

SEQUENCE LISTING

<110> OXFORD NANOPORE TECHNOLOGIES LIMITED

<120> METHOD

<130> N416641W0

<150> GB 1907244.6

<151> 2019-05-22

<160> 12

<170> PatentIn version 3.5

<210> 1

<211> 485

<212> PRT

<213> Escherichia coli

<400> 1

Met	Met	Asn	Asp	Gly	Lys	Gln	Gln	Ser	Thr	Phe	Leu	Phe	His	Asp	Tyr
1				5					10					15	

Glu	Thr	Phe	Gly	Thr	His	Pro	Ala	Leu	Asp	Arg	Pro	Ala	Gln	Phe	Ala
			20					25					30		

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

Phe	Tyr	Cys	Lys	Pro	Ala	Asp	Asp	Tyr	Leu	Pro	Gln	Pro	Gly	Ala	Val
	50					55					60				

Leu	Ile	Thr	Gly	Ile	Thr	Pro	Gln	Glu	Ala	Arg	Ala	Lys	Gly	Glu	Asn
65					70					75					80

Glu	Ala	Ala	Phe	Ala	Ala	Arg	Ile	His	Ser	Leu	Phe	Thr	Val	Pro	Lys
			85						90					95	

Thr	Cys	Ile	Leu	Gly	Tyr	Asn	Asn	Val	Arg	Phe	Asp	Asp	Glu	Val	Thr
			100					105					110		

Arg	Asn	Ile	Phe	Tyr	Arg	Asn	Phe	Tyr	Asp	Pro	Tyr	Ala	Trp	Ser	Trp
		115					120					125			

Gln His Asp Asn Ser Arg Trp Asp Leu Leu Asp Val Met Arg Ala Cys
130 135 140

Tyr Ala Leu Arg Pro Glu Gly Ile Asn Trp Pro Glu Asn Asp Asp Gly
145 150 155 160

Leu Pro Ser Phe Arg Leu Glu His Leu Thr Lys Ala Asn Gly Ile Glu
165 170 175

His Ser Asn Ala His Asp Ala Met Ala Asp Val Tyr Ala Thr Ile Ala
180 185 190

Met Ala Lys Leu Val Lys Thr Arg Gln Pro Arg Leu Phe Asp Tyr Leu
195 200 205

Phe Thr His Arg Asn Lys His Lys Leu Met Ala Leu Ile Asp Val Pro
210 215 220

Gln Met Lys Pro Leu Val His Val Ser Gly Met Phe Gly Ala Trp Arg
225 230 235 240

Gly Asn Thr Ser Trp Val Ala Pro Leu Ala Trp His Pro Glu Asn Arg
245 250 255

Asn Ala Val Ile Met Val Asp Leu Ala Gly Asp Ile Ser Pro Leu Leu
260 265 270

Glu Leu Asp Ser Asp Thr Leu Arg Glu Arg Leu Tyr Thr Ala Lys Thr
275 280 285

Asp Leu Gly Asp Asn Ala Ala Val Pro Val Lys Leu Val His Ile Asn
290 295 300

Lys Cys Pro Val Leu Ala Gln Ala Asn Thr Leu Arg Pro Glu Asp Ala
305 310 315 320

Asp Arg Leu Gly Ile Asn Arg Gln His Cys Leu Asp Asn Leu Lys Ile
325 330 335

Leu Arg Glu Asn Pro Gln Val Arg Glu Lys Val Val Ala Ile Phe Ala
340 345 350

Glu Ala Glu Pro Phe Thr Pro Ser Asp Asn Val Asp Ala Gln Leu Tyr
355 360 365

Asn Gly Phe Phe Ser Asp Ala Asp Arg Ala Ala Met Lys Ile Val Leu
370 375 380

Glu Thr Glu Pro Arg Asn Leu Pro Ala Leu Asp Ile Thr Phe Val Asp
385 390 395 400

Lys Arg Ile Glu Lys Leu Leu Phe Asn Tyr Arg Ala Arg Asn Phe Pro
405 410 415

Gly Thr Leu Asp Tyr Ala Glu Gln Gln Arg Trp Leu Glu His Arg Arg
420 425 430

Gln Val Phe Thr Pro Glu Phe Leu Gln Gly Tyr Ala Asp Glu Leu Gln
435 440 445

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

Lys Ala Leu Trp Gln Tyr Ala Glu Glu Ile Val Ser Gly Ser Gly His
465 470 475 480

His His His His His
485

<210> 2
<211> 268
<212> PRT
<213> Escherichia coli

<400> 2

Met Lys Phe Val Ser Phe Asn Ile Asn Gly Leu Arg Ala Arg Pro His
1 5 10 15

Gln Leu Glu Ala Ile Val Glu Lys His Gln Pro Asp Val Ile Gly Leu
20 25 30

Gln Glu Thr Lys Val His Asp Asp Met Phe Pro Leu Glu Glu Val Ala

35

40

45

Lys Leu Gly Tyr Asn Val Phe Tyr His Gly Gln Lys Gly His Tyr Gly
50 55 60

Val Ala Leu Leu Thr Lys Glu Thr Pro Ile Ala Val Arg Arg Gly Phe
65 70 75 80

Pro Gly Asp Asp Glu Glu Ala Gln Arg Arg Ile Ile Met Ala Glu Ile
85 90 95

Pro Ser Leu Leu Gly Asn Val Thr Val Ile Asn Gly Tyr Phe Pro Gln
100 105 110

Gly Glu Ser Arg Asp His Pro Ile Lys Phe Pro Ala Lys Ala Gln Phe
115 120 125

Tyr Gln Asn Leu Gln Asn Tyr Leu Glu Thr Glu Leu Lys Arg Asp Asn
130 135 140

Pro Val Leu Ile Met Gly Asp Met Asn Ile Ser Pro Thr Asp Leu Asp
145 150 155 160

Ile Gly Ile Gly Glu Glu Asn Arg Lys Arg Trp Leu Arg Thr Gly Lys
165 170 175

Cys Ser Phe Leu Pro Glu Glu Arg Glu Trp Met Asp Arg Leu Met Ser
180 185 190

Trp Gly Leu Val Asp Thr Phe Arg His Ala Asn Pro Gln Thr Ala Asp
195 200 205

Arg Phe Ser Trp Phe Asp Tyr Arg Ser Lys Gly Phe Asp Asp Asn Arg
210 215 220

Gly Leu Arg Ile Asp Leu Leu Leu Ala Ser Gln Pro Leu Ala Glu Cys
225 230 235 240

Cys Val Glu Thr Gly Ile Asp Tyr Glu Ile Arg Ser Met Glu Lys Pro
245 250 255

Ser Asp His Ala Pro Val Trp Ala Thr Phe Arg Arg
260 265

<210> 3
<211> 425
<212> PRT
<213> Thermus thermophilus

<400> 3

Met Phe Arg Arg Lys Glu Asp Leu Asp Pro Pro Leu Ala Leu Leu Pro
1 5 10 15

Leu Lys Gly Leu Arg Glu Ala Ala Ala Leu Leu Glu Glu Ala Leu Arg
20 25 30

Gln Gly Lys Arg Ile Arg Val His Gly Asp Tyr Asp Ala Asp Gly Leu
35 40 45

Thr Gly Thr Ala Ile Leu Val Arg Gly Leu Ala Ala Leu Gly Ala Asp
50 55 60

Val His Pro Phe Ile Pro His Arg Leu Glu Glu Gly Tyr Gly Val Leu
65 70 75 80

Met Glu Arg Val Pro Glu His Leu Glu Ala Ser Asp Leu Phe Leu Thr
85 90 95

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

Asn Gly Val Glu Val Ile Val Thr Asp His His Thr Pro Gly Lys Thr
115 120 125

Pro Pro Pro Gly Leu Val Val His Pro Ala Leu Thr Pro Asp Leu Lys
130 135 140

Glu Lys Pro Thr Gly Ala Gly Val Ala Phe Leu Leu Leu Trp Ala Leu
145 150 155 160

His Glu Arg Leu Gly Leu Pro Pro Pro Leu Glu Tyr Ala Asp Leu Ala
165 170 175

Ala Val Gly Thr Ile Ala Asp Val Ala Pro Leu Trp Gly Trp Asn Arg
180 185 190

Ala Leu Val Lys Glu Gly Leu Ala Arg Ile Pro Ala Ser Ser Trp Val
195 200 205

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

Glu Val Ala Phe Arg Ile Ala Pro Arg Ile Asn Ala Ala Ser Arg Leu
225 230 235 240

Gly Glu Ala Glu Lys Ala Leu Arg Leu Leu Thr Asp Asp Ala Ala
245 250 255

Glu Ala Gln Ala Leu Val Gly Glu Leu His Arg Leu Asn Ala Arg Arg
260 265 270

Gln Thr Leu Glu Glu Ala Met Leu Arg Lys Leu Leu Pro Gln Ala Asp
275 280 285

Pro Glu Ala Lys Ala Ile Val Leu Leu Asp Pro Glu Gly His Pro Gly
290 295 300

Val Met Gly Ile Val Ala Ser Arg Ile Leu Glu Ala Thr Leu Arg Pro
305 310 315 320

Val Phe Leu Val Ala Gln Gly Lys Gly Thr Val Arg Ser Leu Ala Pro
325 330 335

Ile Ser Ala Val Glu Ala Leu Arg Ser Ala Glu Asp Leu Leu Leu Arg
340 345 350

Tyr Gly Gly His Lys Glu Ala Ala Gly Phe Ala Met Asp Glu Ala Leu
355 360 365

Phe Pro Ala Phe Lys Ala Arg Val Glu Ala Tyr Ala Ala Arg Phe Pro
370 375 380

Asp Pro Val Arg Glu Val Ala Leu Leu Asp Leu Leu Pro Glu Pro Gly
385 390 395 400

Leu Leu Pro Gln Val Phe Arg Glu Leu Ala Leu Leu Glu Pro Tyr Gly
405 410 415

Glu Gly Asn Pro Glu Pro Leu Phe Leu
420 425

<210> 4
<211> 226
<212> PRT
<213> Bacteriophage lambda

<400> 4

Met Thr Pro Asp Ile Ile Leu Gln Arg Thr Gly Ile Asp Val Arg Ala
1 5 10 15

Val Glu Gln Gly Asp Asp Ala Trp His Lys Leu Arg Leu Gly Val Ile
20 25 30

Thr Ala Ser Glu Val His Asn Val Ile Ala Lys Pro Arg Ser Gly Lys
35 40 45

Lys Trp Pro Asp Met Lys Met Ser Tyr Phe His Thr Leu Leu Ala Glu
50 55 60

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

Gly Lys Gln Tyr Glu Asn Asp Ala Arg Thr Leu Phe Glu Phe Thr Ser
85 90 95

Gly Val Asn Val Thr Glu Ser Pro Ile Ile Tyr Arg Asp Glu Ser Met
100 105 110

Arg Thr Ala Cys Ser Pro Asp Gly Leu Cys Ser Asp Gly Asn Gly Leu
115 120 125

Glu Leu Lys Cys Pro Phe Thr Ser Arg Asp Phe Met Lys Phe Arg Leu
130 135 140

Gly Gly Phe Glu Ala Ile Lys Ser Ala Tyr Met Ala Gln Val Gln Tyr
145 150 155 160

Ser Met Trp Val Thr Arg Lys Asn Ala Trp Tyr Phe Ala Asn Tyr Asp
165 170 175

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

Glu Lys Tyr Met Ala Ser Phe Asp Glu Ile Val Pro Glu Phe Ile Glu
195 200 205

Lys Met Asp Glu Ala Leu Ala Glu Ile Gly Phe Val Phe Gly Glu Gln
210 215 220

Trp Arg
225

<210> 5
<211> 608
<212> PRT
<213> Bacillus subtilis phage Phi 29

<400> 5

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Ala Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
130 135 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
325 330 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
355 360 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
500 505 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys Ser
565 570 575

Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
595 600 605

<210> 6
<211> 970
<212> PRT
<213> Citromicrobium bathyomarinum

<400> 6

Met Leu Ser Val Ala Asn Val Arg Ser Pro Ser Ala Ala Ala Ser Tyr
1 5 10 15

Phe Ala Ser Asp Asn Tyr Tyr Ala Ser Ala Asp Ala Asp Arg Ser Gly
20 25 30

Gln Trp Ile Gly Asp Gly Ala Lys Arg Leu Gly Leu Glu Gly Lys Val
35 40 45

Glu Ala Arg Ala Phe Asp Ala Leu Leu Arg Gly Glu Leu Pro Asp Gly
50 55 60

Ser Ser Val Gly Asn Pro Gly Gln Ala His Arg Pro Gly Thr Asp Leu
65 70 75 80

Thr Phe Ser Val Pro Lys Ser Trp Ser Leu Leu Ala Leu Val Gly Lys
85 90 95

Asp Glu Arg Ile Ile Ala Ala Tyr Arg Glu Ala Val Val Glu Ala Leu

100

105

110

His Trp Ala Glu Lys Asn Ala Ala Glu Thr Arg Val Val Glu Lys Gly
 115 120 125

Met Val Val Thr Gln Ala Thr Gly Asn Leu Ala Ile Gly Leu Phe Gln
 130 135 140

His Asp Thr Asn Arg Asn Gln Glu Pro Asn Leu His Phe His Ala Val
 145 150 155 160

Ile Ala Asn Val Thr Gln Gly Lys Asp Gly Lys Trp Arg Thr Leu Lys
 165 170

Asn Asp Arg Leu Trp Gln Leu Asn Thr Thr Leu Asn Ser Ile Ala Met
 180 185 190

Ala Arg Phe Arg Val Ala Val Glu Lys Leu Gly Tyr Glu Pro Gly Pro
 195 200 205

Val Leu Lys His Gly Asn Phe Glu Ala Arg Gly Ile Ser Arg Glu Gln
 210 215 220

Val Met Ala Phe Ser Thr Arg Arg Lys Glu Val Leu Glu Ala Arg Arg
 225 230 235 240

Gly Pro Gly Leu Asp Ala Gly Arg Ile Ala Ala Leu Asp Thr Arg Ala
 245 250 255

Ser Lys Glu Gly Ile Glu Asp Arg Ala Thr Leu Ser Lys Gln Trp Ser
 260 265 270

Glu Ala Ala Gln Ser Ile Gly Leu Asp Leu Lys Pro Leu Val Asp Arg
 275 280 285

Ala Arg Thr Lys Ala Leu Gly Gln Gly Met Glu Ala Thr Arg Ile Gly
 290 295 300

Ser Leu Val Glu Arg Gly Arg Ala Trp Leu Ser Arg Phe Ala Ala His
 305 310 315 320

Val Arg Gly Asp Pro Ala Asp Pro Leu Val Pro Pro Ser Val Leu Lys
325 330 335

Gln Asp Arg Gln Thr Ile Ala Ala Ala Gln Ala Val Ala Ser Ala Val
340 345 350

Arg His Leu Ser Gln Arg Glu Ala Ala Phe Glu Arg Thr Ala Leu Tyr
355 360 365

Lys Ala Ala Leu Asp Phe Gly Leu Pro Thr Thr Ile Ala Asp Val Glu
370 375 380

Lys Arg Thr Arg Ala Leu Val Arg Ser Gly Asp Leu Ile Ala Gly Lys
385 390 395 400

Gly Glu His Lys Gly Trp Leu Ala Ser Arg Asp Ala Val Val Thr Glu
405 410 415

Gln Arg Ile Leu Ser Glu Val Ala Ala Gly Lys Gly Asp Ser Ser Pro
420 425 430

Ala Ile Thr Pro Gln Lys Ala Ala Ala Ser Val Gln Ala Ala Ala Leu
435 440 445

Thr Gly Gln Gly Phe Arg Leu Asn Glu Gly Gln Leu Ala Ala Ala Arg
450 455 460

Leu Ile Leu Ile Ser Lys Asp Arg Thr Ile Ala Val Gln Gly Ile Ala
465 470 475 480

Gly Ala Gly Lys Ser Ser Val Leu Lys Pro Val Ala Glu Val Leu Arg
485 490 495

Asp Glu Gly His Pro Val Ile Gly Leu Ala Ile Gln Asn Thr Leu Val
500 505 510

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

Phe Leu Gly Gly Trp Asn Lys Leu Leu Asp Asp Pro Gly Asn Val Ala

530

535

540

Leu Arg Ala Glu Ala Gln Ala Ser Leu Lys Asp His Val Leu Val Leu
 545 550 555 560

Asp Glu Ala Ser Met Val Ser Asn Glu Asp Lys Glu Lys Leu Val Arg
 565 570 575

Leu Ala Asn Leu Ala Gly Val His Arg Leu Val Leu Ile Gly Asp Arg
 580 585 590

Lys Gln Leu Gly Ala Val Asp Ala Gly Lys Pro Phe Ala Leu Leu Gln
 595 600 605

Arg Ala Gly Ile Ala Arg Ala Glu Met Ala Thr Asn Leu Arg Ala Arg
 610 615 620

Asp Pro Val Val Arg Glu Ala Gln Ala Ala Ala Gln Ala Gly Asp Val
 625 630 635 640

Arg Lys Ala Leu Arg His Leu Lys Ser His Thr Val Glu Ala Arg Gly
 645 650 655

Asp Gly Ala Gln Val Ala Ala Glu Thr Trp Leu Ala Leu Asp Lys Glu
 660 665 670

Thr Arg Ala Arg Thr Ser Ile Tyr Ala Ser Gly Arg Ala Ile Arg Ser
 675 680 685

Ala Val Asn Ala Ala Val Gln Gln Gly Leu Leu Ala Ser Arg Glu Ile
 690 695 700

Gly Pro Ala Lys Met Lys Leu Glu Val Leu Asp Arg Val Asn Thr Thr
 705 710 715 720

Arg Glu Glu Leu Arg His Leu Pro Ala Tyr Arg Ala Gly Arg Val Leu
 725 730 735

Glu Val Ser Arg Lys Gln Gln Ala Leu Gly Leu Phe Ile Gly Glu Tyr
 740 745 750

Arg Val Ile Gly Gln Asp Arg Lys Gly Lys Leu Val Glu Val Glu Asp
755 760 765

Lys Arg Gly Lys Arg Phe Arg Phe Asp Pro Ala Arg Ile Arg Ala Gly
770 775 780

Lys Gly Asp Asp Asn Leu Thr Leu Leu Glu Pro Arg Lys Leu Glu Ile
785 790 795 800

His Glu Gly Asp Arg Ile Arg Trp Thr Arg Asn Asp His Arg Arg Gly
805 810 815

Leu Phe Asn Ala Asp Gln Ala Arg Val Val Glu Ile Ala Asn Gly Lys
820 825 830

Val Thr Phe Glu Thr Ser Lys Gly Asp Leu Val Glu Leu Lys Lys Asp
835 840 845

Asp Pro Met Leu Lys Arg Ile Asp Leu Ala Tyr Ala Leu Asn Val His
850 855 860

Met Ala Gln Gly Leu Thr Ser Asp Arg Gly Ile Ala Val Met Asp Ser
865 870 875 880

Arg Glu Arg Asn Leu Ser Asn Gln Lys Thr Phe Leu Val Thr Val Thr
885 890 895

Arg Leu Arg Asp His Leu Thr Leu Val Val Asp Ser Ala Asp Lys Leu
900 905 910

Gly Ala Ala Val Ala Arg Asn Lys Gly Glu Lys Ala Ser Ala Ile Glu
915 920 925

Val Thr Gly Ser Val Lys Pro Thr Ala Thr Lys Gly Ser Gly Val Asp
930 935 940

Gln Pro Lys Ser Val Glu Ala Asn Lys Ala Glu Lys Glu Leu Thr Arg
945 950 955 960

Ser Lys Ser Lys Thr Leu Asp Phe Gly Ile

965

970

<210> 7

<211> 760

<212> PRT

<213> Methanococcoides burtonii

<400> 7

Met Met Ile Arg Glu Leu Asp Ile Pro Arg Asp Ile Ile Gly Phe Tyr
 1 5 10 15

Glu Asp Ser Gly Ile Lys Glu Leu Tyr Pro Pro Gln Ala Glu Ala Ile
 20 25 30

Glu Met Gly Leu Leu Glu Lys Lys Asn Leu Leu Ala Ala Ile Pro Thr
 35 40 45

Ala Ser Gly Lys Thr Leu Leu Ala Glu Leu Ala Met Ile Lys Ala Ile
 50 55 60

Arg Glu Gly Gly Lys Ala Leu Tyr Ile Val Pro Leu Arg Ala Leu Ala
 65 70 75 80

Ser Glu Lys Phe Glu Arg Phe Lys Glu Leu Ala Pro Phe Gly Ile Lys
 85 90 95

Val Gly Ile Ser Thr Gly Asp Leu Asp Ser Arg Ala Asp Trp Leu Gly
 100 105 110

Val Asn Asp Ile Ile Val Ala Thr Ser Glu Lys Thr Asp Ser Leu Leu
 115 120 125

Arg Asn Gly Thr Ser Trp Met Asp Glu Ile Thr Thr Val Val Val Asp
 130 135 140

Glu Ile His Leu Leu Asp Ser Lys Asn Arg Gly Pro Thr Leu Glu Val
 145 150 155 160

Thr Ile Thr Lys Leu Met Arg Leu Asn Pro Asp Val Gln Val Val Ala
 165 170 175

Leu Ser Ala Thr Val Gly Asn Ala Arg Glu Met Ala Asp Trp Leu Gly
180 185 190

Ala Ala Leu Val Leu Ser Glu Trp Arg Pro Thr Asp Leu His Glu Gly
195 200 205

Val Leu Phe Gly Asp Ala Ile Asn Phe Pro Gly Ser Gln Lys Lys Ile
210 215 220

Asp Arg Leu Glu Lys Asp Asp Ala Val Asn Leu Val Leu Asp Thr Ile
225 230 235 240

Lys Ala Glu Gly Gln Cys Leu Val Phe Glu Ser Ser Arg Arg Asn Cys
245 250 255

Ala Gly Phe Ala Lys Thr Ala Ser Ser Lys Val Ala Lys Ile Leu Asp
260 265 270

Asn Asp Ile Met Ile Lys Leu Ala Gly Ile Ala Glu Glu Val Glu Ser
275 280 285

Thr Gly Glu Thr Asp Thr Ala Ile Val Leu Ala Asn Cys Ile Arg Lys
290 295 300

Gly Val Ala Phe His His Ala Gly Leu Asn Ser Asn His Arg Lys Leu
305 310 315 320

Val Glu Asn Gly Phe Arg Gln Asn Leu Ile Lys Val Ile Ser Ser Thr
325 330 335

Pro Thr Leu Ala Ala Gly Leu Asn Leu Pro Ala Arg Arg Val Ile Ile
340 345 350

Arg Ser Tyr Arg Arg Phe Asp Ser Asn Phe Gly Met Gln Pro Ile Pro
355 360 365

Val Leu Glu Tyr Lys Gln Met Ala Gly Arg Ala Gly Arg Pro His Leu
370 375 380

Asp Pro Tyr Gly Glu Ser Val Leu Leu Ala Lys Thr Tyr Asp Glu Phe
385 390 395 400

Ala Gln Leu Met Glu Asn Tyr Val Glu Ala Asp Ala Glu Asp Ile Trp
405 410 415

Ser Lys Leu Gly Thr Glu Asn Ala Leu Arg Thr His Val Leu Ser Thr
420 425 430

Ile Val Asn Gly Phe Ala Ser Thr Arg Gln Glu Leu Phe Asp Phe Phe
435 440 445

Gly Ala Thr Phe Phe Ala Tyr Gln Gln Asp Lys Trp Met Leu Glu Glu
450 455 460

Val Ile Asn Asp Cys Leu Glu Phe Leu Ile Asp Lys Ala Met Val Ser
465 470 475 480

Glu Thr Glu Asp Ile Glu Asp Ala Ser Lys Leu Phe Leu Arg Gly Thr
485 490 495

Arg Leu Gly Ser Leu Val Ser Met Leu Tyr Ile Asp Pro Leu Ser Gly
500 505 510

Ser Lys Ile Val Asp Gly Phe Lys Asp Ile Gly Lys Ser Thr Gly Gly
515 520 525

Asn Met Gly Ser Leu Glu Asp Asp Lys Gly Asp Asp Ile Thr Val Thr
530 535 540

Asp Met Thr Leu Leu His Leu Val Cys Ser Thr Pro Asp Met Arg Gln
545 550 555 560

Leu Tyr Leu Arg Asn Thr Asp Tyr Thr Ile Val Asn Glu Tyr Ile Val
565 570 575

Ala His Ser Asp Glu Phe His Glu Ile Pro Asp Lys Leu Lys Glu Thr
580 585 590

Asp Tyr Glu Trp Phe Met Gly Glu Val Lys Thr Ala Met Leu Leu Glu
595 600 605

Glu Trp Val Thr Glu Val Ser Ala Glu Asp Ile Thr Arg His Phe Asn
610 615 620

Val Gly Glu Gly Asp Ile His Ala Leu Ala Asp Thr Ser Glu Trp Leu
625 630 635 640

Met His Ala Ala Ala Lys Leu Ala Glu Leu Leu Gly Val Glu Tyr Ser
645 650 655

Ser His Ala Tyr Ser Leu Glu Lys Arg Ile Arg Tyr Gly Ser Gly Leu
660 665 670

Asp Leu Met Glu Leu Val Gly Ile Arg Gly Val Gly Arg Val Arg Ala
675 680 685

Arg Lys Leu Tyr Asn Ala Gly Phe Val Ser Val Ala Lys Leu Lys Gly
690 695 700

Ala Asp Ile Ser Val Leu Ser Lys Leu Val Gly Pro Lys Val Ala Tyr
705 710 715 720

Asn Ile Leu Ser Gly Ile Gly Val Arg Val Asn Asp Lys His Phe Asn
725 730 735

Ser Ala Pro Ile Ser Ser Asn Thr Leu Asp Thr Leu Leu Asp Lys Asn
740 745 750

Gln Lys Thr Phe Asn Asp Phe Gln
755 760

<210> 8

<211> 439

<212> PRT

<213> Enterobacteria phage T4

<400> 8

Met Thr Phe Asp Asp Leu Thr Glu Gly Gln Lys Asn Ala Phe Asn Ile
1 5 10 15

Val Met Lys Ala Ile Lys Glu Lys Lys His His Val Thr Ile Asn Gly
20 25 30

Pro Ala Gly Thr Gly Lys Thr Thr Leu Thr Lys Phe Ile Ile Glu Ala
35 40 45

Leu Ile Ser Thr Gly Glu Thr Gly Ile Ile Leu Ala Ala Pro Thr His
50 55 60

Ala Ala Lys Lys Ile Leu Ser Lys Leu Ser Gly Lys Glu Ala Ser Thr
65 70 75 80

Ile His Ser Ile Leu Lys Ile Asn Pro Val Thr Tyr Glu Glu Asn Val
85 90 95

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

Ile Cys Asp Glu Val Ser Met Tyr Asp Arg Lys Leu Phe Lys Ile Leu
115 120 125

Leu Ser Thr Ile Pro Pro Trp Cys Thr Ile Ile Gly Ile Gly Asp Asn
130 135 140

Lys Gln Ile Arg Pro Val Asp Pro Gly Glu Asn Thr Ala Tyr Ile Ser
145 150 155 160

Pro Phe Phe Thr His Lys Asp Phe Tyr Gln Cys Glu Leu Thr Glu Val
165 170 175

Lys Arg Ser Asn Ala Pro Ile Ile Asp Val Ala Thr Asp Val Arg Asn
180 185 190

Gly Lys Trp Ile Tyr Asp Lys Val Val Asp Gly His Gly Val Arg Gly
195 200 205

Phe Thr Gly Asp Thr Ala Leu Arg Asp Phe Met Val Asn Tyr Phe Ser
210 215 220

Ile Val Lys Ser Leu Asp Asp Leu Phe Glu Asn Arg Val Met Ala Phe
225 230 235 240

Thr Asn Lys Ser Val Asp Lys Leu Asn Ser Ile Ile Arg Lys Lys Ile

245

250

255

Phe Glu Thr Asp Lys Asp Phe Ile Val Gly Glu Ile Ile Val Met Gln
 260 265 270

Glu Pro Leu Phe Lys Thr Tyr Lys Ile Asp Gly Lys Pro Val Ser Glu
 275 280 285

Ile Ile Phe Asn Asn Gly Gln Leu Val Arg Ile Ile Glu Ala Glu Tyr
 290 295 300

Thr Ser Thr Phe Val Lys Ala Arg Gly Val Pro Gly Glu Tyr Leu Ile
 305 310 315 320

Arg His Trp Asp Leu Thr Val Glu Thr Tyr Gly Asp Asp Glu Tyr Tyr
 325 330 335

Arg Glu Lys Ile Lys Ile Ile Ser Ser Asp Glu Glu Leu Tyr Lys Phe
 340 345 350

Asn Leu Phe Leu Gly Lys Thr Ala Glu Thr Tyr Lys Asn Trp Asn Lys
 355 360 365

Gly Gly Lys Ala Pro Trp Ser Asp Phe Trp Asp Ala Lys Ser Gln Phe
 370 375 380

Ser Lys Val Lys Ala Leu Pro Ala Ser Thr Phe His Lys Ala Gln Gly
 385 390 395 400

Met Ser Val Asp Arg Ala Phe Ile Tyr Thr Pro Cys Ile His Tyr Ala
 405 410 415

Asp Val Glu Leu Ala Gln Gln Leu Leu Tyr Val Gly Val Thr Arg Gly
 420 425 430

Arg Tyr Asp Val Phe Tyr Val
 435

<210> 9

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of a polynucleotide strand discussed in the example

<220>

<221> misc_feature

<222> (1)..(1)

<223> 5Biosg

<220>

<221> misc_feature

<222> (35)..(35)

<223> iSp18

<220>

<221> misc_feature

<222> (36)..(36)

<223> iSp18

<220>

<221> misc_feature

<222> (37)..(37)

<223> iSp18

<220>

<221> misc_feature

<222> (38)..(38)

<223> iSp18

<220>

<221> misc_feature

<222> (39)..(39)

<223> iBNA-C

<220>

<221> misc_feature

<222> (40)..(40)

<223> iBNA-C

<220>

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<223> iBNA-A

<220>

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<223> iBNA-C

<220>

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<222> (43)..(43)
 <223> iBNA-A

<220>
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 <222> (66)..(66)
 <223> 3Bio

<400> 9
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 attgcn 66

<210> 10
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence of a polynucleotide strand discussed in the
 example ("Test" strand).

<400> 10
 ggttaaacac ccaagcagac gccaaaaaaa agg 33

<210> 11
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence of a polynucleotide strand discussed in the
 example.

<220>
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 <222> (1)..(1)
 <223> 5phos

<220>
 <221> misc_feature
 <222> (24)..(24)
 <223> iBNA-T

<220>
 <221> misc_feature
 <222> (25)..(25)
 <223> iBNA-G

<220>
 <221> misc_feature

<222> (26)..(26)
<223> iBNA-T

<220>
<221> misc_feature
<222> (27)..(27)
<223> iBNA-G

<220>
<221> misc_feature
<222> (28)..(28)
<223> iBNA-G

<400> 11
ngcaatacgt aactgaacga agtnnnnn 28

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of a polynucleotide strand discussed in the
example ("Test -10" strand).

<400> 12
ccaagcagac gccaaaaaaa agg 23