

101823-02pct.ST25.txt
SEQUENCE LISTING

<110> Biotec Pharmacon ASA
<120> A method of removing nucleic acid contamination in reverse transcription and amplification reactions
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<150> GB0912637.6
<151> 2009-07-21
<150> US61/235177
<151> 2009-08-19
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<170> PatentIn version 3.3
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Phe Tyr Glu Leu Ile Arg Val Cys Phe Asp Pro Ala Asn Glu Thr Thr
Page 1

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ctc gcc cag gac aaa aaa gtt gtc cct gct cct gca tta aca tgg aag Leu Ala Gln Asp Lys Lys Val Val Pro Ala Pro Ala Leu Thr Trp Lys 290 295 300	912
gtg atc tat gag aag gac act aac cga gct gct gct att gtt gga ata Val Ile Tyr Glu Lys Asp Thr Asn Arg Ala Ala Ala Ile Val Gly Ile 305 310 315 320	960
aac aac ccc cac atc acc acg gca cca gaa cct ctt tgt acc gac atc Asn Asn Pro His Ile Thr Thr Ala Pro Glu Pro Leu Cys Thr Asp Ile 325 330 335	1008
tgc tcc agc ctc aca tgg ctg gac ttt gat ttt ggg gac ctt gtc cat Cys Ser Ser Leu Thr Trp Leu Asp Phe Asp Phe Gly Asp Leu Val His 340 345 350	1056
ggc tac acc tac tgc tgc tct gta gct gat ctc agg gca gcc att ccc Gly Tyr Thr Tyr Cys Cys Ser Val Ala Asp Leu Arg Ala Ala Ile Pro 355 360 365	1104
aat gtt cca gat tta gga gac gtt gat atc tta gac gaa taa Asn Val Pro Asp Leu Gly Asp Val Asp Ile Leu Asp Glu 370 375 380	1146

<210> 7
<211> 381

<212> PRT
 <213> Pandalus borealis

<220>
 <221> MUTAGEN
 <222> (214)..(214)

<400> 7

Glu Asp Cys Val Trp Asp Asn Asp Val Asp Tyr Pro Glu Tyr Pro Pro
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Leu Ile Leu Asp Ser Ser Phe Gln Leu Val Leu Pro Val Leu Glu Gly
 20 25 30

Asp Gln Arg Ile Thr Ser Val Gln Ser Gly Ser Lys Leu Ile Leu Ala
 35 40 45

Cys Pro Gly Arg Gly Ile Ser Ala Leu Gly Ser Glu Asp Ala Gln Ala
 50 55 60

Thr Cys Leu Gly Gly Lys Leu Val Glu Val Asp Gly Lys Glu Trp Asn
 65 70 75 80

Ile Val Glu Leu Gly Cys Thr Lys Met Ala Ser Glu Thr Ile His Arg
 85 90 95

Asn Leu Gly Gln Cys Gly Asp Gln Asp Leu Gly Ile Tyr Glu Val Ile
 100 105 110

Gly Phe Asp Leu Pro Thr Thr Gly His Phe Tyr Glu Leu Ile Arg Val
 115 120 125

Cys Phe Asp Pro Ala Asn Glu Thr Thr Ile Phe Ser Glu Asn Ile Val
 130 135 140

His Gly Ala Ser Ile Ala Ala Lys Asp Ile Asp Pro Gly Arg Pro Ser
 145 150 155 160

Phe Lys Thr Ser Thr Gly Phe Phe Ser Val Ser Met Ile Ser Val Tyr
 165 170 175

Ser Gln Arg Ser Gln Leu Glu Leu Met Lys Asn Leu Leu Gly Asp Asp
 180 185 190

Glu Leu Ala Ala Thr Ile Ile Asp Pro Ser Glu Gln Phe Tyr Phe Ala
 195 200 205

Lys Gly His Met Ala Ala Asp Ala Asp Phe Val Thr Val Val Glu Gln
 210 215 220

Asp Ala Thr Tyr Tyr Tyr Ile Asn Ala Leu Pro Gln Trp Gln Ala Phe
 225 230 235 240

Asn Asn Gly Asn Trp Lys Tyr Leu Glu Tyr Asp Thr Arg Asp Leu Ala
245 250 255

Glu Lys His Gly Thr Asp Leu Thr Val Tyr Ser Gly Gly Trp Gly Val
260 265 270

Leu Glu Leu Glu Asp Ile Asn Gly Asn Pro Val Glu Ile Tyr Leu Gly
275 280 285

Leu Ala Gln Asp Lys Lys Val Val Pro Ala Pro Ala Leu Thr Trp Lys
290 295 300

Val Ile Tyr Glu Lys Asp Thr Asn Arg Ala Ala Ala Ile Val Gly Ile
305 310 315 320

Asn Asn Pro His Ile Thr Thr Ala Pro Glu Pro Leu Cys Thr Asp Ile
325 330 335

Cys Ser Ser Leu Thr Trp Leu Asp Phe Asp Phe Gly Asp Leu Val His
340 345 350

Gly Tyr Thr Tyr Cys Cys Ser Val Ala Asp Leu Arg Ala Ala Ile Pro
355 360 365

Asn Val Pro Asp Leu Gly Asp Val Asp Ile Leu Asp Glu
370 375 380

<210> 8
<211> 1146
<212> DNA
<213> *Pandalus borealis*

<220>
<221> CDS
<222> (1)..(1146)

<220>
<221> mutation
<222> (640)..(640)

<400> 8
gag gac tgt gtc tgg gac aat gat gta gac tat cct gag tat cct cct 48
Glu Asp Cys Val Trp Asp Asn Asp Val Asp Tyr Pro Glu Tyr Pro Pro
1 5 10 15

ctg atc ctg gat tca tcc ttt cag ctg gtt ctg cca gtg ttg gaa gga 96
Leu Ile Leu Asp Ser Ser Phe Gln Leu Val Leu Pro Val Leu Glu Gly
20 25 30

gac caa agg ata acc agt gtc caa tct ggg agt aag ctg atc ttg gct 144
Asp Gln Arg Ile Thr Ser Val Gln Ser Gly Ser Lys Leu Ile Leu Ala
35 40 45

tgt cct ggg agg gga att tca gcc ctg ggg tca gag gat gca caa gcc 192
Cys Pro Gly Arg Gly Ile Ser Ala Leu Gly Ser Glu Asp Ala Gln Ala
50 55 60

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act tgt ctt ggt ggc aag ctc gtc gaa gtc gat ggc aaa gaa tgg aat Thr Cys Leu Gly Gly Lys Leu Val Glu Val Asp Gly Lys Glu Trp Asn 65 70 75 80	240
ata gtc gaa ctc ggc tgc aca aaa atg gca tct gaa acc atc cat aga Ile Val Glu Leu Gly Cys Thr Lys Met Ala Ser Glu Thr Ile His Arg 85 90 95	288
aac ctt gga caa tgt ggt gat caa gac ctg gga att tac gaa gtc att Asn Leu Gly Gln Cys Gly Asp Gln Asp Leu Gly Ile Tyr Glu Val Ile 100 105 110	336
ggt ttc gac ctt cca aca acg gga cac ttc tat gaa ttg ata cga gtt Gly Phe Asp Leu Pro Thr Thr Gly His Phe Tyr Glu Leu Ile Arg Val 115 120 125	384
tgc ttt gac ccg gca aat gag acc act att ttt tcc gag aac atc gtt Cys Phe Asp Pro Ala Asn Glu Thr Thr Ile Phe Ser Glu Asn Ile Val 130 135 140	432
cac gga gcc agc atc gcc gcc aaa gac att gac ccg ggt cgt cca tct His Gly Ala Ser Ile Ala Ala Lys Asp Ile Asp Pro Gly Arg Pro Ser 145 150 155 160	480
ttc aaa aca tcc act ggg ttc ttc agt gta tcg atg ata tct gtc tat Phe Lys Thr Ser Thr Gly Phe Phe Ser Val Ser Met Ile Ser Val Tyr 165 170 175	528
tcg caa aga agt cag ctg gag ctc atg aag aac ctc tta gga gat gat Ser Gln Arg Ser Gln Leu Glu Leu Met Lys Asn Leu Leu Gly Asp Asp 180 185 190	576
gaa tta gct gcg aca atc atc gat cct tca gag cag ttc tac ttt gct Glu Leu Ala Ala Thr Ile Ile Asp Pro Ser Glu Gln Phe Tyr Phe Ala 195 200 205	624
aaa gga cat atg gct gct gac gcg gac ttt gtg aca gta gtt gag cag Lys Gly His Met Ala Ala Asp Ala Asp Phe Val Thr Val Val Glu Gln 210 215 220	672
gac gca aca tac tat tac atc aac gcg ttg cct caa tgg cag gcc ttt Asp Ala Thr Tyr Tyr Tyr Ile Asn Ala Leu Pro Gln Trp Gln Ala Phe 225 230 235 240	720
aac aat gga aac tgg aag tac ttg gaa tac gac acc cgt gac ctg gct Asn Asn Gly Asn Trp Lys Tyr Leu Glu Tyr Asp Thr Arg Asp Leu Ala 245 250 255	768
gaa aaa cat ggc act gac ctg acc gtc tac agt ggt ggc tgg ggg gtt Glu Lys His Gly Thr Asp Leu Thr Val Tyr Ser Gly Gly Trp Gly Val 260 265 270	816
cta gag ctt gaa gac atc aac gga aac ccc gtt gaa atc tat ctt ggc Leu Glu Leu Glu Asp Ile Asn Gly Asn Pro Val Glu Ile Tyr Leu Gly 275 280 285	864
ctc gcc cag gac aaa aaa gtt gtc cct gct cct gca tta aca tgg aag Leu Ala Gln Asp Lys Lys Val Val Pro Ala Pro Ala Leu Thr Trp Lys 290 295 300	912
gtg atc tat gag aag gac act aac cga gct gct gct att gtt gga ata Val Ile Tyr Glu Lys Asp Thr Asn Arg Ala Ala Ala Ile Val Gly Ile 305 310 315 320	960
aac aac ccc cac atc acc acg gca cca gaa cct ctt tgt acc gac atc Asn Asn Pro His Ile Thr Thr Ala Pro Glu Pro Leu Cys Thr Asp Ile 325 330 335	1008

101823-02pct.ST25.txt

tgc tcc agc ctc aca tgg ctg gac ttt gat ttt ggg gac ctt gtc cat 1056
Cys Ser Ser Leu Thr Trp Leu Asp Phe Asp Phe Gly Asp Leu Val His
340 345 350

ggc tac acc tac tgc tgc tct gta gct gat ctc agg gca gcc att ccc 1104
Gly Tyr Thr Tyr Cys Cys Ser Val Ala Asp Leu Arg Ala Ala Ile Pro
355 360 365

aat gtt cca gat tta gga gac gtt gat atc tta gac gaa taa 1146
Asn Val Pro Asp Leu Gly Asp Val Asp Ile Leu Asp Glu
370 375 380

<210> 9
<211> 23
<212> PRT
<213> Pandalus borealis

<220>
<221> SIGNAL
<222> (1)..(23)

<400> 9

Met Ile Gly Arg Thr Thr Phe Ile Ala Leu Phe Val Lys Val Leu Thr
1 5 10 15

Ile Trp Ser Phe Thr Lys Gly
20

<210> 10
<211> 15
<212> DNA
<213> Artificial

<220>
<223> 5' FAM and 3' TAMRA labelled oligonucleotide probe for measuring
DNase activity

<400> 10 15
cgccatcgga gggttc

<210> 11
<211> 15
<212> DNA
<213> Artificial

<220>
<223> complementary sequence of SEQ ID No. 10

<400> 11 15
gaacctccga tggcg

<210> 12
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Forward primer for amplifying a section of the E. coli 23SrRNA
gene

<400> 12
gaaaggcgcg cgatacag 18

<210> 13
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Reverse primer for amplifying a section of the E. coli 23SrRNA

<400> 13
gtccccgccct actcatcga 19

<210> 14
<211> 26
<212> DNA
<213> Artificial

<220>
<223> 5' FAM and 3' BHQ labelled oligonucleotide probe complementary to a section of the E. coli 23SrRNA gene between the regions complementary to SEQ ID No. 13 and SEQ ID No. 14

<400> 14
ccccgtacac aaaaatgcac atgctg 26

<210> 15
<211> 381
<212> PRT
<213> Paralithodes camtschatica

<400> 15

Gln Asp Cys Val Trp Asp Lys Asp Thr Asp Phe Pro Glu Asp Pro Pro
1 5 10 15

Leu Ile Phe Asp Ser Asn Leu Glu Leu Ile Arg Pro Val Leu Glu Asn
20 25 30

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

Cys Ser Gly Ser Glu Leu Ile Asn Leu Gly Met Glu Ala Val Glu Ala
50 55 60

Lys Cys Ala Gly Gly Val Met Leu Ala Ile Glu Gly Thr Glu Trp Glu
65 70 75 80

Ile Trp Ser Leu Gly Cys Ser Asn His Val Lys Glu Thr Ile Arg Arg
85 90 95

Asn Leu Gly Thr Cys Gly Glu Ala Asp Gln Gly Asp Arg His Ser Ile
100 105 110

Gly Phe Glu Tyr Tyr Gly Gly Ser Ile Tyr Tyr Glu Leu Ile Ser Val
115 120 125

Cys Phe Gly Pro Val Ser Glu Thr Thr Leu Arg Thr Glu His Val Leu
 130 135 140
 His Gly Ala Asn Ile Ala Ala Lys Asp Ile Glu Thr Ser Arg Pro Ser
 145 150 155 160
 Phe Lys Thr Ser Thr Gly Phe Phe Ser Val Ser Met Ser Thr Val Tyr
 165 170 175
 Ser Gln Ala Ser Gln Leu Gln Leu Met Thr Asp Ile Leu Gly Asp Ser
 180 185 190
 Asp Leu Ala Asn Asn Ile Ile Asp Pro Ser Gln Gln Leu Tyr Phe Ala
 195 200 205
 Lys Gly His Met Ser Pro Asp Ala Asp Phe Val Thr Val Ala Glu Gln
 210 215 220
 Asp Ala Thr Tyr Tyr Phe Ile Asn Ala Leu Pro Gln Trp Gln Ala Phe
 225 230 235 240
 Asn Asn Gly Asn Trp Lys Tyr Leu Glu Tyr Ala Thr Arg Asp Leu Ala
 245 250 255
 Glu Ser His Gly Ser Asp Leu Arg Val Tyr Ser Gly Gly Trp Ser Leu
 260 265 270
 Leu Gln Leu Asp Asp Ile Asn Gly Asn Pro Val Asp Ile Leu Leu Gly
 275 280 285
 Leu Ser Glu Gly Lys Glu Val Val Pro Val Pro Ser Leu Thr Trp Lys
 290 295 300
 Val Val Tyr Glu Glu Ser Ser Ser Lys Ala Ala Ala Ile Val Gly Ile
 305 310 315 320
 Asn Asn Pro His Ile Thr Thr Ala Pro Ser Pro Leu Cys Ser Asp Leu
 325 330 335
 Cys Ser Ser Leu Thr Trp Ile Asp Phe Asn Leu Asp Asp Leu Ala His
 340 345 350
 Gly Tyr Thr Tyr Cys Cys Ala Val Asp Asp Leu Arg Gln Ala Ile Pro
 355 360 365
 Tyr Ile Pro Asp Leu Gly Asn Val Gly Leu Leu Thr Asn
 370 375 380