

SEQUENCE LISTING

<110> DAIICHI SANKYO COMPANY LIMITED

<120> Novel Endo-Beta, N-acetylglucosaminidase

<130> FP1734

<150> JP2016-234808

<151> 2016-12-02

<160> 23

<170> PatentIn version 3.5

<210> 1

<211> 696

<212> PRT

<213> Rhizomucor pusillus

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Asn	Ala	Ser	Arg	Ala	Asn	Ile	Ala	Thr	Ile	Pro	Leu	His	Gln	Arg	Ser
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Asn	Leu	Asp	Pro	Ala	Glu	Pro	Arg	Leu	Ile	Val	Thr	His	Asp	Met	Ala
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Gly	Gly	Tyr	Lys	Glu	Asp	Ser	Asn	Ile	Gln	Gly	Asn	Thr	Tyr	Asp	Thr
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Ile	Tyr	Ser	Cys	Gln	Tyr	Trp	Gln	Tyr	Val	Asp	Thr	Phe	Ile	Tyr	Phe
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Ser	His	His	Arg	Val	Thr	Ile	Pro	Pro	Val	Asn	Trp	Ile	Asn	Ala	Cys
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His	Arg	Asn	Gly	Val	Lys	Thr	Leu	Gly	Thr	Phe	Ile	Val	Glu	Gly	Ala
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Ala	Gly	Met	Phe	Ala	Leu	Glu	Arg	Phe	Val	Tyr	Gly	Pro	Glu	Pro	Gly
	130					135					140				

Gln	Arg	Asn	Ser	Trp	Ser	Pro	Tyr	Tyr	Ala	Asp	Lys	Leu	Val	Asp	Ile	
145					150					155					160	
Ala	Glu	Phe	Tyr	Gly	Phe	Asp	Gly	Trp	Leu	Leu	Asn	Ile	Glu	Ser	Asp	
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Phe	Phe	Pro	Leu	Tyr	Arg	Asn	Pro	Ser	Leu	Lys	Ala	Ile	His	Leu	Ala	
			180					185					190			
Lys	Leu	Leu	Arg	Tyr	Leu	Lys	Asn	Ala	Met	His	Ala	Arg	Val	Pro	Gly	
		195					200					205				
Ser	Glu	Ile	Ile	Trp	Tyr	Asp	Ser	Met	Thr	Thr	Asn	Gly	Ser	Val	Gln	
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Trp	Gln	Asn	Asn	Ile	Thr	Pro	Lys	Asn	Ser	Ile	Phe	Phe	Glu	Ala	Ala	
225					230					235					240	
Asp	Gly	Ile	Phe	Leu	Asn	Tyr	Trp	Trp	Asn	Ala	Thr	Val	Pro	Pro	Leu	
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Ala	Leu	Gln	Val	Ala	His	Arg	Leu	Gly	Arg	Gln	Gly	Ser	Asp	Val	Tyr	
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Phe	Gly	Thr	Asp	Val	Trp	Gly	Arg	Gly	Thr	Phe	Gly	Gly	Gly	Gly	Phe	
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Asp	Ser	Tyr	Leu	Ala	Val	Gly	Thr	Ala	Arg	Ala	Phe	Lys	Thr	Ser	Ser	
	290					295					300					
Ala	Leu	Phe	Gly	Thr	Ala	Trp	Ile	Tyr	Glu	His	Phe	Gly	Lys	Lys	Asp	
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Phe	Glu	Leu	Met	Asp	Arg	Leu	Leu	Trp	Leu	Gly	Gly	Asp	Gln	Ser	Glu	
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Tyr	Pro	Ala	Gln	Glu	Gly	Glu	Gln	Asn	Arg	Thr	Val	Lys	Val	Thr	Ser	
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His	Leu	Gly	Arg	His	Pro	Gly	Ile	Ala	Asp	Val	Ser	Pro	Val	Arg	Ser	
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Ala	Pro	Gly	Lys	Thr	Trp	Phe	Ala	Thr	Trp	Phe	Asp	Arg	Gly	Tyr	Gly	
	370					375					380					

Thr Gly Phe Tyr Tyr Gln Gly Lys Lys Leu Leu Ser Gln Pro Trp Ser
 385 390 395 400

His Leu Ser His Gln Ser Ile Pro Pro Asn Leu Ile Ala Arg Leu Gln
 405 410 415

Arg Glu Glu Asn His Gly Leu Ser Tyr Phe Leu Ala Asp Asp Asp Ala
 420 425 430

Tyr Ile Gly Gly Thr Ser Leu Leu Ile Ala Ala Glu Ile Thr Gln Glu
 435 440 445

Arg Gln Leu Pro Leu Tyr Gln Leu Glu Tyr Asp Val Thr Glu Gly Cys
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Glu Val Gln Phe Ile Tyr Lys Ser Pro Glu Pro Asp Met Gln Gly Lys
 465 470 475 480

Ile Asp Ile Tyr Leu Asn Leu Gln Val Thr Asp Ile Leu Pro Asp Glu
 485 490 495

Leu Ala Phe Tyr Trp Gln Asp Val Thr Asp Ala Ser Ser Gln Ala Asp
 500 505 510

Ala Thr Thr Ala Met Arg Leu Tyr Leu Asn Glu Asn Thr Val Ile Tyr
 515 520 525

Leu Lys Pro Ser Arg Lys Gln Glu Leu Ala Glu Gly Trp Leu Leu Cys
 530 535 540

Ser Val Arg Val Pro Pro Thr Tyr Pro Leu Gly Ile Ala Thr Ile Lys
 545 550 555 560

Glu Leu Gly Ile His Val Asp Gly Lys Glu Thr Val Leu Phe Arg Leu
 565 570 575

Gly Leu Leu Thr Ile Ile Pro Leu Gly Asp Ala Pro Ser Ala Leu Ser
 580 585 590

Arg Ile Thr Gln Val Gln Leu Gln Arg Asp Glu Asp Ile His Ser Lys
 595 600 605

Cys Pro Ser Ser Ser Cys Glu Leu Trp Ala Thr Leu Ser Trp Met Met
610 615 620

Glu His Asn Ser Lys Glu Asp Trp Asp Gln Val Asp His Tyr Met Ile
625 630 635 640

Phe Phe Lys Asn Val Asp Ser Lys Ala Glu Pro Ile Phe Leu Gly Thr
645 650 655

Ser Phe Ser Thr Glu Tyr Arg Ile Ser Gly Leu Glu Ile Lys Lys His
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Gly Asn Ser Ile Glu Ile Trp Ala Val Asn Arg Leu Gly Thr Val Ile
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Ala Arg Gln Asp Ile Asp Ile Gln
690 695

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<213> Rhizomucor pusillus

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Ser Met Pro Leu Gln Thr Met Asn Glu Leu Gly Ser Trp Glu Pro Ser
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Asn Ala Ser Arg Ala Asn Ile Ala Thr Ile Pro Leu His Gln Arg Ser
35 40 45

Asn Leu Asp Pro Ala Glu Pro Arg Leu Ile Val Thr His Asp Met Ala
50 55 60

Gly Gly Tyr Lys Glu Asp Ser Asn Ile Gln Gly Asn Thr Tyr Asp Thr
65 70 75 80

Ile Tyr Ser Cys Gln Tyr Trp Gln Tyr Val Asp Thr Phe Ile Tyr Phe
85 90 95

Ser His His Arg Val Thr Ile Pro Pro Val Asn Trp Ile Asn Ala Cys
100 105 110

His Arg Asn Gly Val Lys Thr Leu Gly Thr Phe Ile Val Glu Gly Thr
115 120 125

Ala Gly Met Phe Ala Leu Glu Arg Phe Val Tyr Gly Pro Glu Pro Gly
130 135 140

Gln Arg Asn Ser Trp Ser Pro Tyr Tyr Ala Asp Lys Leu Val Asp Ile
145 150 155 160

Ala Glu Phe Tyr Gly Phe Asp Gly Trp Leu Leu Asn Ile Glu Ser Asp
165 170 175

Phe Phe Pro Leu Tyr Arg Asn Pro Ser Leu Lys Ala Ile His Leu Ala
180 185 190

Lys Leu Leu Arg Tyr Leu Lys Asn Ala Met His Ala Arg Val Pro Gly
195 200 205

Ser Glu Ile Ile Trp Tyr Asp Ser Met Thr Thr Asn Gly Ser Val Gln
210 215 220

Trp Gln Asn Asn Ile Thr Pro Lys Asn Ser Ile Phe Phe Glu Ala Ala
225 230 235 240

Asp Gly Ile Phe Leu Asn Tyr Trp Trp Asn Ala Thr Val Pro Pro Leu
245 250 255

Ala Leu Gln Val Ala His Arg Leu Gly Arg Gln Gly Ser Asp Val Tyr
260 265 270

Phe Gly Thr Asp Val Trp Gly Arg Gly Thr Phe Gly Gly Gly Gly Phe
275 280 285

Asp Ser Tyr Leu Ala Val Gly Thr Ala Arg Ala Phe Lys Thr Ser Ser
290 295 300

Ala Leu Phe Gly Thr Ala Trp Ile Tyr Glu His Phe Gly Lys Lys Asp
305 310 315 320

Phe Glu Leu Met Asp Arg Leu Leu Trp Leu Gly Gly Asp Gln Ser Glu
325 330 335

Tyr Pro Ala Gln Glu Gly Glu Gln Asn Arg Thr Val Lys Val Thr Ser

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His	Leu	Gly	Arg	His	Pro	Gly	Ile	Ala	Asp	Val	Ser	Pro	Val	Arg	Ser	
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Thr	Gly	Phe	Tyr	Tyr	Gln	Gly	Lys	Lys	Leu	Leu	Ser	Gln	Pro	Trp	Ser	
385					390					395					400	
His	Leu	Ser	His	Gln	Ser	Ile	Pro	Pro	Asn	Leu	Ile	Ala	Arg	Leu	Gln	
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Arg	Glu	Glu	Asn	His	Gly	Leu	Ser	Tyr	Phe	Leu	Ala	Asp	Asp	Asp	Ala	
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Tyr	Ile	Gly	Gly	Thr	Ser	Leu	Leu	Ile	Ala	Ala	Glu	Ile	Thr	Gln	Glu	
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Leu	Lys	Pro	Ser	Arg	Lys	Gln	Glu	Leu	Ala	Glu	Gly	Trp	Leu	Leu	Cys	
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Ser	Val	Arg	Val	Pro	Pro	Thr	Tyr	Pro	Leu	Gly	Ile	Ala	Thr	Ile	Lys	
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Glu	Leu	Gly	Ile	His	Val	Asp	Gly	Thr	Glu	Thr	Val	Leu	Phe	Arg	Leu	
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Gly Leu Leu Thr Ile Ile Pro Leu Gly Asp Ala Pro Ser Ala Leu Ser
580 585 590

Arg Ile Thr Gln Val Gln Leu Gln Arg Asp Glu Asp Ile His Ser Lys
595 600 605

Cys Pro Ser Ser Ser Cys Glu Leu Trp Ala Thr Leu Ser Trp Met Met
610 615 620

Glu His Asn Ser Lys Glu Asp Trp Asp Gln Val Asp His Tyr Met Ile
625 630 635 640

Phe Phe Lys Asn Val Asp Ser Lys Ala Glu Pro Ile Phe Leu Gly Thr
645 650 655

Ser Phe Ser Thr Glu Tyr Arg Ile Ser Gly Leu Glu Ile Lys Lys His
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Gly Asn Ser Ile Glu Ile Trp Ala Val Asn Arg Leu Gly Thr Val Ile
675 680 685

Ala Arg Gln Asp Ile Asp Ile Gln
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Met Pro Ser Leu Glu Leu Gln Gln Ala Ala Asp Thr Arg Leu Phe Glu
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Ser Met Pro Leu Gln Thr Met Asn Glu Leu Gly Ser Trp Glu Pro Ser
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Asn Ala Ser Arg Ala Asn Ile Ala Thr Ile Pro Leu His Gln Arg Ser
35 40 45

Asn Leu Asp Pro Ala Glu Pro Arg Leu Ile Val Thr His Asp Met Ala
50 55 60

Gly Gly Tyr Lys Glu Asp Ser Asn Ile Gln Gly Asn Thr Tyr Asp Thr
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Ile	Tyr	Ser	Cys	Gln	Tyr	Trp	Gln	Tyr	Val	Asp	Thr	Phe	Ile	Tyr	Phe	
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Ser	His	His	Arg	Val	Thr	Ile	Pro	Pro	Val	Asn	Trp	Ile	Asn	Ala	Cys	
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His	Arg	Asn	Gly	Val	Lys	Thr	Leu	Gly	Thr	Phe	Ile	Val	Glu	Gly	Ala	
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Ala	Gly	Met	Phe	Ala	Leu	Glu	Arg	Phe	Val	Tyr	Gly	Pro	Glu	Pro	Gly	
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Gln	Arg	Asn	Ser	Trp	Ser	Pro	Tyr	Tyr	Ala	Asp	Lys	Leu	Val	Asp	Ile	
145					150					155					160	
Ala	Glu	Phe	Tyr	Gly	Phe	Asp	Gly	Trp	Leu	Leu	Asn	Ile	Glu	Ser	Asp	
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Phe	Phe	Pro	Leu	Tyr	Arg	Asn	Pro	Ser	Leu	Lys	Ala	Ile	His	Leu	Ala	
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Lys	Leu	Leu	Arg	Tyr	Leu	Lys	Asn	Ala	Met	His	Ala	Arg	Val	Pro	Gly	
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Ser	Glu	Ile	Ile	Trp	Tyr	Asp	Ser	Met	Thr	Thr	Asn	Gly	Ser	Val	Gln	
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Trp	Gln	Asn	Asn	Ile	Thr	Pro	Lys	Asn	Ser	Ile	Phe	Phe	Glu	Ala	Ala	
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Asp	Gly	Ile	Phe	Leu	Asn	Tyr	Trp	Trp	Asn	Ala	Thr	Val	Pro	Pro	Leu	
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Ala	Leu	Gln	Val	Ala	His	Arg	Leu	Gly	Arg	Gln	Gly	Ser	Asp	Val	Tyr	
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Phe	Gly	Thr	Asp	Val	Trp	Gly	Arg	Gly	Thr	Phe	Gly	Gly	Gly	Gly	Phe	
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Asp	Ser	Tyr	Leu	Ala	Val	Gly	Thr	Ala	Arg	Ala	Phe	Lys	Thr	Ser	Ser	
	290					295					300					

Ala Leu Phe Gly Thr Ala Trp Ile Tyr Glu His Phe Gly Lys Lys Asp
 305 310 315 320

Phe Glu Leu Met Asp Arg Leu Leu Trp Leu Gly Gly Gly Gln Ser Glu
 325 330 335

Tyr Pro Ala Gln Glu Gly Glu Gln Asn Arg Thr Val Lys Val Thr Ser
 340 345 350

His Leu Gly Arg His Pro Gly Ile Ala Asp Val Ser Pro Val Arg Ser
 355 360 365

Ala Pro Gly Lys Thr Trp Phe Ala Thr Trp Phe Asp Arg Gly Tyr Gly
 370 375 380

Thr Gly Phe Tyr Tyr Gln Gly Lys Lys Leu Leu Ser Gln Pro Trp Ser
 385 390 395 400

His Leu Ser His Gln Ser Ile Pro Pro Asn Leu Ile Ala Arg Leu Gln
 405 410 415

Arg Glu Glu Asn His Gly Leu Ser Tyr Phe Leu Ala Asp Asp Asp Ala
 420 425 430

Tyr Leu Gly Gly Thr Ser Leu Leu Ile Ala Ala Glu Ile Thr Gln Glu
 435 440 445

Arg Gln Leu Pro Leu Tyr Gln Leu Glu Tyr Asp Val Thr Glu Gly Cys
 450 455 460

Glu Val Gln Phe Ile Tyr Lys Ser Pro Glu Pro Asp Met Gln Gly Lys
 465 470 475 480

Ile Asp Ile Tyr Leu Asn Leu Gln Val Thr Asp Ile Leu Pro Asp Glu
 485 490 495

Leu Ala Phe Tyr Trp Gln Asp Val Thr Asp Ala Ser Ser Gln Ala Asp
 500 505 510

Ala Thr Thr Ala Met Arg Leu Tyr Leu Asn Glu Asn Thr Val Val Tyr
 515 520 525

Leu Lys Pro Ser Arg Lys Gln Glu Leu Ala Glu Gly Trp Leu Leu Cys
 530 535 540

Ser Val Arg Val Pro Pro Thr Tyr Pro Leu Gly Ile Ala Thr Ile Lys
 545 550 555 560

Glu Leu Gly Ile His Val Asp Gly Thr Glu Thr Val Leu Phe Arg Leu
 565 570 575

Gly Leu Leu Thr Ile Ile Pro Leu Gly Asp Ala Pro Ser Ala Leu Ser
 580 585 590

Arg Ile Thr Gln Val Gln Leu Gln Arg Asp Glu Asp Ile His Ser Lys
 595 600 605

Cys Ser Ser Ser Ser Cys Glu Leu Trp Ala Thr Leu Ser Trp Met Met
 610 615 620

Glu Arg Asn Ser Lys Glu Asp Trp Asp Gln Val Asp His Tyr Met Ile
 625 630 635 640

Phe Phe Lys Asn Val Asp Ser Lys Ala Glu Pro Ile Phe Leu Gly Thr
 645 650 655

Ser Phe Ser Thr Glu Tyr Arg Ile Ser Gly Leu Glu Ile Lys Lys His
 660 665 670

Gly Asn Ser Ile Glu Ile Trp Ala Val Asn Arg Leu Gly Thr Val Ile
 675 680 685

Ala Arg Gln Asp Ile Asp Ile Gln
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<400> 4

Met Pro Ser Leu Glu Leu Gln Gln Ala Ala Asp Thr Arg Leu Phe Glu
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Ser Met Pro Leu Gln Thr Met Asn Glu Leu Gly Ser Trp Glu Pro Ser
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Asn	Leu	Asp	Pro	Ala	Glu	Pro	Arg	Leu	Ile	Val	Thr	His	Asp	Met	Ala
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Gly	Gly	Tyr	Lys	Glu	Asp	Ser	Asn	Ile	Gln	Gly	Asn	Thr	Tyr	Asp	Thr
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Ile	Tyr	Ser	Cys	Gln	Tyr	Trp	Gln	Tyr	Val	Asp	Thr	Phe	Ile	Tyr	Phe
			85					90					95		
Ser	His	His	Arg	Val	Thr	Ile	Pro	Pro	Val	Asn	Trp	Ile	Asn	Ala	Cys
			100				105						110		
His	Arg	Asn	Gly	Val	Lys	Thr	Leu	Gly	Thr	Phe	Ile	Val	Glu	Gly	Ala
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Ala	Gly	Met	Phe	Ala	Leu	Glu	Arg	Phe	Val	Tyr	Gly	Pro	Glu	Pro	Gly
	130					135					140				
Gln	Arg	Asn	Ser	Trp	Ser	Pro	Tyr	Tyr	Ala	Asp	Lys	Leu	Val	Asp	Ile
145				150					155						160
Ala	Glu	Phe	Tyr	Gly	Phe	Asp	Gly	Trp	Leu	Leu	Asn	Ile	Glu	Ser	Asp
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Phe	Phe	Pro	Leu	Tyr	Arg	Asn	Pro	Ser	Leu	Lys	Ala	Ile	His	Leu	Ala
			180					185					190		
Lys	Leu	Leu	Arg	Tyr	Leu	Lys	Asn	Ala	Met	His	Ala	Arg	Val	Pro	Gly
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Ser	Glu	Ile	Ile	Trp	Tyr	Asp	Ser	Met	Thr	Thr	Asn	Gly	Ser	Val	Gln
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Trp	Gln	Asn	Asn	Ile	Thr	Pro	Lys	Asn	Ser	Ile	Phe	Phe	Glu	Ala	Ala
225				230					235						240
Asp	Gly	Ile	Phe	Leu	Asn	Tyr	Trp	Trp	Asn	Ala	Thr	Val	Pro	Pro	Leu
				245				250					255		
Ala	Leu	Gln	Val	Ala	His	Arg	Leu	Gly	Arg	Gln	Gly	Ser	Asp	Val	Tyr
			260				265						270		

Phe Gly Thr Asp Val Trp Gly Arg Gly Thr Phe Gly Gly Gly Gly Phe
275 280 285

Asp Ser Tyr Leu Ala Val Gly Thr Ala Arg Ala Phe Lys Thr Ser Ser
290 295 300

Ala Leu Phe Gly Thr Ala Trp Ile Tyr Glu His Phe Gly Lys Lys Asp
305 310 315 320

Phe Glu Leu Met Asp Arg Leu Leu Trp Leu Gly Gly Asp Gln Ser Glu
325 330 335

Tyr Pro Ala Gln Glu Gly Glu Gln Asn Arg Thr Val Lys Val Thr Ser
340 345 350

His Leu Gly Arg His Pro Gly Ile Ala Asp Val Ser Pro Val Arg Ser
355 360 365

Ala Pro Gly Lys Thr Trp Phe Ala Thr Trp Phe Asp Arg Gly Tyr Gly
370 375 380

Thr Gly Phe Tyr Tyr Gln Gly Lys Lys Leu Leu Ser Gln Pro Trp Ser
385 390 395 400

His Leu Ser His Gln Ser Ile Pro Pro Asn Leu Ile Ala Arg Leu Gln
405 410 415

Arg Glu Glu Asn His Gly Leu Ser Tyr Phe Leu Ala Asp Asp Asp Ala
420 425 430

Tyr Ile Gly Gly Thr Ser Leu Leu Ile Ala Ala Glu Ile Thr Gln Glu
435 440 445

Arg Gln Leu Pro Leu Tyr Gln Leu Glu Tyr Asp Ala Thr Glu Gly Cys
450 455 460

Glu Val Gln Phe Ile Tyr Lys Ser Pro Glu Pro Asp Met Gln Gly Lys
465 470 475 480

Ile Asp Ile Tyr Leu Asn Leu Gln Val Thr Asp Ile Leu Pro Asp Glu
485 490 495

Leu Ala Phe Tyr Trp Gln Asp Val Thr Asp Ala Ser Ser Gln Ala Asp

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

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

Asp Gly Ile Phe Leu Asn Tyr Trp Trp Asn Ala Thr Val Pro Pro Leu
 245 250 255

Ala Leu Gln Val Ala His Arg Leu Gly Arg Gln Gly Ser Asp Val Tyr
 260 265 270

Phe Gly Thr Asp Val Trp Gly Arg Gly Thr Phe Gly Gly Gly Gly Phe
 275 280 285

Asp Ser Tyr Leu Ala Val Gly Thr Ala Arg Ala Phe Lys Thr Ser Ser
 290 295 300

Ala Leu Phe Gly Thr Ala Trp Ile Tyr Glu His Phe Gly Lys Lys Asp
 305 310 315 320

Phe Glu Leu Met Asp Arg Leu Leu Trp Leu Gly Gly Asp Gln Ser Glu
 325 330 335

Tyr Pro Ala Gln Glu Gly Glu Gln Asn Arg Thr Val Lys Val Thr Ser
 340 345 350

His Leu Gly Arg His Pro Gly Ile Ala Asp Val Ser Pro Val Arg Ser
 355 360 365

Ala Pro Gly Lys Thr Trp Phe Ala Thr Trp Phe Asp Arg Gly Tyr Gly
 370 375 380

Thr Gly Phe Tyr Tyr Gln Gly Lys Lys Leu Leu Ser Gln Pro Trp Ser
 385 390 395 400

His Leu Ser His Gln Ser Ile Pro Pro Asn Leu Ile Ala Arg Leu Gln
 405 410 415

Arg Glu Glu Asn His Gly Leu Ser Tyr Phe Leu Ala Asp Asp Asp Ala
 420 425 430

Tyr Ile Gly Gly Thr Ser Leu Leu Ile Ala Ala Glu Ile Thr Gln Glu
 435 440 445

Arg Gln Leu Pro Leu Tyr Gln Leu Glu Tyr Asp Val Thr Glu Gly Cys
 450 455 460

Glu Val Gln Phe Ile Tyr Lys Ser Pro Glu Pro Asp Met Gln Gly Lys
 465 470 475 480

Ile Asp Ile Tyr Leu Asn Leu Gln Val Thr Asp Ile Leu Pro Asp Glu
 485 490 495

Leu Ala Phe Tyr Trp Gln Asp Val Thr Asp Ala Ser Ser Gln Ala Asp
 500 505 510

Ala Thr Thr Ala Met Arg Leu Tyr Leu Asn Glu Asn Thr Val Ile Tyr
 515 520 525

Leu Lys Pro Ser Arg Lys Gln Glu Leu Ala Glu Gly Trp Leu Leu Cys
 530 535 540

Ser Val Arg Val Pro Pro Thr Tyr Pro Leu Gly Ile Ala Thr Ile Lys
 545 550 555 560

Glu Leu Gly Ile His Val Asp Gly Thr Glu Thr Val Leu Phe Arg Leu
 565 570 575

Gly Leu Leu Thr Ile Ile Pro Leu Gly Asp Ala Pro Ser Ala Leu Ser
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Arg Ile Thr Gln Val Gln Leu Gln Arg Asp Glu Asp Ile His Ser Lys
 595 600 605

Cys Pro Ser Ser Ser Cys Glu Leu Trp Ala Thr Leu Ser Trp Met Met
 610 615 620

Glu His Asn Ser Lys Glu Asp Trp Asp Gln Val Asp His Tyr Met Ile
 625 630 635 640

Phe Phe Lys Asn Val Asp Ser Lys Ala Glu Pro Ile Phe Leu Gly Thr
 645 650 655

Ser Phe Ser Thr Glu Tyr Arg Ile Ser Gly Leu Glu Ile Lys Lys His
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Gly Asn Ser Ile Glu Ile Trp Ala Val Asn Arg Leu Gly Thr Val Ile
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Ala Arg Gln Asp Ile Asp Ile Gln
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 <211> 697
 <212> PRT
 <213> Rhizomucor miehei

<400> 6

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Ser Thr Pro Leu Met Thr Met Asp Glu Leu Gly Ser Trp Asp Pro Ser
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Asn Ala Leu Arg Ala Ser Ile Ala Thr Val Pro Leu His Pro Arg Pro
 35 40 45

Ser Ile Asp Pro Thr Glu Pro Arg Leu Ile Val Thr His Asp Met Ala
 50 55 60

Gly Gly Tyr Lys Glu Asp Phe Ser Ile Gln Gly Asn Ala Tyr Asp Thr
 65 70 75 80

Val Tyr Thr Cys Gln Tyr Trp Gln Tyr Val Asp Ile Phe Ile Tyr Phe
 85 90 95

Ser His His Arg Val Thr Ile Pro Pro Val Asn Trp Thr Asn Ala Cys
 100 105 110

His Arg Asn Gly Val Lys Ser Leu Gly Thr Phe Ile Val Glu Gly Ala
 115 120 125

Ala Gly Met Phe Ala Leu Glu Arg Phe Val Tyr Gly Pro Asn Pro Gly
 130 135 140

Gln Arg Lys Ser Trp Ser Pro Tyr Tyr Ala Asp Lys Leu Val Asp Ile
 145 150 155 160

Ala Glu Phe Tyr Gly Phe Asp Gly Trp Leu Ile Asn Ile Glu Ser Asp
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Phe Phe Pro Leu Tyr Arg Ser Pro Ser Met Lys Ala Lys His Leu Ala
 180 185 190

Lys Leu Leu Leu Tyr Leu Arg Asn Ala Met His Ala Arg Val Pro Gly

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225					230					235					240
Asp	Gly	Ile	Phe	Leu	Asn	Tyr	Trp	Trp	Asn	Ala	Thr	Tyr	Pro	Pro	Phe
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Ala	Met	Gln	Val	Ala	His	Tyr	Leu	Gly	Arg	Gln	Gly	Ser	Asp	Val	Tyr
			260					265					270		
Phe	Gly	Ser	Asp	Ile	Trp	Gly	Arg	Gly	Thr	Phe	Gly	Gly	Gly	Gly	Phe
		275					280					285			
Asp	Ser	Tyr	Leu	Ala	Val	Ala	Thr	Ala	Ser	Ala	Phe	Lys	Thr	Ser	Ser
	290					295					300				
Ala	Leu	Phe	Gly	Thr	Ala	Trp	Thr	Tyr	Glu	His	Phe	Glu	Lys	Lys	Asp
305					310					315					320
Phe	Glu	Leu	Met	Asp	Arg	Leu	Leu	Trp	Leu	Gly	Gly	Asp	Gln	Ser	Glu
				325					330					335	
Tyr	Pro	Ala	Gln	Ala	Glu	Gly	Gln	Glu	Ser	Ile	Ala	Lys	Ser	Gly	Ser
			340					345					350		
Arg	Leu	Gly	Arg	His	Pro	Gly	Ile	Thr	Asp	Val	Ala	Ala	Val	Arg	Ser
		355					360					365			
Ala	Pro	Gly	Arg	Arg	Trp	Phe	Val	Thr	Trp	Phe	Asp	Arg	Gly	His	Gly
	370					375					380				
Thr	Gly	Phe	Tyr	His	Gln	Gly	Lys	Lys	Leu	Leu	Ser	Gln	Pro	Trp	Ser
385					390					395					400
His	Leu	Ser	His	Gln	Ser	Ile	Pro	Pro	Asn	Leu	Val	Ala	Arg	Leu	Gln
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Arg	Lys	Glu	Asp	Asp	Gly	Val	Ser	Tyr	Phe	Leu	Ala	Asp	Asp	Asp	Ala
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Tyr Ile Gly Gly Thr Ser Leu Leu Ile Ala Ala Glu Gly Thr Gln Glu
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Arg Gln Ile Pro Leu Tyr Gln Leu Asn Tyr Asp Ala Thr Asn Gly Cys
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Glu Val Gln Phe Val Tyr Lys Ser Pro Glu Pro Asp Met Gln Ser Lys
465 470 475 480

Val Gln Ile Tyr Leu Asn Leu Arg Val Thr Asp Val Leu Pro Asp Glu
485 490 495

Leu Ala Tyr Tyr Trp His Asp Val Ala Ala Thr Ser Pro Gln Pro Gln
500 505 510

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

Leu Asn Thr Ser Lys Thr Gln Glu Leu Ala Glu Gly Trp Val Leu Cys
530 535 540

Ser Val Arg Val Pro Ser Val His Pro Leu Gly Glu Ala Ala Ile Glu
545 550 555 560

Glu Leu Gly Ile Tyr Leu Asp Gly Thr Glu Asp Val Leu Phe Arg Leu
565 570 575

Gly Leu Leu Thr Ile Val Pro Tyr Thr Asp Thr Ser Ser Thr Leu Ala
580 585 590

Ser Lys Ile Thr His Ile Gln Leu Gln Arg Asp Ala Asp Val Ser Ser
595 600 605

Lys Cys Leu Ser Ser Ser Cys Glu Leu Trp Ala Thr Leu Ser Trp Met
610 615 620

Met Glu Ser Asn Ser Ser Glu Glu Trp Asn Gln Val Asp His Tyr Leu
625 630 635 640

Ile Ser Tyr Gly Asp Ile Asn Ala Asp Gly Ala Ala Thr Phe Leu Gly
645 650 655

Thr Thr Phe Thr Thr Glu Tyr Arg Ile Ser Gly Leu Glu Met Lys Asn

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660
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<211> 701
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<220>
<223> The assumed amino acid sequence derived from publicly available
genomic DNA sequence of Rhizomucor pusillus strain CBS 183.67,
which has been assumed to be endo-beta-N-acetylglucosaminidase.
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Ser Met Pro Leu Gln Thr Met Asn Glu Leu Gly Ser Trp Glu Pro Ser
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35 40 45
Asn Leu Asp Pro Ala Glu Pro Arg Leu Ile Val Thr His Asp Met Ala
50 55 60
Gly Gly Tyr Lys Glu Asp Ser Asn Ile Gln Gly Asn Thr Tyr Asp Thr
65 70 75 80
Ile Tyr Ser Cys Gln Tyr Trp Gln Tyr Val Asp Thr Phe Ile Tyr Phe
85 90 95
Ser His His Arg Val Thr Ile Pro Pro Val Asn Trp Ile Asn Ala Cys
100 105 110
His Arg Asn Gly Val Lys Thr Leu Gly Thr Phe Ile Val Glu Gly Ala
115 120 125
Ala Gly Met Phe Ala Leu Glu Arg Phe Val Tyr Gly Pro Glu Pro Gly
130 135 140

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Gln Arg Asn Ser Trp Ser Pro Tyr Tyr Ala Asp Lys Leu Val Asp Ile
 145 150 155 160

Ala Glu Phe Tyr Gly Phe Asp Gly Trp Leu Leu Asn Ile Glu Ser Asp
 165 170 175

Phe Phe Pro Leu Tyr Arg Asn Pro Ser Leu Lys Ala Ile His Leu Ala
 180 185 190

Asn Thr Tyr Tyr Ile Arg Leu Leu Arg Tyr Leu Lys Asn Ala Met His
 195 200 205

Ala Arg Val Pro Gly Ser Glu Ile Ile Trp Tyr Asp Ser Met Thr Thr
 210 215 220

Asn Gly Ser Val Gln Trp Gln Asn Asn Ile Thr Pro Lys Asn Ser Ile
 225 230 235 240

Phe Phe Glu Ala Ala Asp Gly Ile Phe Leu Asn Tyr Trp Trp Asn Ala
 245 250 255

Thr Val Pro Pro Leu Ala Leu Gln Val Ala His Arg Leu Gly Arg Gln
 260 265 270

Gly Ser Asp Val Tyr Phe Gly Thr Asp Val Trp Gly Arg Gly Thr Phe
 275 280 285

Gly Gly Gly Gly Phe Asp Ser Tyr Leu Ala Val Gly Thr Ala Arg Ala
 290 295 300

Phe Lys Thr Ser Ser Ala Leu Phe Gly Thr Ala Trp Ile Tyr Glu His
 305 310 315 320

Phe Gly Lys Lys Asp Phe Glu Leu Met Asp Arg Leu Leu Trp Leu Gly
 325 330 335

Gly Asp Gln Ser Glu Tyr Pro Ala Gln Glu Gly Glu Gln Asn Arg Thr
 340 345 350

Val Lys Val Thr Ser His Leu Gly Arg His Pro Gly Ile Ala Asp Val
 355 360 365

Ser Pro Val Arg Ser Ala Pro Gly Lys Thr Trp Phe Ala Thr Trp Phe

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Ile	Ala	Arg	Leu	Gln	Arg	Glu	Glu	Asn	His	Gly	Leu	Ser	Tyr	Phe	Leu	
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Ala	Asp	Asp	Asp	Ala	Tyr	Ile	Gly	Gly	Thr	Ser	Leu	Leu	Ile	Ala	Ala	
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Val	Leu	Phe	Arg	Leu	Gly	Leu	Leu	Thr	Ile	Ile	Pro	Leu	Gly	Asp	Ala	
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Pro	Ser	Ala	Leu	Ser	Arg	Ile	Thr	Gln	Val	Gln	Leu	Gln	Arg	Asp	Glu	
		595					600					605				

Asp Ile His Ser Lys Cys Pro Ser Ser Ser Cys Glu Leu Trp Ala Thr
610 615 620

Leu Ser Trp Met Met Glu His Asn Ser Lys Glu Asp Trp Asp Gln Val
625 630 635 640

Asp His Tyr Met Ile Phe Phe Lys Asn Val Asp Ser Lys Ala Glu Pro
645 650 655

Ile Phe Leu Gly Thr Ser Phe Ser Thr Glu Tyr Arg Ile Ser Gly Leu
660 665 670

Glu Ile Lys Lys His Gly Asn Ser Ile Glu Ile Trp Ala Val Asn Arg
675 680 685

Leu Gly Thr Val Ile Ala Arg Gln Asp Ile Asp Ile Gln
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<211> 2091
<212> DNA
<213> Rhizomucor pusillus

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120

actattcctt tgcatacagcg atccaatctt gatccggcag agccgcgctt gatcgtaact
180

cacgatatgg ctggaggcta caaggaagac tcaaataattc agggcaatac gtatgataca
240

atztatagct gtcaatattg gcaatatgtg gatactttta tctattttctc gcatcatcga
300

gttacgatac ctctgtcaa ttggataaat gcatgccaca gaaacggtgt caaaacgcta
360

ggaacattca ttgtggaagg agctgcgggc atgtttgcct tggagagatt cgtctacgga
420

cctgagcctg gacagagaaa cagctggagc ccttactatg ctgataagct ggtggacata
480

gccgagtttt acggttttcga cggctggctg cttaacattg agagtgattt cttcccttta
540

tattcgaaatc cgtctctgaa agcgatccat ctagcaaagc tgctgcgata tctgaagaat
600

gcaatgcacg ccagagtgcc aggttcagag atcatctggt atgacagcat gacgacaaac
660

ggaagtgtgc agtggcaaaa caatatcacg cccaaaaatt ccatattttt tgaagctgca
720

gatggcatat ttttaaatta ttggtggaac gcgacggttc cgccggttggc tttgcaagta
780

gcacatcgtc taggacgtca aggatctgat gtatactttg gaacggatgt ttggggacga
840

ggaacattcg gtggtggcgg attcgattca tatctcgctg ttggcactgc gagggcattc
900

aaaacatcat ctgcgctttt cggcacagca tggatctatg agcatttttg gaagaaagat
960

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1020

gaaggagagc agaatcgcac agtaaaagtt acatcccatc ttggaagaca tcctggtatc
1080

gccgatgtgt caccggtgcg aagtgctcca gggaaaacat ggttcgcaac gtggtttgat
1140

agaggttacg gaacagggtt ctattatcag ggcaagaaac tattatcaca gccgtggtcg
1200

catttatcgc atcaatctat cccgccgaat cttatagcca gattacagag agaagaaaat
1260

cacggccttt cgtatttctt ggcagacgac gatgcataca tcgggggaac ttcgctgtta
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1380

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1440

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1620

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1680

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1740

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1800

agggatgagg atatccatag taaatgtcca tcctcctcat gcgaactttg ggccacactc
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1980

gagtacagaa tatcaggcct ggagatcaag aaacacggaa attccatcga gatatgggca
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2091

<210> 9

<211> 2109

<212> DNA

<213> Artificial Sequence

<220>

<223> Optimized DNA sequence for expression of Endo-Rp in E. coli

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120

accattccgc tgcattcagcg tagcaatctg gatccggcag aaccgctct gattgttacc
180

catgatatgg caggcggtta taaagaagat agcaatattc agggcaacac ctatgatacc
240

atztatagct gtcagtattg gcagtatgtg gacaccttta tctattttag ccatcaccgt
300

gttaccattc ctccgggttaa ttggattaat gcctgtcatc gtaatgggtg taaaaccctg
360

ggcaccttta ttgttgaagg tgcagcaggt atgtttgcac tggaacgttt tgtttatggg
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ccggaaccgg gtcagcgtaa tagctgggtc ccgtattatg cagataaaact ggttgatata
480

gccgagtttt atgggttttga tggttggtg ctgaacatcg aaagcgattt ttttccgctg
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tattcgtaatc cgagcctgaa agcaattcat ctggcaaaac tgctgcgcta tctgaaaaat
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780

gcacatcgtc tgggtcgtca gggtagtgat gtttattttg gcaccgatgt ttggggtcgt
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1020

gaaggtgaac agaatcgtac cgtaaagtt accagccatc tgggtcgcca tccgggtatt
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gcagatgtta gtccggttcg tagcgcaccg ggtaaaacct ggtttgcaac atggtttgat
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1200

catctgagcc atcagagcat tccgcctaata ctgattgcac gcctgcagcg tgaagaaaat
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1320

attgcagcag aaattaccca agaacgtcag ctgcctctgt atcagctgga atatgatgtt
1380

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1440

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1500

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1560

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1680

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1800

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1980

gaatatcgta ttagcgggtct ggaaatcaaa aaacatggca acagcattga aatctgggca
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2109

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<211> 2091
<212> DNA
<213> Rhizomucor pusillus

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240

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480

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660

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720

gatggcatat ttttaaatta ttggtggaac gcgacggttc cgccggttggc tttgcaagta
780

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840

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aaaacatcat ctgcgctttt cggcacagca tggatctatg agcatttttg gaagaaagat
960

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1020

gaaggagagc agaatcgcac agtaaaagtt acatcccatc ttggaagaca tcctggtatc
1080

gccgatgtgt caccggtgcg aagtgctcca gggaaaacat ggttcgcaac gtggtttgat
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1200

catttatcgc atcaatctat cccgccgaat cttatagcca gattacagag agaagaaaat
1260

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1320

atagcagccg aaatcactca agaacgcaa ttgccgctct atcaactaga gtatgacgtt
1380

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1440

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1500

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1620

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1680

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1800

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1920

ttcttcaaaa atgttgattc caaggcagaa cctattttcc ttggcaccag cttcagtacc
1980

gagtacagaa tatcaggcct ggagatcaag aaacacggaa attccatcga gatatgggca
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2091

<210> 11

<211> 2109

<212> DNA

<213> Artificial Sequence

<220>

<223> Optimized DNA sequence for expression of Endo-Rp2 in E. coli

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120

accattccgc tgcattcagcg tagcaatctg gatccggcag aaccgctct gattgttacc
180

catgatatgg caggcgggta taaagaagat agcaatattc agggcaacac ctatgatacc
240

atztatagct gtcagtattg gcagtatgtg gacaccttta tctattttag ccatcaccgt
300

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360

ggcaccttta ttgttgaagg taccgcaggt atgtttgcac tggaacgttt tgtttatggg
420

ccggaaccgg gtcagcgtaa tagctgggtc ccgtattatg cagataaaact ggttgatata
480

gccgagtttt atgggttttga tggttggtg ctgaacatcg aaagcgattt ttttccgctg
540

tattcgtaatc cgagcctgaa agcaattcat ctggcaaaac tgctgcgcta tctgaaaaat
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720

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780

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900

aaaaccagca gcgcactggt tggtagagca tggatttatg aacacttcgg caaaaaagac
960

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1020

gaaggtgaac agaatcgtac cgtaaagtt accagccatc tgggtcgcca tccgggtatt
1080

gcagatgtta gtccggttcg tagcgcaccg ggtaaaacct ggtttgcaac atggtttgat
1140

cgtgggttatg gcaccgggtt ctattatcag ggtaaaaaac tgctgagcca gccgtggtca
1200

catctgagcc atcagagcat tccgcctaata ctgattgcac gcctgcagcg tgaagaaaat
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1320

attgcagcag aaattaccca agaacgtcag ctgcctctgt atcagctgga atatgatgtt
1380

accgaaggtt gcgaagtga gttcatctat aaaagccctg aaccggatat gcagggcaaa
1440

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1500

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1560

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1620

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1680

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1800

cgtgatgaag atattcatag caaatgtccg agcagcagct gtgaactgtg ggcaaccctg
1860

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1920

tttttcaaaa acgtggatag caaagccgaa ccgatttttc tgggcaccag ctttagcacc
1980

gaatatcgta ttagcgggtct ggaaatcaaa aaacatggca acagcattga aatctgggca
2040

gttaatcgcc tgggcacagt tattgcacgt caggatattg atattcagca tcacaccat
2100

caccattaa
2109

<210> 12
<211> 2091
<212> DNA
<213> Rhizomucor pusillus

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cagactatga atgagcttgg ttcttgggaa cctagcaatg cctcgcgagc caacattgca
120

actattcctt tgcacacgag atccaatctt gatccggcag agccgcgctt gatcgtaact
180

cacgatatgg ctggaggcta caaggaagac tcaaataatc agggcaatac gtatgataca
240

atttatagct gtcaatattg gcaatatgtg gatactttta tctattttctc gcatcatcga
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gttacgatac ctctgtcaa ttggataaat gcatgccaca gaaacgggtg caaaacgcta
360

ggaacattca tcgtggaagg agctgcgggc atgtttgcct tggagagatt cgtctacgga
420

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480

gccgagtttt acggttttga cggctggctg cttaacattg agagtgattt cttcccttta
540

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 660
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 720
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 780
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 aaaacatcat ctgcgctttt cggcacagca tggatctatg agcatttttg gaagaaagat
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 1680

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1800

agggatgagg atatccatag taaatgttca tcctcctcat gcgaactttg ggccacactc
1860

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1920

ttcttcaaaa atgttgattc caaggcagaa cctattttcc ttggcaccag cttcagtacc
1980

gagtacagaa tatcaggcct ggagatcaag aaacacggaa attccatcga gatatgggca
2040

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2091

<210> 13

<211> 2109

<212> DNA

<213> Artificial Sequence

<220>

<223> Optimized DNA sequence for expression of Endo-Rp3 in E. coli

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cagaccatga atgaactggg tagctgggaa ccgagcaatg caagccgtgc aaatattgca
120

accattccgc tgcacacgag tagcaatctg gatccggcag aaccggtct gattgttacc
180

catgatatgg caggcggtta taaagaagat agcaatattc agggcaacac ctatgatacc
240

atttatagct gtcagtattg gcagtatgtg gacaccttta tctattttag ccatcaccgt
300

gttaccattc ctccgggtta ttggattaat gcctgtcatc gtaatgggtg taaaaccctg
360

ggcaccttta ttgttgaagg tgcagcaggt atgtttgcac tggaacgttt tgtttatggg
420

ccggaaccgg gtcagcgtaa tagctgggtc ccgtattatg cagataaaact ggttgatata
480

gccgagtttt atgggttttga tggttggtg ctgaacatcg aaagcgattt ttttccgctg
540

tatcgtaatc cgagcctgaa agcaattcat ctggcaaaac tgctgcgcta tctgaaaaat
 600

gcaatgcatg cacgtgttcc gggtagcgaa attatctggt atgatagcat gaccaccaat
 660

ggtagcgttc agtggcagaa taacattacc ccgaaaaaca gcatcttttt tgaagcagcc
 720

gatggcatct ttctgaatta ttggtggaat gcaaccgttc ctccgctggc actgcaggtt
 780

gcacatcgtc tgggtcgtca gggtagtgat gtttattttg gcaccgatgt ttggggtcgt
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 900

aaaaccagca gcgcactggt tggtagagca tggatttatg aacacttcgg caaaaaagac
 960

ttcgaactga tggatcgtct gctgtggctg ggtggtggtc agagcgaata tccggcacia
 1020

gaaggtgaac agaatcgtac cgtaaagtt accagccatc tgggtcgcca tccgggtatt
 1080

gcagatgtta gtccggttcg tagcgcaccg ggtaaaacct ggtttgcaac atggtttgat
 1140

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 1200

catctgagcc atcagagcat tccgcctaata ctgattgcac gcctgcagcg tgaagaaaat
 1260

catggcctga gctattttct ggcagatgat gatgcatatc tgggtggcac cagcctgctg
 1320

attgcagcag aaattaccca agaacgtcag ctgcctctgt atcagctgga atatgatgtt
 1380

accgaaggtt gcgaagtgca gttcatctat aaaagccctg aaccggatat gcagggcaaa
 1440

attgatatct atctgaatct gcaggttacc gatatcctgc cggatgaact ggcattttat
 1500

tggcaggacg ttaccgatgc aagcagccag gcagatgcaa ccaccgcaat gcgtctgtat
 1560

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 1680

gaactgggca ttcatgtgga tggtagcgaa accgttctgt ttcgcctggg tctgctgacc
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1800

cgtgatgaag atattcatag caaatgtagc agcagcagct gtgaactgtg ggcaaccctg
1860

agctggatga tggaacgtaa tagcaaagaa gattgggatc aggtcgatca ctacatgatc
1920

tttttcaaaa acgtggatag caaagccgaa ccgatttttc tgggcaccag ctttagcacc
1980

gaatatcgta ttagcgggtct ggaaatcaaa aaacatggca acagcattga aatctgggca
2040

gttaatcgcc tgggcacagt tattgcacgt caggatattg atattcagca tcacaccat
2100

caccattaa
2109

<210> 14
<211> 2091
<212> DNA
<213> Rhizomucor pusillus

<400> 14
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cagactatga atgagcttgg ttcttgggaa cctagcaatg cctcgcgagc caacattgca
120

actattcctt tgcacacgag atccaatcct gatccggcag agccgcgctt gatcgtaact
180

cacgatatgg ctggaggcta caaggaagac tcaaataattc agggcaatac gtatgataca
240

atttatagct gtcaatattg gcaatatgtg gatactttta tctattttctc gcatcatcga
300

gttacgatac ctctgtcaa ttggataaat gcatgccaca gaaacgggtgt caaaacgcta
360

ggaacattca ttgtggaagg agctgcgggc atgtttgcct tggagagatt cgtctacgga
420

cctgagcctg gacagagaaa cagctggagc ccttactatg ctgataagct ggtggacata
480

gccgagtttt acggttttga cggctggctg cttaacattg agagtgattt tttcccttta
540

tatcgaaatc cgtctctgaa agcgatccat ctagcaaagc tgctgcgata tctgaagaat
 600

gcaatgcacg ccagagtgcc aggttcagag atcatctggt atgacagcat gacgacaaac
 660

ggaagtgtgc agtggcaaaa caatatcacg cccaaaaatt ccatatTTTT tgaagctgca
 720

gatggcatat ttttaaatta ttggtggaac gcgacggttc cgccgttggc tttgcaagta
 780

gcacatcgtc taggacgtca aggatctgat gtatactttg gaacggatgt ttggggacga
 840

ggaacattcg gtggtggcgg attcgattca tatctcgctg ttggcactgc gagggcattc
 900

aaaacatcat ctgcgctttt cggcacagca tggatctatg agcatttttg gaagaaagat
 960

tttgagctta tggatagact tttgtggtta ggtggtgatc aatcagaata tccagctcag
 1020

gaaggagagc agaatcgcac agtaaaagtt acatcccatc ttggaagaca tcctggtatc
 1080

gccgatgtgt caccggtgcg aagtgtcca gggaaaacat ggttcgcaac gtggtttgat
 1140

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 1200

catttatcgc atcaatctat cccgccgaat cttatagcca gattacagag agaagaaaat
 1260

cacggccttt cgtatttctt ggcagacgac gatgcataca tcgggggaac ttcgctgtta
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atagcagccg aaatcactca agaacgcaa ttgccgctct atcaactaga gtatgacgct
 1380

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 1440

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 1500

tggcaagatg ttacggatgc ttctcccag gccgatgcaa cgacagccat gcgtttatat
 1560

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 1620

tggttgctct gttccgtgcg tgtgccacct acttatccac ttggtatcgc aacgatcaag
 1680

gaactagggga tccatgtgga tggtagacagaa acagtgcctat ttaggctggg tctccttaca
1740

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1800

agggatgagg atatccatag taaatgtcca tcctcctcat gcgaactttg ggccacactc
1860

tcgtggatga tggaacacaa ctcaaaagag gactgggacc aggtcgatca ctatatgatt
1920

ttcttcaaaa atgttgattc caaggcagaa cctatcttcc ttggcaccag cttcagtacc
1980

gagtacagaa tatcaggcct ggagatcaag aaacacggaa attccatcga gatatgggca
2040

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<210> 15

<211> 2109

<212> DNA

<213> Artificial Sequence

<220>

<223> Optimized DNA sequence for expression of Endo-Rp4 in E. coli

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120

accattccgc tgcattcagcg tagcaatctg gatccggcag aaccgctct gattgttacc
180

catgatatgg caggcgggta taaagaagat agcaatattc agggcaacac ctatgatacc
240

atztatagct gtcagtattg gcagtatgtg gacaccttta tctatcttag ccatcaccgt
300

gttaccattc ctccgggttaa ttggattaat gcctgtcatc gtaatgggtg taaaaccctg
360

ggcaccttta ttgttgaagg tgcagcaggt atgtttgcac tggaacgttt tgtttatggg
420

ccggaaccgg gtcagcgtaa tagctgggtc ccgtattatg cagataaaact ggttgatata
480

gccgagtttt atgggttttga tgggtggctg ctgaacatcg aaagcgattt ttttccgctg
540

tatcgtaatc cgagcctgaa agcaattcat ctggcaaaac tgctgcgcta tctgaaaaat
 600

gcaatgcatg cacgtgttcc gggtagcgaa attatctggg atgatagcat gaccaccaat
 660

ggtagcgttc agtggcagaa taacattacc ccgaaaaaca gcatcttttt tgaagcagcc
 720

gatggcatct ttctgaatta ttgggtggaat gcaaccgttc ctccgctggc actgcaggtt
 780

gcacatcgtc tgggtcgta gggtagtgat gtttattttg gcaccgatgt ttggggtcgt
 840

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 900

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 960

ttcgaactga tggatcgctc gctgtggctg ggtgggtgat agagcgaata tccggcacia
 1020

gaaggtgaac agaatcgta cgttaaagtt accagccatc tgggtcgcca tccgggtatt
 1080

gcagatgtta gtccggttcg tagcgaccg ggtaaaacct ggtttgcaac atggtttgat
 1140

cgtgggttatg gcaccgggtt ctattatcag ggtaaaaaac tgctgagcca gccgtgggtc
 1200

catctgagcc atcagagcat tccgccta atctgattgcac gcctgcagcg tgaagaaaat
 1260

catggcctga gctattttct ggcagatgat gatgcatata ttgggtggcac cagcctgctg
 1320

attgcagcag aaattaccca agaacgtcag ctgcctctgt atcagctgga atatgatgca
 1380

accgaagggt gcgaagtga gttcatctat aaaagccctg aaccggatat gcagggcaaa
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 1500

tggcaggacg ttaccgatgc aagcagccag gcagatgcaa ccaccgcaat gcgtctgtat
 1560

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 1680

gaactgggca ttcatgtgga tggtagcgaa accgttctgt ttcgcctggg tctgctgacc
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1800

cgtgatgaag atattcatag caaatgtccg agcagcagct gtgaactgtg ggcaaccctg
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1920

tttttcaaaa acgtggatag caaagccgaa ccgatttttc tgggcaccag ctttagcacc
1980

gaatatcgta ttagcgggtct ggaaatcaaa aaacatggca acagcattga aatctgggca
2040

gttaatcgcc tgggcacagt tattgcacgt caggatattg atattcagca tcacaccat
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caccattaa
2109

<210> 16
<211> 2091
<212> DNA
<213> Rhizomucor pusillus

<400> 16
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cagactatga atgagcttgg ttcttgggaa cctagcaatg cctcgcgagc caacattgca
120

actattcctt tgcacacgag atccaatctt gatccggcag agccgcgctt gatcgtaact
180

cacgatatgg ctggaggcta caaggaagac tcaaatatc agggcaatac gtatgataca
240

atztatagct gtcaatattg gcaatatgtg gatactttta tctattttctc gcatcatcga
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420

cctgagcctg gacagagaaa cagctggagc cttactatg ctgataagct ggtggacata
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540

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 780

gcacatcgtc taggacgtca aggatctgat gtatactttg gaacggatgt ttggggacga
 840

ggaacattcg gtggtggcgg attcgattca tatctcgctg ttggcactgc gagggcattc
 900

aaaacatcat ctgcgctttt cggcacagca tggatctatg agcatttttg gaagaaagat
 960

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 1020

gaaggagagc agaatcgcac agtaaaagtt acatcccatc ttggaagaca tcctggtatc
 1080

gccgatgtgt caccggtgcg aagtgtcca gggaaaacat ggttcgcaac gtggtttgat
 1140

agaggttacg gaacaggttt ctattatcag ggcaagaaac tattatcaca gccgtggtcg
 1200

catttatcgc atcaatctat cccgccgaat cttatagcca gattacagag agaagaaaat
 1260

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atagcagccg aaatcactca agaacgcaa ttgccgtct atcaactaga gtatgacgtt
 1380

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 1500

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gaactagggga tccatgtgga tggtagacagaa acagtgcctat ttaggctggg tctccttaca
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1800

agggatgagg atatccatag taaatgtcca tcctcctcat gcgaactttg ggccacactc
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1920

ttcttcaaaa atgttgattc caaggcagaa cctatcttcc ttggcaccag cttcagtacc
1980

gagtacagaa tatcaggcct ggagatcaag aaacacggaa attccatcga gatatgggca
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gtaaatcgct taggaaccgt cattgcacgg caagacatcg atatccaata g
2091

<210> 17

<211> 2109

<212> DNA

<213> Artificial Sequence

<220>

<223> Optimized DNA sequence for expression of Endo-Rp5 in E. coli

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120

accattccgc tgcacacagc tagcaatctg gatccggcag aaccgctct gattgttacc
180

catgatatgg caggcgggta taaagaagat agcaatattc agggcaacac ctatgatacc
240

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300

gttaccattc ctccgggtta ttggattaat gcctgtcatc gtaatgggtg taaaaccctg
360

ggcaccttta ttgttgaagg tgcagcaggt atgtttgcac tggaacgttt tgtttatggg
420

ccggaaccgg gtcagcgtaa tagctgggtc ccgtattatg cagataaaact ggttgatata
480

gccgagtttt atgggttttga tggttggtg ctgaacatcg aaagcgattt ttttccgctg
540

tattcgtaatc cgagcctgaa agcaattcat ctggcaaaac tgctgcgcta tctgaaaaat
600

gcaatgcatg cacgtgttcc gggtagcgaa attatctggt atgatagcat gaccaccaat
660

ggtagcgttc agtggcagaa taacattacc ccgaaaaaca gcatcttttt tgaagcagcc
720

gatggcatct ttctgaatta ttggtggaat gcaaccgttc ctccgctggc actgcaggtt
780

gcacatcgtc tgggtcgta gggtagtgat gtttatcttg gcaccgatgt ttggggtcgt
840

ggcacctttg gtggtggtgg ctttgatagt tatctggcag ttggcaccgc acgtgcattt
900

aaaaccagca gcgcactggt tggtagagca tggatttatg aacacttcgg caaaaaagac
960

ttcgaactga tggatcgctc gctgtggctg ggtggtgatc agagcgaata tccggcacia
1020

gaaggtgaac agaatcgta cgttaaagtt accagccatc tgggtcgcca tccgggtatt
1080

gcagatgtta gtccggttcg tagcgcaccg ggtaaaacct ggtttgcaac atggtttgat
1140

cgtgggttatg gcaccgggtt ctattatcag ggtaaaaaac tgctgagcca gccgtggta
1200

catctgagcc atcagagcat tccgcctaatt ctgattgcac gcctgcagcg tgaagaaaat
1260

catggcctga gctatcttct ggcagatgat gatgcatata ttggtggcac cagcctgctg
1320

attgcagcag aaattaccca agaacgtcag ctgcctctgt atcagctgga atatgatgtt
1380

accgaaggtt gcgaagtga gttcatctat aaaagccctg aaccggatat gcagggcaaa
1440

attgatattc atctgaattc gcaggttacc gatatcctgc cggatgaact ggcattttat
1500

tggcaggacg ttaccgatgc aagcagccag gcagatgcaa ccaccgcaat gcgtctgtat
1560

ctgaatgaaa ataccgtgat ttatctgaaa ccgagccgta aacaagaact ggcggaaggc
1620

tggctgctgt gtagcggttcg tgttccgcct acctatccgc tgggtattgc caccattaaa
1680

gaactgggca ttcatgtgga tggtagcgaa accgttctgt ttcgcctggg tctgctgacc
1740

attatccgcg tgggtgatgc accgagcgca ctgagccgta ttaccaggt tcagctgcaa
1800

cgtgatgaag atattcatag caaatgtccg agcagcagct gtgaactgtg ggcaaccctg
1860

agctggatga tggaacataa tagcaaagaa gattgggatc aggtcgatca ctacatgatc
1920

tttttcaaaa acgtggatag caaagccgaa ccgatttttc tgggcaccag ctttagcacc
1980

gaatatcgta ttagcgggtct ggaaatcaaa aaacatggca acagcattga aatctgggca
2040

gttaatcgcc tgggcacagt tattgcacgt caggatattg atattcagca tcatcaccat
2100

caccattaa
2109

<210> 18
<211> 2094
<212> DNA
<213> Rhizomucor miehei

<400> 18
atgccctcac tcgaacttca gcaagccgtg gacacaagac tcttcgagtc aacaccactt
60

atgactatgg atgagcttgg ctctgggat cctagcaatg ctttgcgagc cagcattgcg
120

acagttcctc tgcacccgag accaagcatc gatccgacag aaccacgctt gattgtgaca
180

cacgatatgg caggaggcta caaggaagac tttagtattc agggcaatgc atatgacacc
240

gtttacacct gccaatattg gcaatacgtg gacattttta tctacttctc gcatcatcga
300

gttacgatac caccgtaaa ctggacgaat gcttgccaca ggaacggtgt caaaagtctc
360

ggaacattta ttgttgaagg agcagcaggc atgtttgccc tggagagggt cgtgtatggc
420

cctaaccctg ggcaaaggaa gagctggagc ccatattatg cagataagct agtggacatt
480

gccgaatttt atggtttcga tggatggttg atcaatattg aaagcgattt tttccctctg
540

tatcgaagcc cgtcaatgaa ggcgaaacat ttggcaaagc tgctgctata tctcaggaat
 600

gctatgcatg ccagagtacc gggttcgcag atcatctggt atgacagcat gaccacaagt
 660

ggatacgttc aatggcaaaa caatattaca cctcagaatg agatattctt tgaggctgcc
 720

gatggtatat ttttgaatta ctggtggaat gcaacatacc caccttttgc catgcaggta
 780

gcgcattatc tgggtcgcca aggatccgat gtatactttg gttctgacat ttggggacga
 840

ggaacttttg gtggtggtgg cttcgattca tacctggcag ttgctaccgc gagtgctttt
 900

aagacgtcat ctgcactttt cggcacagca tggacttatg aacattttga aaagaaggac
 960

tttgagctga tggataggct actgtggtta ggcggtgatc aatcagagta tccagctcaa
 1020

gcagaagggc aggaaagcat agcaaagtct gggtcgcgac tcggaagaca cccaggcatt
 1080

accgatgtgg ctgcagttcg tagcgctcca ggtcgaagat ggtttgtaac ttggttcgat
 1140

agaggacatg gaaccggttt ctatcatcaa ggaaagaaac tactatcaca accatggtcc
 1200

catttgcttc atcaatctat accgcccaat ctcgtcgcca gactgcaaag gaaagaagat
 1260

gacggcgttt cgtacttctt ggccgacgat gatgcttaca ttggaggaac gtctctatta
 1320

atagcagcag agggtagcca agaacgtcag ataccacttt atcaactgaa ttatgacgcc
 1380

acaaacggat gtgaagtgca gtttgtttat aagtccccag agccggatat gcaaagcaaa
 1440

gtgcagatat atttgaacct cagagtgaca gatgttctac ctgacgaact cgcttactac
 1500

tggcacgacg ttgcagctac ctctccccag cctcaggcaa caacagcctc gcgtttgaac
 1560

atcaacgaag acaccagtgt ttatttgaat acttcgaaga cgcaagaatt ggcagaaggc
 1620

tgggtgttgt gctccgttcg agtgccatct gttcacccgc taggcgaagc tgcaattgaa
 1680

gaattaggaa tctatattgga cggaactgag gatgtgctgt tcagattggg gcttttgact
1740

atcgtgccct acacagatac gtcattctact cttgcaagca aaataactca catccagctt
1800

caaagggatg cagacgtcag cagtaaatgc ttatcatctt cgtgcgaact ctgggctacg
1860

ttatcctgga tgatggagtc gaattctagt gaggaatgga accaagtcga tcactatctc
1920

atttcctacg gagatatcaa tgctgatggg gcagctacat ttctcggtac tactttcact
1980

acagagtata ggatatcagg tctggagatg aagaatgaca tcgactatat ccaaatttcg
2040

gcagtgagcc gcctaggcaa tataacttgca cagcaaacga tcggcataca gtag
2094

<210> 19

<211> 2112

<212> DNA

<213> Artificial Sequence

<220>

<223> Optimized DNA sequence for expression of Endo-Rm in E. coli

<400> 19

atgccgagcc tggaactgca gcaggcagtt gatacccgtc tgtttgaaag cacaccgctg
60

atgaccatgg atgaactggg tagctgggat ccgagcaatg cactgcgtgc aagcattgca
120

accgttccgc tgcattccgc tccgagcatt gatccgaccg aaccgcgtct gattgttacc
180

catgatatgg caggcgggta taaagaagat tttagcattc agggcaacgc ctatgatacc
240

gtttatacct gtcagtattg gcagtatgtg gacatcttta tctatatttag ccatcaccgt
300

gttaccattc cgctgttaa ttggaccaat gcatgtcatc gtaatgggtg taaaagcctg
360

ggcaccttta ttgttgaagg tgcagcaggt atgtttgcac tggaacgttt tgtttatggg
420

ccgaatccgg gtcagcgtaa aagctgggtc ccgtattatg cagataaact ggttgatata
480

gccgagtttt atggttttga tggttggtg attaacatcg agagcgattt ttttccgctg
540

tatcgtagcc cgagcatgaa agcaaaacat ctggcaaaac tgctgctgta tctgcgtaat
 600

gcaatgcatg cccgtgttcc gggtagccag attattttgt atgatagcat gaccaccagt
 660

ggttatgttc agtggcagaa taacattaca ccgcagaacg aaatcttttt tgaagcagcc
 720

gatggcatct ttctgaatta ttggtggaat gcaacctatc cgccttttgc aatgcaggtt
 780

gcacattatc tgggtcgtca gggtagtgat gtttattttg gtagcgatat ttggggtcgt
 840

ggcacctttg gtggtggtgg ctttgatagt tatctggcag ttgcaaccgc aagcgcatth
 900

aaaaccagca gcgcactgtt tggcaccgca tggacctatg aacattttga gaaaaaagac
 960

ttcgagctga tggatcgtct gctgtggctg ggtggtgatc agagcgaata tccggcacag
 1020

gcagaaggtc aagaaagcat tgccaaaagc ggtagccgtc tgggtcgcca tccgggtatt
 1080

accgatgttg cagcagttcg tagcgcaccg ggtcgtcgtt ggtttggttac ctggtttgat
 1140

cgtggtcatg gcaccgggtt ttatcatcag ggtaaaaaac tgctgagcca gccgtggtca
 1200

catctgagcc atcagagcat tcctccgaat ctggttgcac gtctgcagcg caaagaagat
 1260

gacggcgtta gctattttct ggcagatgat gatgcatata ttggtggcac cagcctgctg
 1320

attgcagcag aaggcaccca agaacgtcag attcctctgt atcagctgaa ttatgatgca
 1380

accaatgggt gtgaagtgca gttcgtgtat aaaagtccgg aaccggatat gcagagcaaa
 1440

gttcagatth atctgaatct gcgtgtgacc gatgttctgc cggatgagct ggcatattat
 1500

tggcatgatg ttgccgcaac cagtccgcag ccgcaggcaa ccaccgcaag ccgtctgaat
 1560

attaacgaag ataccagcgt gtatctgaac accagcaaaa cacaagaact ggccgaaggt
 1620

tgggttctgt gtagcgttcg tgttccgagc gttcatccgc tgggtgaagc agcaattgaa
 1680

gaactgggca tttatctgga tggcaccgaa gatgttctgt ttcgcctggg tctgctgacc
1740

attgttccgt ataccgatac cagcagcacc ctggcaagca aaatcaccca tattcagctg
1800

cagcgtgatg cagatgttag cagcaaatgt ctgagcagca gctgtgaact gtgggcaacc
1860

ctgagctgga tgatggaaag caatagcagc gaagaatgga atcaggtgga tcattatctg
1920

attagctatg gcgatattaa tgcagatggg gcagccacct ttctggggcac cacctttacc
1980

accgaatatc gtattagcgg tctggaaatg aaaaacgaca tcgattacat tcagattagc
2040

gcagttagtc gtctgggtaa tattctggcc cagcagacca ttggtattca gcatcatcac
2100

catcaccact aa
2112

<210> 20
<211> 2106
<212> DNA
<213> Artificial Sequence

<220>
<223> The assumed DNA sequence derived from publicly available genomic
DNA sequence of *Rhizomucor pusillus* strain CBS 183.67, which has
been assumed to encode endo-beta-N-acetylglucosaminidase.

<400> 20
atgccttcac tcgaactaca gcaagctgct gacacgagac ttttcgagtc tatgccactt
60

cagactatga atgagcttgg ttcttgggaa cctagcaatg cctcgcgagc caacattgca
120

actattcctt tgcatacagc atccaatctt gatccggcag agccgcgctt gatcgtaact
180

cacgatatgg ctggaggcta caaggaagac tcaaatatc agggcaatac gtatgatata
240

atttatagct gtcaatattg gcaatatgtg gatactttta tctattttctc gcatcatcga
300

gttacgatac ctctgtcaa ttggataaat gcatgccaca gaaacggtgt caaaacgcta
360

ggaacattca ttgtggaagg agctgcgggc atgtttgcct tggagagatt cgtctacgga
420

cctgagcctg gacagagaaa cagctggagc ccttactatg ctgataagct ggtggacata
480

gccgagtttt acggttttcga cggctggctg cttaacattg agagtgattt cttcccttta
540

tatcgaaatc cgtctctgaa agcgatccat ctagcaaata catattatat aaggctgctg
600

cgatatctga agaatgcaat gcacgccaga gtgccagggt cagagatcat ctggtatgac
660

agcatgacga caaacggaag tgtgcagtgg caaaacaata tcacgccccaa aaattccata
720

ttttttgaag ctgcagatgg catattttta aattattggt ggaacgcgac ggttccgccg
780

ttggctttgc aagtagcaca tcgtctagga cgtcaaggat ctgatgtata ctttggaaacg
840

gatgtttggg gacgaggaac attcgggtgt ggcggattcg attcatatct cgctgttggc
900

actgcgaggg cattcaaaac atcatctgcg cttttcggca cagcatggat ctatgagcat
960

tttggaaga aagattttga gcttatggat agacttttgt ggtaggtgg tgatcaatca
1020

gaatatccag ctcaggaagg agagcagaat cgcacagtaa aagttacatc ccatcttggc
1080

agacatcctg gtatcgccga tgtgtcaccg gtgcgaagtg ctccagggaa aacatggttc
1140

gcaacgtggt ttgatagagg ttacggaaca ggtttctatt atcagggcaa gaaactatta
1200

tcacagccgt ggtcgcattt atcgcatcaa tctatcccgc cgaatcttat agccagatta
1260

cagagagaag aaaatcacgg cttttcgtat ttcttggcag acgacgatgc atacatcggg
1320

ggaacttcgc tgtaaatagc agccgaaatc actcaagaac gccaatggcc gctctatcaa
1380

ctagagtatg acgttactga aggctgagag gtgcagttta tatacaagtc tccggaacca
1440

gatatgcaag gaaaaataga tatatatttg aacttgcaag ttacagacat actgcctgat
1500

gagctagcct ttactggca agatgttacg gatgcttcct ccagggccga tgcaacgaca
1560

gccatgcgtt tataatctaaa cgaaaacaca gttatattatc taaagccgtc caggaaacaa
1620

gagctagccg aaggctgggt gctctgttcc gtgcgtgtgc cacctactta tccacttggt
1680

atcgcaacga tcaaggaact agggatccat gtggatggta cagaaacagt gctatttagg
1740

ctgggtctcc ttacaattat accccttgga gatgcgccgt ctgcgctttc cagaattacc
1800

cagggtccagc ttcaaaggga tgaggatata catagtaaata gtccatcctc ctcatgcgaa
1860

ctttgggcca cactctcgtg gatgatggaa cacaactcaa aagaggactg ggaccaggtc
1920

gatcactata tgattttctt caaaaatggt gattccaagg cagaacctat tttccttggc
1980

accagcttca gtaccgagta cagaatatca ggccctggaga tcaagaaaca cggaaattcc
2040

atcgagatat gggcagtaaa tcgcttagga accgtcattg cacggcaaga catcgatatc
2100

caatag
2106

<210> 21
<211> 2124
<212> DNA
<213> Artificial Sequence

<220>
<223> Optimized DNA sequence for expression of the assumed amino acid
sequence of SEQ ID NO:7 in E. coli

<400> 21
atgccgagcc tggaactgca gcaggcagca gatacccgtc tgtttgaaag catgccgctg
60

cagaccatga atgaactggg tagctgggaa ccgagcaatg caagccgtgc aaatattgca
120

accattccgc tgcatacgcg tagcaatctg gatccggcag aaccgcgtct gattgttacc
180

catgatatgg caggcgggta taaagaagat agcaatattc agggcaacac ctatgatacc
240

atttatagct gtcagtattg gcagtatgtg gacaccttta tctatttttag ccatcaccgt
300

gttaccattc ctccgggttaa ttggattaat gcctgtcatc gtaatgggtg taaaaccctg
360

ggcaccttta ttgttgaagg tgcagcaggt atgtttgcac tggaacgttt tgtttatggt
420

ccggaaccgg gtcagcgtaa tagctgggtca ccgtattatg cagataaact ggttgatatc
480

gccgagtttt atggttttga tggttggctg ctgaacatcg aaagcgattt ttttccgctg
540

tatcgtaatc cgagcctgaa agcaattcat ctggcaaaca cctattatat ccgtctgctg
600

cgctatctga aaaatgcaat gcatgcacgt gttccgggta gcgaaattat ctggtatgat
660

agcatgacca ccaatggtag cgttcagtgg cagaataaca ttaccccgaa aaacagcatc
720

ttttttgaag cagccgatgg catctttctg aattattggt ggaatgcaac cgttcctccg
780

ctggcactgc aggttgcaca tcgtctgggt cgtcagggta gtgatgttta ttttggcacc
840

gatgtttggg gtcgtggcac ctttgggtgg ggtggctttg atagttatct ggcagttggc
900

accgcacgtg catttaaaac cagcagcgca ctgtttggta cagcatggat ttatgaacac
960

ttcggcaaaa aagacttcga actgatggat cgtctgctgt ggctgggtgg tgatcagagc
1020

gaatatccgg cacaagaagg tgaacagaat cgtaccgtta aagttaccag ccacttgggt
1080

cgccatccgg gtattgcaga tgtagtccg gttcgtagcg caccgggtaa aacctggttt
1140

gcaacatggg ttgatcgtgg ttatggcacc ggtttctatt atcagggtaa aaaactgctg
1200

agccagccgt ggtcacatct gagccatcag agcattccgc ctaatctgat tgcacgcctg
1260

cagcgtgaag aaaatcatgg cctgagctat tttctggcag atgatgatgc atatattggt
1320

ggcaccagcc tgctgattgc agcagaaatt acccaagaac gtcagctgcc tctgtatcag
1380

ctggaatatg atgttaccga aggttgcgaa gtgcagttca tctataaaaag ccctgaaccg
1440

gatatgcagg gcaaaattga tatctatctg aatctgcagg ttaccgatat cctgccggat
1500

gaactggcat tttattggca ggacgttacc gatgcaagca gccaggcaga tgcaaccacc
1560

gcaatgcgtc tgtatctgaa tgaaaatacc gtgatttatc tgaaaccgag ccgtaaacia
1620

gaactggcgg aaggctggct gctgtgtagc gttcgtgttc cgcctaccta tccgctgggt
1680

attgccacca ttaaagaact gggcattcat gtggatggta ccgaaaccgt tctgtttcgc
1740

ctgggtctgc tgaccattat cccgctgggt gatgcaccga gcgcactgag ccgtattacc
1800

caggttcagc tgcaacgtga tgaagatatt catagcaaat gtccgagcag cagctgtgaa
1860

ctgtgggcaa ccctgagctg gatgatggaa cataatagca aagaagattg ggatcaggtc
1920

gatcactaca tgatcttttt caaaaacgtg gatagcaaag ccgaaccgat ttttctgggc
1980

accagcttta gcaccgaata tcgtattagc ggtctggaaa tcaaaaaaca tggcaacagc
2040

attgaaatct gggcagttaa tcgcctgggc acagttattg cacgtcagga tattgatatt
2100

cagcatcatc accatcacca ttaa
2124

<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for cloning of Endo-Rp gene

<400> 22
atgccttcac tcgaactaca gcaagc
26

<210> 23
<211> 696
<212> PRT
<213> Artificial Sequence

<220>
<223> Possible mutations in Endo-Rp amino acid sequence, which are confirmed to work in working examples.

<220>

<221> mutation
 <222> (128)..(128)
 <223> The position can be various amino acid, preferably Ala or Thr

<220>
 <221> mutation
 <222> (172)..(172)
 <223> The position can be various amino acid, preferably Asn, Asp, Gln, Glu, Ala, Cys, His, Phe, Gly, Leu, Ile, Lys, Met, Pro, Ser, Thr or Val.

<220>
 <221> mutation
 <222> (176)..(176)
 <223> The position can be various amino acid, preferably Asp or Arg.

<220>
 <221> mutation
 <222> (214)..(214)
 <223> The position can be various amino acid with large side chain, preferably Tyr or Phe.

<220>
 <221> mutation
 <222> (216)..(216)
 <223> The position can be various amino acid with small side chain, preferably Ser, Ala or Val.

<220>
 <221> mutation
 <222> (245)..(245)
 <223> The position can be various amino acid, preferably Leu or Ser.

<220>
 <221> mutation
 <222> (246)..(246)
 <223> The position can be various amino acid, preferably Asn or Asp.

<220>
 <221> mutation
 <222> (275)..(275)
 <223> The position can be various amino acid, preferably Thr or Ile.

<220>
 <221> mutation
 <222> (278)..(278)
 <223> The position can be various amino acid with hydrophobic side chain, preferably, Phe, Tyr, Ala, Leu or Ile.

<220>
 <221> mutation
 <222> (283)..(283)
 <223> The position can be various amino acid, preferably Phe or Ser.

<220>
 <221> mutation
 <222> (306)..(306)
 <223> The position can be various amino acid, preferably Leu or Ile.

<220>
 <221> mutation
 <222> (307)..(307)
 <223> The position can be various amino acid, preferably Phe, Tyr or His.

<220>
 <221> mutation
 <222> (310)..(310)
 <223> The position can be various amino acid with poler or charged side chain, preferably Asp, Glu,

<220>
 <221> mutation
 <222> (314)..(314)
 <223> The position can be various amino acid, preferably Glu or Gln.

<220>
 <221> mutation
 <222> (333)..(333)
 <223> The position can be various amino acid, preferably Asp or Gly.

<220>
 <221> mutation
 <222> (434)..(434)
 <223> The position can be various amino acid, preferably Ile or Leu.

<220>
 <221> mutation
 <222> (460)..(460)
 <223> The position can be various amino acid, preferably Val or Ala.

<220>
 <221> mutation
 <222> (527)..(527)
 <223> The position can be various amino acid, preferably Ile or Val.

<220>
 <221> mutation
 <222> (569)..(569)
 <223> The position an be various amino acid, preferably Lys or Thr

<220>
 <221> mutation
 <222> (610)..(610)
 <223> The position can be various amino acid, preferably Phe or Ser.

<220>
 <221> mutation
 <222> (626)..(626)
 <223> The position can be various amino acid, preferably His or Arg.

<400> 23

Met Pro Ser Leu Glu Leu Gln Gln Ala Ala Asp Thr Arg Leu Phe Glu
 1 5 10 15

Ser Met Pro Leu Gln Thr Met Asn Glu Leu Gly Ser Trp Glu Pro Ser
 20 25 30

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

Asn Leu Asp Pro Ala Glu Pro Arg Leu Ile Val Thr His Asp Met Ala
 50 55 60

Gly Gly Tyr Lys Glu Asp Ser Asn Ile Gln Gly Asn Thr Tyr Asp Thr
 65 70 75 80

Ile Tyr Ser Cys Gln Tyr Trp Gln Tyr Val Asp Thr Phe Ile Tyr Phe
 85 90 95

Ser His His Arg Val Thr Ile Pro Pro Val Asn Trp Ile Asn Ala Cys
 100 105 110

His Arg Asn Gly Val Lys Thr Leu Gly Thr Phe Ile Val Glu Gly Xaa
 115 120 125

Ala Gly Met Phe Ala Leu Glu Arg Phe Val Tyr Gly Pro Glu Pro Gly
 130 135 140

Gln Arg Asn Ser Trp Ser Pro Tyr Tyr Ala Asp Lys Leu Val Asp Ile
 145 150 155 160

Ala Glu Phe Tyr Gly Phe Asp Gly Trp Leu Leu Xaa Ile Glu Ser Xaa
 165 170 175

Phe Phe Pro Leu Tyr Arg Asn Pro Ser Leu Lys Ala Ile His Leu Ala
 180 185 190

Lys Leu Leu Arg Tyr Leu Lys Asn Ala Met His Ala Arg Val Pro Gly
 195 200 205

Ser Glu Ile Ile Trp Xaa Asp Xaa Met Thr Thr Asn Gly Ser Val Gln
 210 215 220

Trp Gln Asn Asn Ile Thr Pro Lys Asn Ser Ile Phe Phe Glu Ala Ala
 225 230 235 240

Asp Gly Ile Phe Xaa Xaa Tyr Trp Trp Asn Ala Thr Val Pro Pro Leu

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

Ile	Asp	Ile	Tyr	Leu	Asn	Leu	Gln	Val	Thr	Asp	Ile	Leu	Pro	Asp	Glu	
				485					490					495		
Leu	Ala	Phe	Tyr	Trp	Gln	Asp	Val	Thr	Asp	Ala	Ser	Ser	Gln	Ala	Asp	
			500					505					510			
Ala	Thr	Thr	Ala	Met	Arg	Leu	Tyr	Leu	Asn	Glu	Asn	Thr	Val	Xaa	Tyr	
			515				520					525				
Leu	Lys	Pro	Ser	Arg	Lys	Gln	Glu	Leu	Ala	Glu	Gly	Trp	Leu	Leu	Cys	
	530					535					540					
Ser	Val	Arg	Val	Pro	Pro	Thr	Tyr	Pro	Leu	Gly	Ile	Ala	Thr	Ile	Lys	
545					550					555					560	
Glu	Leu	Gly	Ile	His	Val	Asp	Gly	Xaa	Glu	Thr	Val	Leu	Phe	Arg	Leu	
				565					570					575		
Gly	Leu	Leu	Thr	Ile	Ile	Pro	Leu	Gly	Asp	Ala	Pro	Ser	Ala	Leu	Ser	
			580					585					590			
Arg	Ile	Thr	Gln	Val	Gln	Leu	Gln	Arg	Asp	Glu	Asp	Ile	His	Ser	Lys	
		595				600						605				
Cys	Xaa	Ser	Ser	Ser	Cys	Glu	Leu	Trp	Ala	Thr	Leu	Ser	Trp	Met	Met	
	610					615					620					
Glu	Xaa	Asn	Ser	Lys	Glu	Asp	Trp	Asp	Gln	Val	Asp	His	Tyr	Met	Ile	
625					630					635					640	
Phe	Phe	Lys	Asn	Val	Asp	Ser	Lys	Ala	Glu	Pro	Ile	Phe	Leu	Gly	Thr	
				645					650					655		
Ser	Phe	Ser	Thr	Glu	Tyr	Arg	Ile	Ser	Gly	Leu	Glu	Ile	Lys	Lys	His	
			660					665					670			
Gly	Asn	Ser	Ile	Glu	Ile	Trp	Ala	Val	Asn	Arg	Leu	Gly	Thr	Val	Ile	
		675					680					685				
Ala	Arg	Gln	Asp	Ile	Asp	Ile	Gln									
	690					695										