

SEQUENCE LISTING

<110> Novozymes A/S

<120> POLYPEPTIDES HAVING ESTERASE ACTIVITY AND NUCLEIC ACIDS ENCODING THE SAME

<130> 10776.204-WO

<140> EP09151012.3

<141> 2009-01-21

<160> 15

<170> PatentIn version 3.3

<210> 1

<211> 1684

<212> DNA

<213> Myrothecium sp.

<220>

<221> sig_peptide

<222> (1)..(60)

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<221> CDS

<222> (1)..(1560)

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ggt	ggt	caa	gct	tcg	agt	tgt	tcc	cca	gaa	gtc	ttc	tca	tct	gtc	ggg	96
Val	Val	Gln	Ala	Ser	Ser	Cys	Ser	Pro	Glu	Val	Phe	Ser	Ser	Val	Gly	
		20					25					30				
att	ccc	aaa	ggc	gaa	ggt	ctg	tct	ctg	acg	gct	gag	ctc	gcg	gaa	act	144
Ile	Pro	Lys	Gly	Glu	Val	Leu	Ser	Leu	Thr	Ala	Glu	Leu	Ala	Glu	Thr	
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ctc	cca	tcg	caa	caa	acg	gcg	aac	aat	tgg	ccc	atc	ttc	tcc	aac	acg	192
Leu	Pro	Ser	Gln	Gln	Thr	Ala	Asn	Asn	Trp	Pro	Ile	Phe	Ser	Asn	Thr	
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acg	act	ctg	act	tgc	cag	gtc	acg	atc	cag	tac	acc	cat	ccg	gga	tgg	240
Thr	Thr	Leu	Thr	Cys	Gln	Val	Thr	Ile	Gln	Tyr	Thr	His	Pro	Gly	Trp	
65				70				75						80		
aac	gac	acc	atc	aac	acc	tac	gtg	tgg	ctt	ccc	gtc	gag	gac	tgg	aat	288
Asn	Asp	Thr	Ile	Asn	Thr	Tyr	Val	Trp	Leu	Pro	Val	Glu	Asp	Trp	Asn	
	85						90					95				
ggt	cgc	ttc	gtc	ggc	gtc	ggt	ggc	gga	gga	tgg	gca	gca	ggc	cag	ccg	336
Gly	Arg	Phe	Val	Gly	Val	Gly	Gly	Gly	Gly	Trp	Ala	Ala	Gly	Gln	Pro	
	100					105							110			
act	gat	ctg	ggt	ctc	cag	gtg	gcc	aga	gga	tac	gct	gcc	ggt	acc	acg	384
Thr	Asp	Leu	Gly	Leu	Gln	Val	Ala	Arg	Gly	Tyr	Ala	Ala	Val	Thr	Thr	

115	120	125	
gac ggt ggt cat cct ttt Asp Gly Gly His Pro Phe 130	gag cgc tct gat Glu Arg Ser 135	gac ctg gat tac tgg gcc Asp Leu Asp Tyr Trp Ala 140	432
atg gtg ggg aaa gac agc atc aat tgg tac aat atg ctg aat ttc ttc Met Val Gly Lys Asp Ser Ile Asn Trp Tyr Asn Met Leu Asn Phe Phe 145 150 155 160			480
tcc gtg gcc cta gac gat gca gct aca ttg ggc aag gca gcc gtt gtc Ser Val Ala Leu Asp Asp Ala Ala Thr Leu Gly Lys Ala Ala Val Val 165 170 175			528
gcc tac tat gga cga gaa caa gaa tac tcg tac tgg aac ggc tgt tcg Ala Tyr Tyr Gly Arg Glu Gln Glu Tyr Ser Tyr Trp Asn Gly Cys Ser 180 185 190			576
aca gga gga cgt caa ggc ttc atg atg gcc cag aga tac cca gaa cag Thr Gly Gly Arg Gln Gly Phe Met Met Ala Gln Arg Tyr Pro Glu Gln 195 200 205			624
tac gat ggc att ctc gcc tct gcg ccc gcc att aac tgg ggc cag ctg Tyr Asp Gly Ile Leu Ala Ser Ala Pro Ala Ile Asn Trp Gly Gln Leu 210 215 220			672
gtc atc agc atg tac ttg ccc att ctg acc atg aga tca ttg gac tat Val Ile Ser Met Tyr Leu Pro Ile Leu Thr Met Arg Ser Leu Asp Tyr 225 230 235 240			720
tac cca tcc aac tgc gag ctc aat gct att aca agc gct gct gtt gaa Tyr Pro Ser Asn Cys Glu Leu Asn Ala Ile Thr Ser Ala Ala Val Glu 245 250 255			768
gca tgt gat gaa gct gac ggt ctg aag gac gac gta gtt gtg cgg aca Ala Cys Asp Glu Ala Asp Gly Leu Lys Asp Asp Val Val Val Arg Thr 260 265 270			816
tgg gag tgc gaa ttc gat gct tcg agc gtc gtc ggc cag aag tac agc Trp Glu Cys Glu Phe Asp Ala Ser Ser Val Val Gly Gln Lys Tyr Ser 275 280 285			864
tgc gga aac gag tct ggt atc atc acc tcc cag gct gcc gag gtt gct Cys Gly Asn Glu Ser Gly Ile Ile Thr Ser Gln Ala Ala Glu Val Ala 290 295 300			912
tcc aca acc tgg agt ggc tcc gtc ttc cag aac ggc cga cgt gct gga Ser Thr Thr Trp Ser Gly Ser Val Phe Gln Asn Gly Arg Arg Ala Gly 305 310 315 320			960
tgg gga ctt gct cca tcg gct ccc ttg gtt ggc att gct aac gtt gtt Trp Gly Leu Ala Pro Ser Ala Pro Leu Val Gly Ile Ala Asn Val Val 325 330 335			1008
tgc tcc tcg ccc ggt gat tgt gaa ccg gca ccc ttc atc ctc tca acc Cys Ser Ser Pro Gly Asp Cys Glu Pro Ala Pro Phe Ile Leu Ser Thr 340 345 350			1056
caa tgg atc tcc aag ttc gtt ctt gag aac agc gat gcg gac ctc tcc Gln Trp Ile Ser Lys Phe Val Leu Glu Asn Ser Asp Ala Asp Leu Ser 355 360 365			1104

acc ctt acg gac gag gag tat ctc agc ctc ttc cgc caa tcg gcc aac 1152
 Thr Leu Thr Asp Glu Glu Tyr Leu Ser Leu Phe Arg Gln Ser Ala Asn
 370 375 380

aag tac agc tca ctc tcc gac acg aac gat ccg gat ctg acc gac ttc 1200
 Lys Tyr Ser Ser Leu Ser Asp Thr Asn Asp Pro Asp Leu Thr Asp Phe
 385 390 395 400

aag ttg gcc ggc ggc aag atg att aca tgg cac ggc ggc gac gat atc 1248
 Lys Leu Ala Gly Gly Lys Met Ile Thr Trp His Gly Gly Asp Asp Ile
 405 410 415

ctc att cca tac aac agt acc gtc gat tac tac gag aaa gtt gct gca 1296
 Leu Ile Pro Tyr Asn Ser Thr Val Asp Tyr Tyr Glu Lys Val Ala Ala
 420 425 430

ctg gac gca gac gtc ttg gac tac ttc aga ttc ttc tca gcg ccc gga 1344
 Leu Asp Ala Asp Val Leu Asp Tyr Phe Arg Phe Phe Ser Ala Pro Gly
 435 440 445

gtt cag cac tgc cag gac gga gct ggg tgg ttc ccc ggt gag gcg ttt 1392
 Val Gln His Cys Gln Asp Gly Ala Gly Trp Phe Pro Gly Glu Ala Phe
 450 455 460

gag tcc ctg gtc gac tgg gtt gag aat ggc aaa gct cca gag acg ctg 1440
 Glu Ser Leu Val Asp Trp Val Glu Asn Gly Lys Ala Pro Glu Thr Leu
 465 470 475 480

tat ggc agg cct cgt ggt agc aac ttc act gga gag aga gaa gcc aac 1488
 Tyr Gly Arg Pro Arg Gly Ser Asn Phe Thr Gly Glu Arg Glu Ala Asn
 485 490 495

ttg tgc ctg tat ccc aag cag atc cgt tac att ggg gga gac ccg gag 1536
 Leu Cys Leu Tyr Pro Lys Gln Ile Arg Tyr Ile Gly Gly Asp Pro Glu
 500 505 510

gtt gct tct tct ttc gag tgt cag tgagaaactg ccggttttgt caaggcagag 1590
 Val Ala Ser Ser Phe Glu Cys Gln
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 <213> Myrothecium sp.

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Ile Pro Lys Gly Glu Val Leu Ser Leu Thr Ala Glu Leu Ala Glu Thr
35 40 45

Leu Pro Ser Gln Gln Thr Ala Asn Asn Trp Pro Ile Phe Ser Asn Thr
50 55 60

Thr Thr Leu Thr Cys Gln Val Thr Ile Gln Tyr Thr His Pro Gly Trp
65 70 75 80

Asn Asp Thr Ile Asn Thr Tyr Val Trp Leu Pro Val Glu Asp Trp Asn
85 90 95

Gly Arg Phe Val Gly Val Gly Gly Gly Gly Trp Ala Ala Gly Gln Pro
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Thr Asp Leu Gly Leu Gln Val Ala Arg Gly Tyr Ala Ala Val Thr Thr
115 120 125

Asp Gly Gly His Pro Phe Glu Arg Ser Asp Asp Leu Asp Tyr Trp Ala
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Met Val Gly Lys Asp Ser Ile Asn Trp Tyr Asn Met Leu Asn Phe Phe
145 150 155 160

Ser Val Ala Leu Asp Asp Ala Ala Thr Leu Gly Lys Ala Ala Val Val
165 170 175

Ala Tyr Tyr Gly Arg Glu Gln Glu Tyr Ser Tyr Trp Asn Gly Cys Ser
180 185 190

Thr Gly Gly Arg Gln Gly Phe Met Met Ala Gln Arg Tyr Pro Glu Gln
195 200 205

Tyr Asp Gly Ile Leu Ala Ser Ala Pro Ala Ile Asn Trp Gly Gln Leu
210 215 220

Val Ile Ser Met Tyr Leu Pro Ile Leu Thr Met Arg Ser Leu Asp Tyr
225 230 235 240

Tyr Pro Ser Asn Cys Glu Leu Asn Ala Ile Thr Ser Ala Ala Val Glu
245 250 255

Ala Cys Asp Glu Ala Asp Gly Leu Lys Asp Asp Val Val Val Arg Thr
260 265 270

Trp Glu Cys Glu Phe Asp Ala Ser Ser Val Val Gly Gln Lys Tyr Ser

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