcagatcaa ccgaatggat gcccatgcta catggatacc ttttaataca	120
acagaggatg ccttgcttgg agatccacaa tcctcgccca actatattgtc tttgaatggg	180
atgtggaaat tcgcctatgc agagactccg gatcaacgca tacgtaactt ttttgaaaaa	240
aactatgatt gcagttcttg ggctgaactg aacgttcctt ctcatgggca gatgcatgga	300
tatgactacc ctcaagtatac gaatgtacgg tatccctgga gtgaacgtga gccggagctc	360
aaaccgcctt ttgctccac ccaatataat ccggttgggt cttatgtacg aaccttctct	420
gtaccggagg actggagcgg gaagcctggt ttcatcagct ttcaaggtgt ggagtctgcc	480
ttctatgttt ggctcaatgg agagttgggt ggatacagcg aggatacctt caccctgcg	540
gaatttgact taactcctta tctaataccg ggagacaata agcttgccgt tgaagtgtat	600

H 3831W0 - SeqL_ST25

cgttggtgtg acgccagttg gctggaggat caggatttct ggagacttag cggcatat	660
agagatgtct atctatatac aacaccggaa gcccatat	720
gaactggatg agcagtaccg gcatgctgaa ttgcagctgg atgtgaagct tatggattat	780
tttgaaagaa ccgctgaggc agttattgtg catgcgagc tttatgatca cgatcagaac	840
gctatctttg atcagccgct ttcacagaca gtctacttca atagcgcttc taccagacg	900
ctccaattct cttcttctat tattgacccg ttaaaatgga gtgcggaaca tccgaatcta	960
tatacgttag tgttgtcttt acatcatgtg gatggagagc tcatggaagc cgttagctgc	1020
cgtgttggct ttcgtacatt cgagctaaag gacggtttaa tgaagattaa tggaaaacgg	1080
atcgtcttta agggcgtgaa ccgccatgaa ttctcatgcg ataccggcag atcaattgat	1140
gtcgaatgata tggtagcggga cattctactg atgaaagcac acaacatcaa tgccgttcgg	1200
acttcgcatt atccgaatca gaccatatgg tatgacctt gtgaccaata tgggctgtat	1260
gtaattgatg agaccaatct ggagacacat ggttcgtgga gctatggaca gacagactta	1320
ggcggaaaata cggtagccgg cagtagacct gaatggcgcg cgaatgtact ggatcggtgt	1380
aattcaatgc tccaaagga caaaaaccac cttccatcg tcacttggtc actcggtaac	1440
gagtcctttg gcggtgataa ctttgtggct atgcatgatt ttcttaagaa agaagacccc	1500
tcccggttg tccattatga aggcctctt cactatcgcg agagcgatgt tgcctcggac	1560
attgagagca ccatgtacat tagtccggcc gatgtggaac agtatgcgct taatgatcca	1620
aagaagcctt atattctatg cgagtatagc catgcaatgg gcaactcctg cgggggattg	1680
catctatact gggaagtttt tgagaaatat gatattttac aggggtgcctt tatctgggac	1740
tggattgatc aagcgattcg acttaagcaa gccgacggat ccatgcatat ggcctacggc	1800
ggagacttcg gggaatcccc tcatgacggc aacttctgcg gaaatggctt gattttcgct	1860
gaccgttcag tatctcctaa gctgtatgag gtcaagaaat gctaccagaa tggttaaattt	1920
gaggctgtcg atttagagcg aggcatttat cgggtaacca atcagaatct atttacggat	1980
ttggcggagt acgcactggc ttgggaagta agctgtaacg gcaatcctgt gcttaagggt	2040
actgttgatc tggctgtccc tgcaggagaa tcggcagaaa tttcggttcc cgtggctgat	2100
gaacctaacc tgcaatccga gggcgagcat gtcctcacgt ttagcctgca attgaagaaa	2160

H 3831W0 - SeqL_ST25

tccacccttt	gggcagacgc	aggccatgaa	gtggcatggg	aacaattcct	gctgcctaca	2220
cctcagttta	tggcgggtca	ggatcaagac	tctgttttga	catcagatcg	tggtgtgatt	2280
gtggaggaac	aagcagggcg	tttaactgtt	caggcggcgg	atgtctccct	tcaattcagt	2340
acttcaagcg	gttatctgat	ctctatgcaa	aataaaggca	aggaactgct	gctcgaacct	2400
gttcgtccga	atttctggcg	tgcatgttacg	gataacgatc	tagggaacaa	acaccatgag	2460
cgttgcgcg	tttgaatac	agcgggagct	ggctgtacac	tagcttcctt	tgaatcgcat	2520
aagaatgtag	atggcgtaac	tgttctgtgct	aagtacaccg	taccaccgt	accatttct	2580
tcactgatat	tggaatatag	aatccaagaa	aatggctcca	ttgaagtctt	tgaagagcta	2640
tcaccgggca	tgggcttgcc	ggagattcct	gaaattggcc	tcatgtttat	cgttgaagat	2700
cgactcgaca	ccgtttcatg	gtatggccgc	ggaccgcatg	agaattactg	ggaccggaag	2760
acaggcgcca	gacttggata	tttttcggga	agtgtccagg	atcagttcgt	tccgtatata	2820
aggcctcaag	aatgcggaaa	caaaacggat	gtgcgttttg	ccagtatcac	tgggggtata	2880
aacggctcag	gattccgtgt	ggatggcgat	cctgtactgg	aactaaatgc	cttgccttgg	2940
acacccgctg	agttggaagc	gaatgatcac	atatataagc	tgccagccag	taataaaacc	3000
gttgtgcgtg	tgaactacaa	gcaaattgggt	gtaggtggag	acaacagctg	gggcgcgacg	3060
acacatcctg	aattcacttt	gccggcggat	caaacttatg	ggtttcgggt	tacgattcgg	3120
atggtgtaa						3129