

PhoenixTemp3822.tmp.txt
SEQUENCE LISTING

<110> Novozymes A/S
<120> Hafnia phytase
<130> 11202.204-wo
<160> 12
<170> PatentIn version 3.5
<210> 1
<211> 23
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<223> Primer 2123fw

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<223> N designates A, C, G or T.

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<221> misc_feature
<222> (16)..(16)
<223> R designates A or G.

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 <222> (22)..(22)
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 <223> Primer 2328 TSP1dw

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<210> 6
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<212> DNA
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<220>
<223> Primer 2332 TSP2up

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<210> 8
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<220>
<223> Primer 2333 TSP3up

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<222> (1)..(99)

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<221> mat_peptide
<222> (100)..(1338)

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Met Thr Ile Ser Leu Phe Asn Arg Asn Lys Pro Ala Ile Ala Gln Arg
-30 -25 -20

att tta tgt cct ctg atc gtg gct tta ttc tca ggt tta ccg gca tac 96
Ile Leu Cys Pro Leu Ile Val Ala Leu Phe Ser Gly Leu Pro Ala Tyr
-15 -10 -5

gcc agt gat acc gcc cct gct ggg ttc cag ttg gaa aag gtt gtt atc 144
Ala Ser Asp Thr Ala Pro Ala Gly Phe Gln Leu Glu Lys Val Val Ile
-1 1 5 10 15

cta agc aga cat ggt gta cgc gcg cca acc aaa atg aca caa acg atg 192
Leu Ser Arg His Gly Val Arg Ala Pro Thr Lys Met Thr Gln Thr Met
20 25 30

cgc gac gtc aca cct cac cag tgg cct gaa tgg ccg gta aaa ctc ggc 240
Arg Asp Val Thr Pro His Gln Trp Pro Glu Trp Pro Val Lys Leu Gly
35 40 45

tat atc acg cca cgc ggc gaa cat ctg att agc ctg atg ggc ggt ttt 288
Tyr Ile Thr Pro Arg Gly Glu His Leu Ile Ser Leu Met Gly Gly Phe
50 55 60

tat cga gag cgc ttt cag caa caa ggt tta tta cct aag gat aac tgt 336
Tyr Arg Glu Arg Phe Gln Gln Gln Gly Leu Leu Pro Lys Asp Asn Cys
65 70 75

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cct Pro 80	aca Thr	cca Pro	gat Asp	gcc Ala	gtg Val 85	tat Tyr	gtt Val	tgg Trp	gca Ala	gac Asp 90	gtc Val	gat Asp	caa Gln	cgc Arg	aca Thr 95	384
cg Arg	aaa Lys	acc Thr	ggc Gly	gag Glu 100	gct Ala	ttc Phe	tta Leu	gca Ala	gg Gly 105	ctt Leu	gct Ala	ccc Pro	cag Gln	tgt Cys 110	gat Asp	432
tta Leu	gcg Ala	atc Ile	cac His 115	cat His	cag Gln	caa Gln	aac Asn	act Thr 120	cag Gln	cag Gln	gcc Ala	gat Asp	ccg Pro 125	ctg Leu	ttc Phe	480
cac His	cct Pro	gtg Val 130	aaa Lys	gcc Ala	ggt Gly	att Ile	tgt Cys 135	tcg Ser	atg Met	gat Asp	aaa Lys	tca Ser 140	cag Gln	gta Val	cac His	528
gcc Ala	gcg Ala 145	gtt Val	gaa Glu	aag Lys	cag Gln	gca Ala 150	ggc Gly	aca Thr	ccg Pro	att Ile	gag Glu 155	acg Thr	ctc Leu	aat Asn	caa Gln	576
cg Arg 160	tat Tyr	caa Gln	gcc Ala	tct Ser	tta Leu 165	gcg Ala	ctg Leu	atg Met	agt Ser	tcg Ser 170	gta Val	ctc Leu	gat Asp	ttt Phe	cca Pro 175	624
aaa Lys	tcc Ser	ccc Pro	tat Tyr	tgt Cys 180	cag Gln	cag Gln	cac His	aac Asn	att Ile 185	ggc Gly	aaa Lys	ctc Leu	tgc Cys	gat Asp 190	ttt Phe	672
tca Ser	cag Gln	gcg Ala	atg Met 195	cct Pro	agc Ser	aga Arg	ctg Leu	gcg Ala 200	ata Ile	aat Asn	gac Asp	gac Asp	gg Gly 205	aat Asn	aaa Lys	720
gtg Val	gct Ala	ctc Leu 210	gaa Glu	ggt Gly	gcc Ala	gtg Val	gga Gly 215	ctt Leu	gca Ala	tcg Ser	acg Thr	ttg Leu 220	gct Ala	gaa Glu	att Ile	768
ttc Phe 225	ctg Leu	ctg Leu	gaa Glu	cac His	gct Ala	cag Gln 230	gga Gly	atg Met	cct Pro	aaa Lys	gtg Val 235	gct Ala	tgg Trp	ggg Gly	aat Asn	816
att Ile 240	cac His	act Thr	gag Glu	cag Gln	caa Gln 245	tgg Trp	aac Asn	tct Ser	ctg Leu	ttg Leu 250	aaa Lys	ttg Leu	cat His	aat Asn	gcg Ala 255	864
cag Gln	ttt Phe	gac Asp	ttg Leu	atg Met 260	tcg Ser	cg Arg	acg Thr	ccc Pro	tat Tyr 265	atc Ile	gcc Ala	aag Lys	cat His	aac Asn 270	ggt Gly	912
act Thr	cca Pro	ctg Leu 275	ctg Leu	caa Gln	acc Thr	atc Ile	gcc Ala	cac His 280	gca Ala	ctg Leu	ggt Gly	tcc Ser	aat Asn 285	atc Ile	acg Thr	960
agt Ser	cg Arg	cca Pro 290	ctg Leu	ccg Pro	gat Asp	att Ile	tcg Ser 295	cca Pro	gac Asp	aat Asn	aag Lys	atc Ile 300	ctg Leu	ttt Phe	att Ile	1008
gcc Ala	ggt Gly 305	cac His	gac Asp	acc Thr	aat Asn	att Ile 310	gcc Ala	aat Asn	att Ile	tct Ser	ggc Gly 315	atg Met	tta Leu	ggg Gly	atg Met	1056
aca Thr 320	tgg Trp	aca Thr	ctt Leu	ccg Pro	gga Gly 325	caa Gln	cca Pro	gat Asp	aac Asn	acg Thr 330	cct Pro	ccg Pro	ggt Gly	ggc Gly	gct Ala 335	1104
ttg Leu	gtg Val	ttt Phe	gaa Glu	cg Arg 340	tgg Trp	gta Val	gat Asp	aac Asn	gcg Ala 345	ggg Gly	aaa Lys	ccg Pro	tat Tyr	gtt Val 350	agc Ser	1152
gtg Leu	aat Thr	atg Thr	gtg Thr	tat Thr	caa Thr	aca Thr	ctg Thr	gca Thr	cag Thr	ttg Thr	cac Thr	gac Thr	cag Thr	gcg Thr	ccg Thr	1200

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Val Asn Met Val Tyr Gln Thr Leu Ala Gln Leu His Asp Gln Ala Pro
355 360 365

cta acg ttg cag cat cct gcg ggc agc gta cga cta aac ata ccg ggt 1248
Leu Thr Leu Gln His Pro Ala Gly Ser Val Arg Leu Asn Ile Pro Gly
370 375 380

tgc agc gat caa acg ccc gat ggc tat tgc ccg ctc tcc acc ttc agc 1296
Cys Ser Asp Gln Thr Pro Asp Gly Tyr Cys Pro Leu Ser Thr Phe Ser
385 390 395

cgc tta gtc agc cac agc gtt gag cct gcg tgc cag ctt cct 1338
Arg Leu Val Ser His Ser Val Glu Pro Ala Cys Gln Leu Pro
400 405 410

<210> 10

<211> 446

<212> PRT

<213> Hafnia alvei

<400> 10

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-30 -25 -20

Ile Leu Cys Pro Leu Ile Val Ala Leu Phe Ser Gly Leu Pro Ala Tyr
-15 -10 -5

Ala Ser Asp Thr Ala Pro Ala Gly Phe Gln Leu Glu Lys Val Val Ile
-1 1 5 10 15

Leu Ser Arg His Gly Val Arg Ala Pro Thr Lys Met Thr Gln Thr Met
20 25 30

Arg Asp Val Thr Pro His Gln Trp Pro Glu Trp Pro Val Lys Leu Gly
35 40 45

Tyr Ile Thr Pro Arg Gly Glu His Leu Ile Ser Leu Met Gly Gly Phe
50 55 60

Tyr Arg Glu Arg Phe Gln Gln Gln Gly Leu Leu Pro Lys Asp Asn Cys
65 70 75

Pro Thr Pro Asp Ala Val Tyr Val Trp Ala Asp Val Asp Gln Arg Thr
80 85 90 95

Arg Lys Thr Gly Glu Ala Phe Leu Ala Gly Leu Ala Pro Gln Cys Asp
100 105 110

Leu Ala Ile His His Gln Gln Asn Thr Gln Gln Ala Asp Pro Leu Phe
115 120 125

His Pro Val Lys Ala Gly Ile Cys Ser Met Asp Lys Ser Gln Val His
130 135 140

Ala Ala Val Glu Lys Gln Ala Gly Thr Pro Ile Glu Thr Leu Asn Gln
145 150 155

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Arg Tyr Gln Ala Ser Leu Ala Leu Met Ser Ser Val Leu Asp Phe Pro
160 165 170 175

Lys Ser Pro Tyr Cys Gln Gln His Asn Ile Gly Lys Leu Cys Asp Phe
180 185 190

Ser Gln Ala Met Pro Ser Arg Leu Ala Ile Asn Asp Asp Gly Asn Lys
195 200 205

Val Ala Leu Glu Gly Ala Val Gly Leu Ala Ser Thr Leu Ala Glu Ile
210 215 220

Phe Leu Leu Glu His Ala Gln Gly Met Pro Lys Val Ala Trp Gly Asn
225 230 235

Ile His Thr Glu Gln Gln Trp Asn Ser Leu Leu Lys Leu His Asn Ala
240 245 250 255

Gln Phe Asp Leu Met Ser Arg Thr Pro Tyr Ile Ala Lys His Asn Gly
260 265 270

Thr Pro Leu Leu Gln Thr Ile Ala His Ala Leu Gly Ser Asn Ile Thr
275 280 285

Ser Arg Pro Leu Pro Asp Ile Ser Pro Asp Asn Lys Ile Leu Phe Ile
290 295 300

Ala Gly His Asp Thr Asn Ile Ala Asn Ile Ser Gly Met Leu Gly Met
305 310 315

Thr Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly Ala
320 325 330 335

Leu Val Phe Glu Arg Trp Val Asp Asn Ala Gly Lys Pro Tyr Val Ser
340 345 350

Val Asn Met Val Tyr Gln Thr Leu Ala Gln Leu His Asp Gln Ala Pro
355 360 365

Leu Thr Leu Gln His Pro Ala Gly Ser Val Arg Leu Asn Ile Pro Gly
370 375 380

Cys Ser Asp Gln Thr Pro Asp Gly Tyr Cys Pro Leu Ser Thr Phe Ser
385 390 395

Arg Leu Val Ser His Ser Val Glu Pro Ala Cys Gln Leu Pro
400 405 410

<210> 11
<211> 81
<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (1)..(81)

<223> Savinase signal peptide

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1				5				10					15			

tct	ggt	gct	ttt	agt	tca	tcg	atc	gca	tcg	gct	81
Ser	Val	Ala	Phe	Ser	Ser	Ser	Ile	Ala	Ser	Ala	
			20					25			

<210> 12

<211> 27

<212> PRT

<213> Bacillus licheniformis

<400> 12

Met	Lys	Lys	Pro	Leu	Gly	Lys	Ile	Val	Ala	Ser	Thr	Ala	Leu	Leu	Ile
1				5				10					15		

Ser	Val	Ala	Phe	Ser	Ser	Ser	Ile	Ala	Ser	Ala
			20					25		