

SEQUENCE LISTING

<110> UNIVERSITETET I TROMSØ - NORGES ARKTISKE UNIVERSITET

<120> DNA Polymerases

<130> 59.67.134638/01

<150> GB1721053.5

<151> 2017-12-15

<160> 20

<170> PatentIn version 3.5

<210> 1

<211> 32

<212> PRT

<213> Psychrobacillus sp.

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<212> PRT

<213> Psychrobacillus sp.

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Thr	Ser	Glu	Leu	Leu	Gly	Ile	Ala	Leu	Ser	Asp	Gly	Glu	Lys	Gly	Tyr
			35				40					45			

Phe	Ala	Pro	Ala	Asp	Ile	Ala	Phe	Gln	Ser	Lys	Asp	Phe	Cys	Ser	Trp
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Leu Glu Asn Ala Thr Asn Lys Lys Tyr Leu Ala Asp Ser Lys Ala Thr
 65 70 75 80

Gln Ala Val Ser Arg Lys His Asn Val Asn Val His Gly Val Glu Phe
 85 90 95

Asp Leu Leu Leu Ala Ala Tyr Ile Val Asn Pro Ala Ile Ser Ser Glu
 100 105 110

Asp Val Ala Ala Ile Ala Lys Glu Phe Gly Tyr Phe Asn Leu Leu Thr
 115 120 125

Asn Asp Ser Val Tyr Gly Lys Gly Ala Lys Lys Thr Ala Pro Glu Ile
 130 135 140

Glu Lys Ile Ala Glu His Ala Val Arg Lys Ala Arg Ala Ile Trp Asp
 145 150 155 160

Leu Lys Glu Lys Leu Glu Val Lys Leu Glu Glu Asn Glu Gln Tyr Ala
 165 170 175

Leu Tyr Lys Glu Ile Glu Leu Pro Leu Ala Ser Ile Leu Gly Thr Met
 180 185 190

Glu Ser Asp Gly Val Leu Val Asp Lys Gln Ile Leu Val Glu Met Gly
 195 200 205

His Glu Leu Asn Ile Lys Leu Arg Ala Ile Glu Gln Asp Ile Tyr Ala
 210 215 220

Leu Ala Gly Glu Thr Phe Asn Ile Asn Ser Pro Lys Gln Leu Gly Val
 225 230 235 240

Ile Leu Phe Glu Lys Ile Gly Leu Thr Pro Ile Lys Lys Thr Lys Thr
 245 250 255

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

Glu Ile Ile Glu Gln Ile Leu Leu Tyr Arg Gln Leu Gly Lys Leu Asn
275 280 285

Ser Thr Tyr Ile Glu Gly Leu Leu Lys Glu Ile His Glu Asp Asp Gly
290 295 300

Lys Ile His Thr Arg Tyr Gln Gln Ala Leu Thr Ser Thr Gly Arg Leu
305 310 315 320

Ser Ser Ile Asn Pro Asn Leu Gln Asn Ile Pro Val Arg Leu Glu Glu
325 330 335

Gly Arg Lys Ile Arg Lys Ala Phe Val Pro Ser Gln Pro Gly Trp Val
340 345 350

Met Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His
355 360 365

Met Ser Glu Asp Glu Asn Leu Val Glu Ala Phe Asn Asn Asp Leu Asp
370 375 380

Ile His Thr Lys Thr Ala Met Asp Val Phe His Val Glu Gln Glu Ala
385 390 395 400

Val Thr Ser Asp Met Arg Arg Ala Ala Lys Ala Val Asn Phe Gly Ile
405 410 415

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

Arg Lys Glu Ala Ala Thr Phe Ile Glu Asn Tyr Leu Asn Ser Phe Pro
435 440 445

Gly Val Lys Gly Tyr Met Asp Asp Ile Val Gln Asp Ala Lys Gln Thr

450

455

460

Gly Tyr Val Thr Thr Ile Leu Asn Arg Arg Arg Tyr Leu Pro Glu Ile
 465 470 475 480

Thr Ser Ser Asn Phe Asn Leu Arg Ser Phe Ala Glu Arg Thr Ala Met
 485 490 495

Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile Lys Lys Ala Met
 500 505 510

Ile Asp Met Ala Glu Arg Leu Ile Ser Glu Asn Met Gln Thr Lys Met
 515 520 525

Leu Leu Gln Val His Asp Glu Leu Ile Phe Glu Ala Pro Pro Glu Glu
 530 535 540

Ile Ala Met Leu Glu Lys Ile Val Pro Glu Val Met Glu Asn Ala Ile
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Lys Leu Ile Val Pro Leu Lys Val Asp Tyr Ala Phe Gly Ser Ser Trp
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Tyr Asp Thr Lys
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 <212> DNA
 <213> Psychrobacillus sp.

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 caagcagtga gtagaaaaca taatgtgaat gtacatggag tggaattcga ctttctttta 300

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ccaccagagg aaattgcaat gctagaaaaa atagtgccag aggtgatgga aaacgctatt	1680
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<212> PRT
<213> Psychrobacillus sp.

<400> 4

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Ile His Thr Asn Ala Val Tyr Gly Phe Thr Met Met Leu Gln Lys Ile
35 40 45

Met Asp Glu Glu Asn Pro Thr His Met Leu Val Ala Phe Asp Ala Gly
50 55 60

Lys Thr Thr Phe Arg His Ser Thr Phe Gly Asp Tyr Lys Gly Gly Arg
65 70 75 80

Gln Lys Thr Pro Pro Glu Leu Ser Glu Gln Phe Pro Tyr Ile Arg Lys
85 90 95

Leu Ile Asp Ala Tyr Gly Ile Lys Arg Tyr Glu Leu Glu Met Tyr Glu
100 105 110

Ala Asp Asp Ile Ile Gly Thr Leu Ser Lys Arg Ala Asp Glu Lys Gly
115 120 125

Gln Gln Val Val Ile Val Ser Gly Asp Lys Asp Leu Thr Gln Leu Ala
130 135 140

Thr Asp Lys Thr Thr Val Tyr Ile Thr Arg Lys Gly Ile Thr Asp Ile
145 150 155 160

Glu Lys Tyr Thr Pro Glu His Val Gln Glu Lys Tyr Gly Leu Thr Pro

165

170

175

Leu Gln Ile Ile Asp Met Lys Gly Leu Met Gly Asp Ala Ser Asp Asn
 180 185 190

Ile Pro Gly Val Pro Gly Val Gly Glu Lys Thr Ala Ile Lys Leu Leu
 195 200 205

Lys Glu His Gly Ser Val Glu Asp Leu Tyr Lys Ala Leu Asp Thr Val
 210 215 220

Ser Gly Val Lys Leu Lys Glu Lys Leu Ile Ala Asn Glu Glu Gln Ala
 225 230 235 240

Ile Met Ser Lys Ala Leu Ala Thr Ile Glu Thr Ala Ala Pro Ile Gln
 245 250 255

Ile Ser Ile Asp Asp Leu Ser Tyr Thr Gly Pro Asn Met Glu Glu Val
 260 265 270

Ile Glu Val Trp Lys Glu Leu Ala Phe Lys Thr Leu Leu Glu Lys Ser
 275 280 285

Asp Tyr Ile Ser Glu Glu Ser Glu Thr Thr Glu Val Ala Phe Glu Ile
 290 295 300

Val Glu Glu Ile Asp Ser Thr Ile Leu Asp Lys Val Met Ser Val His
 305 310 315 320

Leu Glu Met Tyr Asp Gly Gln Tyr His Thr Ser Glu Leu Leu Gly Ile
 325 330 335

Ala Leu Ser Asp Gly Glu Lys Gly Tyr Phe Ala Pro Ala Asp Ile Ala
 340 345 350

Phe Gln Ser Lys Asp Phe Cys Ser Trp Leu Glu Asn Ala Thr Asn Lys
 355 360 365

Lys Tyr Leu Ala Asp Ser Lys Ala Thr Gln Ala Val Ser Arg Lys His
370 375 380

Asn Val Asn Val His Gly Val Glu Phe Asp Leu Leu Leu Ala Ala Tyr
385 390 395 400

Ile Val Asn Pro Ala Ile Ser Ser Glu Asp Val Ala Ala Ile Ala Lys
405 410 415

Glu Phe Gly Tyr Phe Asn Leu Leu Thr Asn Asp Ser Val Tyr Gly Lys
420 425 430

Gly Ala Lys Lys Thr Ala Pro Glu Ile Glu Lys Ile Ala Glu His Ala
435 440 445

Val Arg Lys Ala Arg Ala Ile Trp Asp Leu Lys Glu Lys Leu Glu Val
450 455 460

Lys Leu Glu Glu Asn Glu Gln Tyr Ala Leu Tyr Lys Glu Ile Glu Leu
465 470 475 480

Pro Leu Ala Ser Ile Leu Gly Thr Met Glu Ser Asp Gly Val Leu Val
485 490 495

Asp Lys Gln Ile Leu Val Glu Met Gly His Glu Leu Asn Ile Lys Leu
500 505 510

Arg Ala Ile Glu Gln Asp Ile Tyr Ala Leu Ala Gly Glu Thr Phe Asn
515 520 525

Ile Asn Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Ile Gly
530 535 540

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

Val Leu Glu Lys Leu Ala Ser Glu His Glu Ile Ile Glu Gln Ile Leu

565

570

575

Leu Tyr Arg Gln Leu Gly Lys Leu Asn Ser Thr Tyr Ile Glu Gly Leu
 580 585 590

Leu Lys Glu Ile His Glu Asp Asp Gly Lys Ile His Thr Arg Tyr Gln
 595 600 605

Gln Ala Leu Thr Ser Thr Gly Arg Leu Ser Ser Ile Asn Pro Asn Leu
 610 615 620

Gln Asn Ile Pro Val Arg Leu Glu Glu Gly Arg Lys Ile Arg Lys Ala
 625 630 635 640

Phe Val Pro Ser Gln Pro Gly Trp Val Met Phe Ala Ala Asp Tyr Ser
 645 650 655

Gln Ile Glu Leu Arg Val Leu Ala His Met Ser Glu Asp Glu Asn Leu
 660 665 670

Val Glu Ala Phe Asn Asn Asp Leu Asp Ile His Thr Lys Thr Ala Met
 675 680 685

Asp Val Phe His Val Glu Gln Glu Ala Val Thr Ser Asp Met Arg Arg
 690 695 700

Ala Ala Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr
 705 710 715 720

Gly Leu Ser Gln Asn Leu Asp Ile Thr Arg Lys Glu Ala Ala Thr Phe
 725 730 735

Ile Glu Asn Tyr Leu Asn Ser Phe Pro Gly Val Lys Gly Tyr Met Asp
 740 745 750

Asp Ile Val Gln Asp Ala Lys Gln Thr Gly Tyr Val Thr Thr Ile Leu
 755 760 765

Asn Arg Arg Arg Tyr Leu Pro Glu Ile Thr Ser Ser Asn Phe Asn Leu
770 775 780

Arg Ser Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser
785 790 795 800

Ala Ala Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Glu Arg Leu
805 810 815

Ile Ser Glu Asn Met Gln Thr Lys Met Leu Leu Gln Val His Asp Glu
820 825 830

Leu Ile Phe Glu Ala Pro Pro Glu Glu Ile Ala Met Leu Glu Lys Ile
835 840 845

Val Pro Glu Val Met Glu Asn Ala Ile Lys Leu Ile Val Pro Leu Lys
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<212> DNA
<213> Psychrobacillus sp.

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acacaactag ctacagataa aacaactgtg tatatcaciaa gaaaaggcat aaccgatatt 480

gaaaaatata cacctgaaca tgtacaagaa aagtatggct taactccatt acagattata	540
gacatgaaaag gtttaaatggg agatgcttct gataatattc caggagttcc tgggtgctgga	600
gaaaaaacag ctattaagct tttaaaagaa catgggttcgg tagaggattt atataaagca	660
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attatgagta aggcattagc tacgattgaa acagctgcac cgatacagat ttctatagac	780
gatctttcat atactgggtcc taatatggaa gaagtaattg aagtttgga ggaactagct	840
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gatatgcgcc gtgctgctaa ggcagttaac tttgggattg tgtatggtat tagtgattat      2160
ggtttatcac aaaacctaga tattactaga aaagaagcgg cgacatttat cgagaattat      2220
ttaaatagct tcccaggtgt aaaaggatat atggatgata tcgttcaaga tgcgaaacaa      2280
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gcagccgata ttattaaaaa agcaatgatc gatatggcgg aaagattaat atcagaaaat      2460
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gaaattgcaa tgctagaaaa aatagtgcc gaggtgatgg aaaacgctat taaactgatt      2580
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<213> Bacillus species C3_41

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<213> Ureibacillus thermosphaericus

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<400> 7

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<212> PRT
<213> Bacillus subtilis

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Ser Asp Tyr Gly Leu Ser Gln Asn Leu Gly Ile Thr Arg Lys Glu Ala
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<212> PRT
<213> Bacillus smithii

<400> 9

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<210> 10
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<212> PRT
<213> Geobacillus stearothermophilus

<400> 10

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<210> 11

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<213> Geobacillus stearothermophilus

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20 25 30

Asp Ala Pro Ile Val Gly Ile Ala Val Val Asn Glu His Gly Arg Phe
35 40 45

Phe Leu Arg Pro Glu Thr Ala Leu Ala Asp Pro Gln Phe Val Ala Trp
50 55 60

Leu Gly Asp Glu Thr Lys Lys Lys Ser Met Phe Asp Ser Lys Arg Ala
65 70 75 80

Ala Val Ala Leu Lys Trp Lys Gly Ile Glu Leu Cys Gly Val Ser Phe
85 90 95

Asp Leu Leu Leu Ala Ala Tyr Leu Leu Asp Pro Ala Gln Gly Val Asp
100 105 110

Asp Val Ala Ala Ala Lys Met Lys Gln Tyr Glu Ala Val Arg Pro
115 120 125

Asp Glu Ala Val Tyr Gly Lys Gly Ala Lys Arg Ala Val Pro Asp Glu
130 135 140

Pro Val Leu Ala Glu His Leu Val Arg Lys Ala Ala Ala Ile Trp Glu
145 150 155 160

Leu Glu Arg Pro Phe Leu Asp Glu Leu Arg Arg Asn Glu Gln Asp Arg
165 170 175

Leu Leu Val Glu Leu Glu Gln Pro Leu Ser Ser Ile Leu Ala Glu Met
180 185 190

Glu Phe Ala Gly Val Lys Val Asp Thr Lys Arg Leu Glu Gln Met Gly
195 200 205

Lys Glu Leu Ala Glu Gln Leu Gly Thr Val Glu Gln Arg Ile Tyr Glu
210 215 220

Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys Gln Leu Gly Val
225 230 235 240

Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys Lys Thr Lys Thr
245 250 255

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

Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu Gly Lys Leu Gln
275 280 285

Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val Arg Pro Asp Thr Lys
290 295 300

Lys Val His Thr Ile Phe Asn Gln Ala Leu Thr Gln Thr Gly Arg Leu
305 310 315 320

Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile Arg Leu Glu Glu
325 330 335

Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu Ser Asp Trp Leu
340 345 350

Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His
355 360 365

Ile Ala Glu Asp Asp Asn Leu Met Glu Ala Phe Arg Arg Asp Leu Asp
370 375 380

Ile His Thr Lys Thr Ala Met Asp Ile Phe Gln Val Ser Glu Asp Glu
385 390 395 400

Val Thr Pro Asn Met Arg Arg Gln Ala Lys Ala Val Asn Phe Gly Ile
405 410 415

Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn Leu Asn Ile Ser
420 425 430

Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe Glu Ser Phe Pro
435 440 445

Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu Ala Lys Gln Lys
450 455 460

Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr Leu Pro Asp Ile
465 470 475 480

Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu Arg Met Ala Met
485 490 495

Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile Lys Lys Ala Met
500 505 510

Ile Asp Leu Asn Ala Arg Leu Lys Glu Glu Arg Leu Gln Ala His Leu
515 520 525

Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala Pro Lys Glu Glu
530 535 540

Met Glu Arg Leu Cys Arg Leu Val Pro Glu Val Met Glu Gln Ala Val
545 550 555 560

Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr Gly Ser Thr Trp
565 570 575

Tyr Asp Ala Lys
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<210> 12
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<400> 12

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20 25 30

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35 40 45

Phe Val Pro Thr Glu Val Leu Gln Lys Ser Glu Arg Leu Lys Ser Tyr
50 55 60

Phe Glu Asp Glu Thr Lys Lys Lys Tyr Met Ser Asp Leu Lys Ala Ala
65 70 75 80

Gln Cys Ile Leu Lys Arg His Gly Ile Asn Leu Arg Gly Val Glu Phe
85 90 95

Asp Leu Leu Leu Ala Ser Tyr Ile Val Asn Pro Ala Ile Ser Gly Asp
100 105 110

Asp Val Ala Thr Leu Ala Lys Glu Phe Gly Tyr Thr Asp Val Arg Ser
115 120 125

Asn Glu Ala Val Tyr Gly Lys Gly Ala Lys Trp Ala Leu Pro Ser Glu
130 135 140

Glu Val Leu Ala Glu His Val Cys Arg Lys Ala Phe Ala Ile Trp Ser
145 150 155 160

Cys Lys Glu Arg Val Ser Asn Lys Leu Lys Glu Asn Glu Gln Phe Asp
165 170 175

Leu Tyr His Asp Leu Glu Leu Pro Leu Ala Val Ile Leu Gly Lys Met
180 185 190

Glu Ser Glu Gly Ile Lys Val Asn Ile Ser Thr Leu Glu Thr Met Gly
195 200 205

Gln Glu Leu Glu Asp Lys Ile Ala Lys Leu Glu Thr Glu Ile Tyr Glu
210 215 220

Leu Ala Gly Glu Thr Phe Asn Ile Asn Ser Pro Lys Gln Leu Gly Val
225 230 235 240

Ile Leu Phe Glu Lys Leu Gly Leu Pro Val Ile Lys Lys Thr Lys Thr
245 250 255

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

Gln Ile Val Gln Leu Ile Leu Glu Tyr Arg Thr Leu Ala Lys Leu Gln
275 280 285

Ser Thr Tyr Ile Glu Gly Leu Ile Lys Glu Val His Pro Lys Asp Ser
290 295 300

Lys Val His Thr Arg Phe Met Gln Ala Leu Thr Ser Thr Gly Arg Leu
305 310 315 320

Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Ile Arg Leu Glu Glu
325 330 335

Gly Arg Lys Ile Arg Lys Ala Phe Val Pro Ser His Asp Gly Trp Leu
340 345 350

Leu Phe Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His

355

360

365

Met Ser Lys Asp Lys Asn Leu Val Glu Ala Phe Asn Gln Gly Met Asp
 370 375 380

Ile His Thr Arg Thr Ala Met Glu Val Phe His Val Ser Gln Asp Asp
 385 390 395 400

Val Thr Ser Asn Met Arg Arg Ala Ala Lys Ala Val Asn Phe Gly Ile
 405 410 415

Ile Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn Leu Asp Ile Ser
 420 425 430

Arg Lys Glu Ala Gly Glu Phe Ile Glu Lys Tyr Phe Glu Ser Phe Pro
 435 440 445

Gly Val Lys Glu Tyr Met Asp Asn Ile Val Gln Glu Ala Lys Leu Lys
 450 455 460

Gly Tyr Val Thr Thr Ile Leu Asn Arg Arg Arg Tyr Leu Pro Asp Ile
 465 470 475 480

Thr Ser Lys Asn Phe Asn Leu Arg Ser Phe Ala Glu Arg Thr Ala Met
 485 490 495

Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile Lys Lys Ala Met
 500 505 510

Leu Asp Ile Asp Ala Arg Leu Asn Ser Glu Gly Leu Gln Ala Lys Leu
 515 520 525

Leu Leu Gln Val His Asp Glu Leu Ile Phe Glu Ala Pro Lys Glu Glu
 530 535 540

Ile Glu Lys Leu Glu Lys Ile Val Pro Glu Val Met Glu Ser Ala Ile
 545 550 555 560

Leu Leu Asp Val Pro Leu Lys Val Asp Ile Ser Tyr Gly Glu Thr Trp
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Tyr Asp Ala Lys
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gcagttgcac tgaaatggaa aggtattgaa ctgtgcggtg tttcatttga tctgctgctg	300
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taa	1743

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<220>
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 <222> (7)..(7)
 <223> labelled with the fluorophore Dabcyl

<220>
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 <222> (32)..(32)
 <223> labelled with the fluorophore FAM

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gtcgtcagaa atttcgcacc ac	82

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<220>

<223> Artificial Sequence

<400> 17

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19

<210> 18

<211> 19

<212> DNA

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<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence

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<222> (20)..(20)

<223> labelled at 3' end with TAMRA fluorophore

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20

<210> 20

<211> 40

<212> DNA

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<220>

<223> Artificial Sequence

<220>

<221> misc_feature

<222> (1)..(1)

<223> labelled at 5' end with Black Hole Quencher 2

<400> 20

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40