

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

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<211> 32

<212> PRT

<213> Psychrobacillus sp.

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<211> 580

<212> PRT

<213> Psychrobacillus sp.

<400> 2

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20 25 30

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
50 55 60

Leu Glu Asn Ala Thr Asn Lys Lys Tyr Leu Ala Asp Ser Lys Ala Thr

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Gln	Ala	Val	Ser	Arg	Lys	His	Asn	Val	Asn	Val	His	Gly	Val	Glu	Phe
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Asp	Leu	Leu	Leu	Ala	Ala	Tyr	Ile	Val	Asn	Pro	Ala	Ile	Ser	Ser	Glu
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Asp	Val	Ala	Ala	Ile	Ala	Lys	Glu	Phe	Gly	Tyr	Phe	Asn	Leu	Leu	Thr
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Glu	Lys	Ile	Ala	Glu	His	Ala	Val	Arg	Lys	Ala	Arg	Ala	Ile	Trp	Asp
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Leu	Lys	Glu	Lys	Leu	Glu	Val	Lys	Leu	Glu	Glu	Asn	Glu	Gln	Tyr	Ala
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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
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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
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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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 ttatcagatg gagaaaaggg ttattttgct cctgctgata tagcttttca atcgaaggat 180
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 atactatttg aaaaaattgg tcttaccct attaaaaaga caaaaacggg ctattcaact 780

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tcagaaaata tgcagaccaa	aatgctacta caagtacatg	atgaattaat ttttgaggct	1620
ccaccagagg aaattgcaat	gctagaaaaa atagtgccag	aggtgatgga aaacgctatt	1680
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 <213> Psychrobacillus sp.

<400> 4

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			20					25					30		

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
850 855 860

Val Asp Tyr Ala Phe Gly Ser Ser Trp Tyr Asp Thr Lys
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<212> DNA

<213> Psychrobacillus sp.

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tatggtatta agcgatacga actggaaatg tacgaagcag acgatattat cgggtacttta	360
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gatattcata	ctaaaacggc	tatggatgta	ttccatgtgg	agcaggaagc	agtaacgtcc	2100	
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 <212> PRT
 <213> Bacillus species C3_41

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Met	Arg	Arg	Ala	Ala	Lys	Ala	Val	Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile
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Ser	Asp	Tyr	Gly	Leu	Ser	Gln	Asn	Leu	Asp	Ile	Thr	Arg	Lys	Glu	Ala
			20				25						30		

<210> 7
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 <212> PRT
 <213> Ureibacillus thermosphaericus

<400> 7

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<210> 8

<211> 32

<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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<210> 9

<211> 32

<212> PRT

<213> Bacillus smithii

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<210> 10

<211> 32

<212> PRT

<213> Geobacillus stearothermophilus

<400> 10

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<210> 11
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<212> PRT
<213> Geobacillus stearothermophilus

<400> 11

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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
580

<210> 12

<211> 580

<212> PRT

<213> Ureibacillus thermosphaericus

<400> 12

Ala Ala Leu Ser Phe Lys Ile Val Arg Glu Ile Ala Glu Asp Leu Phe
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20 25 30

Thr Cys Asn Ile Leu Gly Phe Gly Phe Thr Asp Gly Ser Asn Thr Phe
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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<220>
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gcagcatata ttgttaatcc ggcaattagc agcgaagatg ttgcagcaat tgcaaaagaa	360
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1743

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<220>
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<220>
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<400> 17
gtggtgcgaa atttctgac 19

<210> 18
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<220>
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<400> 18
tatccaccaa tactaccct 19

<210> 19
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<220>
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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

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40