

SEQUENCE LISTING

<110> Lucite International UK Limited

<120> METHODS FOR THE PRODUCTION OF METHACRYLATES

<130> P32701W01

<150> GB1808424.4

<151> 2018-05-23

<160> 33

<170> PatentIn version 3.5

<210> 1

<211> 465

<212> DNA

<213> Escherichia coli

<400> 1

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cgtaacagcg gcaatcagcg gcgatataaa cgtgatgtgt tgcgatatgt tgcaattatc    180
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gagttggatc ggcgcattca taccttagtg gcgctgcgtg acgaactgga cggatgtatt    360
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<213> Escherichia coli

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          20          25          30
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Ser Lys Gly Leu Ile Thr Ser Ile Arg Asn Ser Gly Asn Gln Arg Arg
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35

40

45

Tyr Lys Arg Asp Val Leu Arg Tyr Val Ala Ile Ile Lys Ile Ala Gln
 50 55 60

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

Pro Glu Gly His Thr Leu Ser Ala Lys Glu Trp Lys Gln Leu Ser Ser
 85 90 95

Gln Trp Arg Glu Glu Leu Asp Arg Arg Ile His Thr Leu Val Ala Leu
 100 105 110

Arg Asp Glu Leu Asp Gly Cys Ile Gly Cys Gly Cys Leu Ser Arg Ser
 115 120 125

Asp Cys Pro Leu Arg Asn Pro Gly Asp Arg Leu Gly Glu Glu Gly Thr
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Gly Ala Arg Leu Leu Glu Asp Glu Gln Asn
 145 150

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<211> 648

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<213> Escherichia coli

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gctggcggtta cgcgcggtgc aatctactgg catttttaaag acaagtcgga tttgttcagt 180

gagatctggg aactgtcaga atccaatatt ggtgaactag agcttgagta tcaggcaaaa 240

ttccctggcg atccactctc agtattaaga gagatattaa ttcattgttct tgaatccacg 300

gtgacagaag aacggcgctcg attattgatg gagattatat tccacaaatg cgaatttgctc 360

ggagaaatgg ctgtttgtgca acaggcacaa cgtaatctct gtctggaaag ttatgaccgt 420

atagaacaaa cgtaaaca ttgtattgaa gcgaaaatgt tgcctgcgga tttaatgacg 480

cgtcgcgcag caattattat gcgcggctat atttccggcc tgatggaaaa ctggctcttt 540

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<211> 215
<212> PRT
<213> Escherichia coli

<400> 4

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Leu Asp Val Ala Leu Arg Leu Phe Ser Gln Gln Gly Val Ser Ser Thr
20 25 30

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

Tyr Trp His Phe Lys Asp Lys Ser Asp Leu Phe Ser Glu Ile Trp Glu
50 55 60

Leu Ser Glu Ser Asn Ile Gly Glu Leu Glu Leu Glu Tyr Gln Ala Lys
65 70 75 80

Phe Pro Gly Asp Pro Leu Ser Val Leu Arg Glu Ile Leu Ile His Val
85 90 95

Leu Glu Ser Thr Val Thr Glu Glu Arg Arg Arg Leu Leu Met Glu Ile
100 105 110

Ile Phe His Lys Cys Glu Phe Val Gly Glu Met Ala Val Val Gln Gln
115 120 125

Ala Gln Arg Asn Leu Cys Leu Glu Ser Tyr Asp Arg Ile Glu Gln Thr
130 135 140

Leu Lys His Cys Ile Glu Ala Lys Met Leu Pro Ala Asp Leu Met Thr
145 150 155 160

Arg Arg Ala Ala Ile Ile Met Arg Gly Tyr Ile Ser Gly Leu Met Glu

165

170

175

Asn Trp Leu Phe Ala Pro Gln Ser Phe Asp Leu Lys Lys Glu Ala Arg
 180 185 190

Asp Tyr Val Ala Ile Leu Leu Glu Met Tyr Leu Leu Cys Pro Thr Leu
 195 200 205

Arg Asn Pro Ala Thr Asn Glu
 210 215

<210> 5

<211> 867

<212> DNA

<213> Escherichia coli

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<212> PRT

<213> Escherichia coli

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Tyr Ser Lys Trp His Leu Gln Arg Met Phe Lys Asp Val Thr Gly His
35 40 45

Ala Ile Gly Ala Tyr Ile Arg Ala Arg Arg Leu Ser Lys Ser Ala Val
50 55 60

Ala Leu Arg Leu Thr Ala Arg Pro Ile Leu Asp Ile Ala Leu Gln Tyr
65 70 75 80

Arg Phe Asp Ser Gln Gln Thr Phe Thr Arg Ala Phe Lys Lys Gln Phe
85 90 95

Ala Gln Thr Pro Ala Leu Tyr Arg Arg Ser Pro Glu Trp Ser Ala Phe
100 105 110

Gly Ile Arg Pro Pro Leu Arg Leu Gly Glu Phe Thr Met Pro Glu His
115 120 125

Lys Phe Val Thr Leu Glu Asp Thr Pro Leu Ile Gly Val Thr Gln Ser
130 135 140

Tyr Ser Cys Ser Leu Glu Gln Ile Ser Asp Phe Arg His Glu Met Arg
145 150 155 160

Tyr Gln Phe Trp His Asp Phe Leu Gly Asn Ala Pro Thr Ile Pro Pro
165 170 175

Val Leu Tyr Gly Leu Asn Glu Thr Arg Pro Ser Gln Asp Lys Asp Asp
180 185 190

Glu Gln Glu Val Phe Tyr Thr Thr Ala Leu Ala Gln Asp Gln Ala Asp

195

200

205

Gly Tyr Val Leu Thr Gly His Pro Val Met Leu Gln Gly Gly Glu Tyr
 210 215 220

Val Met Phe Thr Tyr Glu Gly Leu Gly Thr Gly Val Gln Glu Phe Ile
 225 230 235 240

Leu Thr Val Tyr Gly Thr Cys Met Pro Met Leu Asn Leu Thr Arg Arg
 245 250 255

Lys Gly Gln Asp Ile Glu Arg Tyr Tyr Pro Ala Glu Asp Ala Lys Ala
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Gly Asp Arg Pro Ile Asn Leu Arg Cys Glu Leu Leu Ile Pro Ile Arg
 275 280 285

Arg

<210> 7

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<212> DNA

<213> Escherichia coli

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gcacagttaa aggtgctctg ctctatccgc tgcgcggcgt gtattactcc ggttgaactg 180

aaaaaggtat tgtcggtcga cctgggagca ctgaccgta tgctggatcg cctggtctgt 240

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<210> 8

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<213> Escherichia coli

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Leu Ser Pro Leu Asp Ile Thr Ala Ala Gln Phe Lys Val Leu Cys Ser
35 40 45

Ile Arg Cys Ala Ala Cys Ile Thr Pro Val Glu Leu Lys Lys Val Leu
50 55 60

Ser Val Asp Leu Gly Ala Leu Thr Arg Met Leu Asp Arg Leu Val Cys
65 70 75 80

Lys Gly Trp Val Glu Arg Leu Pro Asn Pro Asn Asp Lys Arg Gly Val
85 90 95

Leu Val Lys Leu Thr Thr Gly Gly Ala Ala Ile Cys Glu Gln Cys His
100 105 110

Gln Leu Val Gly Gln Asp Leu His Gln Glu Leu Thr Lys Asn Leu Thr
115 120 125

Ala Asp Glu Val Ala Thr Leu Glu Tyr Leu Leu Lys Lys Val Leu Pro
130 135 140

<210> 9

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<212> DNA

<213> Escherichia coli

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 <213> Escherichia coli

<400> 10

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20 25 30

Ala Gln Tyr Pro Thr Ile Ala Pro Pro Ala Val Thr Ile Ser Ala Ser
35 40 45

Tyr Pro Gly Ala Asp Ala Lys Thr Val Gln Asp Thr Val Thr Gln Val
50 55 60

Ile Glu Gln Asn Met Asn Gly Ile Asp Asn Leu Met Tyr Met Ser Ser
65 70 75 80

Asn Ser Asp Ser Thr Gly Thr Val Gln Ile Thr Leu Thr Phe Glu Ser
85 90 95

Gly Thr Asp Ala Asp Ile Ala Gln Val Gln Val Gln Asn Lys Leu Gln
100 105 110

Leu Ala Met Pro Leu Leu Pro Gln Glu Val Gln Gln Gln Gly Val Ser
115 120 125

Val Glu Lys Ser Ser Ser Ser Phe Leu Met Val Val Gly Val Ile Asn
130 135 140

Thr Asp Gly Thr Met Thr Gln Glu Asp Ile Ser Asp Tyr Val Ala Ala
145 150 155 160

Asn Met Lys Asp Ala Ile Ser Arg Thr Ser Gly Val Gly Asp Val Gln
165 170 175

Leu Phe Gly Ser Gln Tyr Ala Met Arg Ile Trp Met Asn Pro Asn Glu
180 185 190

Leu Asn Lys Phe Gln Leu Thr Pro Val Asp Val Ile Thr Ala Ile Lys
195 200 205

Ala Gln Asn Ala Gln Val Ala Ala Gly Gln Leu Gly Gly Thr Pro Pro
210 215 220

Val Lys Gly Gln Gln Leu Asn Ala Ser Ile Ile Ala Gln Thr Arg Leu

225		230		235		240									
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Glu	Asn	Tyr	Asp	Ile	Ile	Ala	Glu	Phe	Asn	Gly	Gln	Pro	Ala	Ser	Gly
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Leu	Gly	Ile	Lys	Leu	Ala	Thr	Gly	Ala	Asn	Ala	Leu	Asp	Thr	Ala	Ala
	290					295					300				
Ala	Ile	Arg	Ala	Glu	Leu	Ala	Lys	Met	Glu	Pro	Phe	Phe	Pro	Ser	Gly
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Leu	Lys	Ile	Val	Tyr	Pro	Tyr	Asp	Thr	Thr	Pro	Phe	Val	Lys	Ile	Ser
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Ala	Ile	Gly	Leu	Leu	Val	Asp	Asp	Ala	Ile	Val	Val	Val	Glu	Asn	Val
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Glu	Arg	Val	Met	Ala	Glu	Glu	Gly	Leu	Pro	Pro	Lys	Glu	Ala	Thr	Arg
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Lys	Ser	Met	Gly	Gln	Ile	Gln	Gly	Ala	Leu	Val	Gly	Ile	Ala	Met	Val
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Leu Ser Ala Val Phe Val Pro Met Ala Phe Phe Gly Gly Ser Thr Gly
450 455 460

Ala Ile Tyr Arg Gln Phe Ser Ile Thr Ile Val Ser Ala Met Ala Leu
465 470 475 480

Ser Val Leu Val Ala Leu Ile Leu Thr Pro Ala Leu Cys Ala Thr Met
485 490 495

Leu Lys Pro Ile Ala Lys Gly Asp His Gly Glu Gly Lys Lys Gly Phe
500 505 510

Phe Gly Trp Phe Asn Arg Met Phe Glu Lys Ser Thr His His Tyr Thr
515 520 525

Asp Ser Val Gly Gly Ile Leu Arg Ser Thr Gly Arg Tyr Leu Val Leu
530 535 540

Tyr Leu Ile Ile Val Val Gly Met Ala Tyr Leu Phe Val Arg Leu Pro
545 550 555 560

Ser Ser Phe Leu Pro Asp Glu Asp Gln Gly Val Phe Met Thr Met Val
565 570 575

Gln Leu Pro Ala Gly Ala Thr Gln Glu Arg Thr Gln Lys Val Leu Asn
580 585 590

Glu Val Thr His Tyr Tyr Leu Thr Lys Glu Lys Asn Asn Val Glu Ser
595 600 605

Val Phe Ala Val Asn Gly Phe Gly Phe Ala Gly Arg Gly Gln Asn Thr
610 615 620

Gly Ile Ala Phe Val Ser Leu Lys Asp Trp Ala Asp Arg Pro Gly Glu
625 630 635 640

Glu Asn Lys Val Glu Ala Ile Thr Met Arg Ala Thr Arg Ala Phe Ser
645 650 655

Gln Ile Lys Asp Ala Met Val Phe Ala Phe Asn Leu Pro Ala Ile Val

660

665

670

Glu Leu Gly Thr Ala Thr Gly Phe Asp Phe Glu Leu Ile Asp Gln Ala
 675 680 685

Gly Leu Gly His Glu Lys Leu Thr Gln Ala Arg Asn Gln Leu Leu Ala
 690 695 700

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

Leu Glu Asp Thr Pro Gln Phe Lys Ile Asp Ile Asp Gln Glu Lys Ala
 725 730 735

Gln Ala Leu Gly Val Ser Ile Asn Asp Ile Asn Thr Thr Leu Gly Ala
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Ala Trp Gly Gly Ser Tyr Val Asn Asp Phe Ile Asp Arg Gly Arg Val
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Lys Lys Val Tyr Val Met Ser Glu Ala Lys Tyr Arg Met Leu Pro Asp
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Asp Ile Gly Asp Trp Tyr Val Arg Ala Ala Asp Gly Gln Met Val Pro
 785 790 795 800

Phe Ser Ala Phe Ser Ser Ser Arg Trp Glu Tyr Gly Ser Pro Arg Leu
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Glu Arg Tyr Asn Gly Leu Pro Ser Met Glu Ile Leu Gly Gln Ala Ala
 820 825 830

Pro Gly Lys Ser Thr Gly Glu Ala Met Glu Leu Met Glu Gln Leu Ala
 835 840 845

Ser Lys Leu Pro Thr Gly Val Gly Tyr Asp Trp Thr Gly Met Ser Tyr
 850 855 860

Gln Glu Arg Leu Ser Gly Asn Gln Ala Pro Ser Leu Tyr Ala Ile Ser
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Leu Ile Val Val Phe Leu Cys Leu Ala Ala Leu Tyr Glu Ser Trp Ser
885 890 895

Ile Pro Phe Ser Val Met Leu Val Val Pro Leu Gly Val Ile Gly Ala
900 905 910

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915 920 925

Val Gly Leu Leu Thr Thr Ile Gly Leu Ser Ala Lys Asn Ala Ile Leu
930 935 940

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980 985 990

Thr Gly Ala Gly Ser Gly Ala Gln Asn Ala Val Gly Thr Gly Val Met
995 1000 1005

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Asp Ile Glu His Ser His Thr Val Asp His His
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<212> DNA
<213> Escherichia coli

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<212> DNA
<213> Escherichia coli

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<210> 14
<211> 366
<212> PRT
<213> Escherichia coli

<400> 14

Met Arg Gly Lys Lys Arg Ile Gly Leu Leu Phe Leu Leu Ile Ala Val

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Val Val Gly Gly Gly Gly Leu Leu Leu Ala Gln Lys Val Leu His Lys	20	25	30
Thr Ser Asp Thr Ala Phe Cys Leu Ser Cys His Ser Met Ser Lys Pro	35	40	45
Phe Glu Glu Tyr Gln Gly Thr Val His Phe Ser Asn Gln Lys Gly Ile	50	55	60
Arg Ala Glu Cys Ala Asp Cys His Ile Pro Lys Ser Gly Met Asp Tyr	65	70	75
Leu Phe Ala Lys Leu Lys Ala Ser Lys Asp Ile Tyr His Glu Phe Val	85	90	95
Ser Gly Lys Ile Asp Ser Asp Asp Lys Phe Glu Ala His Arg Gln Glu	100	105	110
Met Ala Glu Thr Val Trp Lys Glu Leu Lys Ala Thr Asp Ser Ala Thr	115	120	125
Cys Arg Ser Cys His Ser Phe Asp Ala Met Asp Ile Ala Ser Gln Ser	130	135	140
Glu Ser Ala Gln Lys Met His Asn Lys Ala Gln Lys Asp Ser Glu Thr	145	150	155
Cys Ile Asp Cys His Lys Gly Ile Ala His Phe Pro Pro Glu Ile Lys	165	170	175
Met Asp Asp Asn Ala Ala His Glu Leu Glu Ser Gln Ala Ala Thr Ser	180	185	190
Val Thr Asn Gly Ala His Ile Tyr Pro Phe Lys Thr Ser His Ile Gly	195	200	205
Glu Leu Ala Thr Val Asn Pro Gly Thr Asp Leu Thr Val Val Asp Ala	210	215	220

Ser Gly Lys Gln Pro Ile Val Leu Leu Gln Gly Tyr Gln Met Gln Gly
225 230 235 240

Ser Glu Asn Thr Leu Tyr Leu Ala Ala Gly Gln Arg Leu Ala Leu Ala
245 250 255

Thr Leu Ser Glu Glu Gly Ile Lys Ala Leu Thr Val Asn Gly Glu Trp
260 265 270

Gln Ala Asp Glu Tyr Gly Asn Gln Trp Arg Gln Ala Ser Leu Gln Gly
275 280 285

Ala Leu Thr Asp Pro Ala Leu Ala Asp Arg Lys Pro Leu Trp Gln Tyr
290 295 300

Ala Glu Lys Leu Asp Asp Thr Tyr Cys Ala Gly Cys His Ala Pro Ile
305 310 315 320

Ala Ala Asp His Tyr Thr Val Asn Ala Trp Pro Ser Ile Ala Lys Gly
325 330 335

Met Gly Ala Arg Thr Ser Met Ser Glu Asn Glu Leu Asp Ile Leu Thr
340 345 350

Arg Tyr Phe Gln Tyr Asn Ala Lys Asp Ile Thr Glu Lys Gln
355 360 365

<210> 15
<211> 972
<212> DNA
<213> Escherichia coli

<400> 15
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gagatcatcg aagagatgcg gcgtaataac gagaaagtta tctttctggt gccgcacggt	420
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cccatcaaat aa	972

<210> 16
 <211> 323
 <212> PRT
 <213> Escherichia coli

<400> 16

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

Met	Ala	Gly	Ile	Ala	Leu	Thr	Pro	Pro	Lys	Phe	Arg	Asp	Pro	Ile	Leu
		35					40					45			

Ala	Arg	Leu	Gly	Arg	Phe	Ala	Gly	Arg	Leu	Gly	Lys	Ser	Ser	Arg	Arg
		50				55					60				

Arg	Ala	Leu	Ile	Asn	Leu	Ser	Leu	Cys	Phe	Pro	Glu	Arg	Ser	Glu	Ala
65				70						75				80	

Glu	Arg	Glu	Ala	Ile	Val	Asp	Glu	Met	Phe	Ala	Thr	Ala	Pro	Gln	Ala
				85					90					95	

Met Ala Met Met Ala Glu Leu Ala Ile Arg Gly Pro Glu Lys Ile Gln
100 105 110

Pro Arg Val Asp Trp Gln Gly Leu Glu Ile Ile Glu Glu Met Arg Arg
115 120 125

Asn Asn Glu Lys Val Ile Phe Leu Val Pro His Gly Trp Ala Val Asp
130 135 140

Ile Pro Ala Met Leu Met Ala Ser Gln Gly Gln Lys Met Ala Ala Met
145 150 155 160

Phe His Asn Gln Gly Asn Pro Val Phe Asp Tyr Val Trp Asn Thr Val
165 170 175

Arg Arg Arg Phe Gly Gly Arg Leu His Ala Arg Asn Asp Gly Ile Lys
180 185 190

Pro Phe Ile Gln Ser Val Arg Gln Gly Tyr Trp Gly Tyr Tyr Leu Pro
195 200 205

Asp Gln Asp His Gly Pro Glu His Ser Glu Phe Val Asp Phe Phe Ala
210 215 220

Thr Tyr Lys Ala Thr Leu Pro Ala Ile Gly Arg Leu Met Lys Val Cys
225 230 235 240

Arg Ala Arg Val Val Pro Leu Phe Pro Ile Tyr Asp Gly Lys Thr His
245 250 255

Arg Leu Thr Ile Gln Val Arg Pro Pro Met Asp Asp Leu Leu Glu Ala
260 265 270

Asp Asp His Thr Ile Ala Arg Arg Met Asn Glu Glu Val Glu Ile Phe
275 280 285

Val Gly Pro Arg Pro Glu Gln Tyr Thr Trp Ile Leu Lys Leu Leu Lys
290 295 300

Thr Arg Lys Pro Gly Glu Ile Gln Pro Tyr Lys Arg Lys Asp Leu Tyr

305

310

315

320

Pro Ile Lys

<210> 17

<211> 1917

<212> DNA

<213> Escherichia coli

<400> 17

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gcctataccc aggatggtga aactctagtt ggtcagccgg ctaaactca ggcagtgcg	180
aacccgcaaa acactctgtt tgcgattaaa cgcctgattg gtcgccgctt ccaggacgaa	240
gaagtacagc gtgatgtttc catcatgccg ttcaaaatta ttgctgctga taacggcgac	300
gcatgggtcg aagttaaagg ccagaaaatg gcaccgccgc agatttctgc tgaagtgctg	360
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<210> 18
<211> 638
<212> PRT
<213> Escherichia coli

<400> 18

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Ala Ile Met Asp Gly Thr Thr Pro Arg Val Leu Glu Asn Ala Glu Gly
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Asp Arg Thr Thr Pro Ser Ile Ile Ala Tyr Thr Gln Asp Gly Glu Thr
35 40 45

Leu Val Gly Gln Pro Ala Lys Arg Gln Ala Val Thr Asn Pro Gln Asn
50 55 60

Thr Leu Phe Ala Ile Lys Arg Leu Ile Gly Arg Arg Phe Gln Asp Glu
65 70 75 80

Glu Val Gln Arg Asp Val Ser Ile Met Pro Phe Lys Ile Ile Ala Ala
85 90 95

Asp Asn Gly Asp Ala Trp Val Glu Val Lys Gly Gln Lys Met Ala Pro
100 105 110

Pro Gln Ile Ser Ala Glu Val Leu Lys Lys Met Lys Lys Thr Ala Glu
115 120 125

Asp Tyr Leu Gly Glu Pro Val Thr Glu Ala Val Ile Thr Val Pro Ala
130 135 140

Tyr Phe Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Arg Ile
145 150 155 160

Ala Gly Leu Glu Val Lys Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala
165 170 175

Leu Ala Tyr Gly Leu Asp Lys Gly Thr Gly Asn Arg Thr Ile Ala Val
180 185 190

Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Ile Glu Ile Asp
195 200 205

Glu Val Asp Gly Glu Lys Thr Phe Glu Val Leu Ala Thr Asn Gly Asp
210 215 220

Thr His Leu Gly Gly Glu Asp Phe Asp Ser Arg Leu Ile Asn Tyr Leu
225 230 235 240

Val Glu Glu Phe Lys Lys Asp Gln Gly Ile Asp Leu Arg Asn Asp Pro
245 250 255

Leu Ala Met Gln Arg Leu Lys Glu Ala Ala Glu Lys Ala Lys Ile Glu
260 265 270

Leu Ser Ser Ala Gln Gln Thr Asp Val Asn Leu Pro Tyr Ile Thr Ala
275 280 285

Asp Ala Thr Gly Pro Lys His Met Asn Ile Lys Val Thr Arg Ala Lys
290 295 300

Leu Glu Ser Leu Val Glu Asp Leu Val Asn Arg Ser Ile Glu Pro Leu

305		310		315		320									
Lys	Val	Ala	Leu	Gln	Asp	Ala	Gly	Leu	Ser	Val	Ser	Asp	Ile	Asp	Asp
			325					330						335	
Val	Ile	Leu	Val	Gly	Gly	Gln	Thr	Arg	Met	Pro	Met	Val	Gln	Lys	Lys
		340						345					350		
Val	Ala	Glu	Phe	Phe	Gly	Lys	Glu	Pro	Arg	Lys	Asp	Val	Asn	Pro	Asp
		355					360					365			
Glu	Ala	Val	Ala	Ile	Gly	Ala	Ala	Val	Gln	Gly	Gly	Val	Leu	Thr	Gly
	370					375					380				
Asp	Val	Lys	Asp	Val	Leu	Leu	Leu	Asp	Val	Thr	Pro	Leu	Ser	Leu	Gly
385					390					395					400
Ile	Glu	Thr	Met	Gly	Gly	Val	Met	Thr	Thr	Leu	Ile	Ala	Lys	Asn	Thr
				405					410					415	
Thr	Ile	Pro	Thr	Lys	His	Ser	Gln	Val	Phe	Ser	Thr	Ala	Glu	Asp	Asn
			420					425					430		
Gln	Ser	Ala	Val	Thr	Ile	His	Val	Leu	Gln	Gly	Glu	Arg	Lys	Arg	Ala
		435					440					445			
Ala	Asp	Asn	Lys	Ser	Leu	Gly	Gln	Phe	Asn	Leu	Asp	Gly	Ile	Asn	Pro
	450					455					460				
Ala	Pro	Arg	Gly	Met	Pro	Gln	Ile	Glu	Val	Thr	Phe	Asp	Ile	Asp	Ala
465					470					475					480
Asp	Gly	Ile	Leu	His	Val	Ser	Ala	Lys	Asp	Lys	Asn	Ser	Gly	Lys	Glu
				485					490					495	
Gln	Lys	Ile	Thr	Ile	Lys	Ala	Ser	Ser	Gly	Leu	Asn	Glu	Asp	Glu	Ile
			500					505					510		
Gln	Lys	Met	Val	Arg	Asp	Ala	Glu	Ala	Asn	Ala	Glu	Ala	Asp	Arg	Lys
		515					520					525			

Phe Glu Glu Leu Val Gln Thr Arg Asn Gln Gly Asp His Leu Leu His
530 535 540

Ser Thr Arg Lys Gln Val Glu Glu Ala Gly Asp Lys Leu Pro Ala Asp
545 550 555 560

Asp Lys Thr Ala Ile Glu Ser Ala Leu Thr Ala Leu Glu Thr Ala Leu
565 570 575

Lys Gly Glu Asp Lys Ala Ala Ile Glu Ala Lys Met Gln Glu Leu Ala
580 585 590

Gln Val Ser Gln Lys Leu Met Glu Ile Ala Gln Gln Gln His Ala Gln
595 600 605

Gln Gln Thr Ala Gly Ala Asp Ala Ser Ala Asn Asn Ala Lys Asp Asp
610 615 620

Asp Val Val Asp Ala Glu Phe Glu Glu Val Lys Asp Lys Lys
625 630 635

<210> 19
<211> 1647
<212> DNA
<213> Escherichia coli

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<210> 20
 <211> 548
 <212> PRT
 <213> Escherichia coli

<400> 20

Met	Ala	Ala	Lys	Asp	Val	Lys	Phe	Gly	Asn	Asp	Ala	Arg	Val	Lys	Met
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Leu	Arg	Gly	Val	Asn	Val	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu	Gly
			20					25					30		

Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr

35

40

45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
 50 55 60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
 65 70 75 80

Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
 85 90 95

Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
 100 105 110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val
 115 120 125

Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile
 130 135 140

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

Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
 165 170 175

Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly
 180 185 190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro
 195 200 205

Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp
 210 215 220

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

Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
 245 250 255

Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val Lys
260 265 270

Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
275 280 285

Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val Ile Ser Glu Glu
290 295 300

Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala
305 310 315 320

Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val
325 330 335

Gly Glu Glu Ala Ala Ile Gln Gly Arg Val Ala Gln Ile Arg Gln Gln
340 345 350

Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg
355 360 365

Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala
370 375 380

Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu
385 390 395 400

His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
405 410 415

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

Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu
435 440 445

Ala Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val
450 455 460

Val Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala

465 470 475 480

Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly Ile Leu Asp Pro
485 490 495

Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly
500 505 510

Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Asn Asp
515 520 525

Ala Ala Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met
530 535 540

Gly Gly Met Met
545

<210> 21
<211> 291
<212> DNA
<213> Escherichia coli

<400> 21
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<210> 22
<211> 96
<212> PRT
<213> Escherichia coli

<400> 22

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Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg
20 25 30

Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp
35 40 45

Lys Ser His Ile Trp Leu Leu Val Asn Asp Asp Gln Arg Leu Glu Gln
50 55 60

Met Ile Ser Gln Ile Asp Lys Leu Glu Asp Val Val Lys Val Gln Arg
65 70 75 80

Asn Gln Ser Asp Pro Thr Met Phe Asn Lys Ile Ala Val Phe Phe Gln
85 90 95

<210> 23
<211> 1167
<212> DNA
<213> Escherichia coli

<400> 23
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<210> 24
 <211> 420
 <212> PRT
 <213> Escherichia coli

<400> 24

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			20					25					30		

Gly	Val	Pro	Thr	Gly	Lys	Met	Pro	Glu	Ala	Ile	Asp	Ala	Leu	Val	Ile
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Ser	Leu	Lys	Thr	Arg	Ser	Cys	Pro	Val	Val	Glu	Ala	Thr	Gln	Gln	Ser
	50					55					60				

Leu	Ala	Ala	Leu	Ser	Trp	Leu	Gln	Gln	Gln	Gly	Cys	Lys	Gln	Ile	Tyr
65					70					75				80	

Phe	Lys	Tyr	Cys	Ser	Thr	Phe	Asp	Ser	Thr	Ala	Lys	Gly	Asn	Ile	Gly
				85					90					95	

Pro	Val	Thr	Asp	Ala	Leu	Met	Asp	Ala	Leu	Asp	Thr	Pro	Phe	Thr	Val
			100					105					110		

Phe	Ser	Pro	Ala	Leu	Pro	Val	Asn	Gly	Arg	Thr	Val	Tyr	Gln	Gly	Tyr
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Leu	Phe	Val	Met	Asn	Gln	Leu	Leu	Ala	Glu	Ser	Gly	Met	Arg	His	His
130						135					140				

Pro	Val	Asn	Pro	Met	Thr	Asp	Ser	Tyr	Leu	Pro	Arg	Leu	Val	Glu	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

Gln Ser Leu Gly Ile Lys Gly Phe His Ile Gly Pro Thr Ile Ser Pro
 370 375 380

Gly Val Pro Trp Val Asn Ala Leu Asp Lys Pro Val Ser Leu Ala Leu
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Lys Ser Gly Asn Phe Gly Asp Glu Ala Phe Phe Ser Arg Ala Gln Arg
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Glu Phe Leu Ser
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 <212> DNA
 <213> Escherichia coli

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<211> 1342

<212> PRT

<213> Escherichia coli

<400> 26

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35 40 45

Leu Glu Ala Ala Phe Arg Ser Val Phe Pro Ile Gln Ser Tyr Ser Gly
50 55 60

Asn Ser Glu Leu Gln Tyr Val Ser Tyr Arg Leu Gly Glu Pro Val Phe
65 70 75 80

Asp Val Gln Glu Cys Gln Ile Arg Gly Val Thr Tyr Ser Ala Pro Leu
85 90 95

Arg Val Lys Leu Arg Leu Val Ile Tyr Glu Arg Glu Ala Pro Glu Gly
100 105 110

Thr Val Lys Asp Ile Lys Glu Gln Glu Val Tyr Met Gly Glu Ile Pro
115 120 125

Leu Met Thr Asp Asn Gly Thr Phe Val Ile Asn Gly Thr Glu Arg Val
130 135 140

Ile Val Ser Gln Leu His Arg Ser Pro Gly Val Phe Phe Asp Ser Asp
145 150 155 160

Lys Gly Lys Thr His Ser Ser Gly Lys Val Leu Tyr Asn Ala Arg Ile
165 170 175

Ile Pro Tyr Arg Gly Ser Trp Leu Asp Phe Glu Phe Asp Pro Lys Asp
180 185 190

Asn Leu Phe Val Arg Ile Asp Arg Arg Arg Lys Leu Pro Ala Thr Ile

195

200

205

Ile Leu Arg Ala Leu Asn Tyr Thr Thr Glu Gln Ile Leu Asp Leu Phe
 210 215 220

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

Leu Val Pro Glu Arg Leu Arg Gly Glu Thr Ala Ser Phe Asp Ile Glu
 245 250 255

Ala Asn Gly Lys Val Tyr Val Glu Lys Gly Arg Arg Ile Thr Ala Arg
 260 265 270

His Ile Arg Gln Leu Glu Lys Asp Asp Val Lys Leu Ile Glu Val Pro
 275 280 285

Val Glu Tyr Ile Ala Gly Lys Val Val Ala Lys Asp Tyr Ile Asp Glu
 290 295 300

Ser Thr Gly Glu Leu Ile Cys Ala Ala Asn Met Glu Leu Ser Leu Asp
 305 310 315 320

Leu Leu Ala Lys Leu Ser Gln Ser Gly His Lys Arg Ile Glu Thr Leu
 325 330 335

Phe Thr Asn Asp Leu Asp His Gly Pro Tyr Ile Ser Glu Thr Leu Arg
 340 345 350

Val Asp Pro Thr Asn Asp Arg Leu Ser Ala Leu Val Glu Ile Tyr Arg
 355 360 365

Met Met Arg Pro Gly Glu Pro Pro Thr Arg Glu Ala Ala Glu Ser Leu
 370 375 380

Phe Glu Asn Leu Phe Phe Ser Glu Asp Arg Tyr Asp Leu Ser Ala Val
 385 390 395 400

Gly Arg Met Lys Phe Asn Arg Ser Leu Leu Arg Glu Glu Ile Glu Gly
 405 410 415

Ser Gly Ile Leu Ser Lys Asp Asp Ile Ile Asp Val Met Lys Lys Leu
420 425 430

Ile Asp Ile Arg Asn Gly Lys Gly Glu Val Asp Asp Ile Asp His Leu
435 440 445

Gly Asn Arg Arg Ile Arg Ser Val Gly Glu Met Ala Glu Asn Gln Phe
450 455 460

Arg Val Gly Leu Val Arg Val Glu Arg Ala Val Lys Glu Arg Leu Ser
465 470 475 480

Leu Gly Asp Leu Asp Thr Leu Met Pro Gln Asp Met Ile Asn Ala Lys
485 490 495

Pro Ile Ser Ala Ala Val Lys Glu Phe Phe Gly Ser Ser Gln Leu Ser
500 505 510

Gln Phe Met Asp Gln Asn Asn Pro Leu Ser Glu Ile Thr His Lys Arg
515 520 525

Arg Ile Ser Ala Leu Gly Pro Gly Gly Leu Thr Arg Glu Arg Ala Gly
530 535 540

Phe Glu Val Arg Asp Val His Pro Thr His Tyr Gly Arg Val Cys Pro
545 550 555 560

Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile Asn Ser Leu Ser
565 570 575

Val Tyr Ala Gln Thr Asn Glu Tyr Gly Phe Leu Glu Thr Pro Tyr Arg
580 585 590

Lys Val Thr Asp Gly Val Val Thr Asp Glu Ile His Tyr Leu Ser Ala
595 600 605

Ile Glu Glu Gly Asn Tyr Val Ile Ala Gln Ala Asn Ser Asn Leu Asp
610 615 620

Glu Glu Gly His Phe Val Glu Asp Leu Val Thr Cys Arg Ser Lys Gly

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Glu	Ser	Ser	Leu	Phe	Ser	Arg	Asp	Gln	Val	Asp	Tyr	Met	Asp	Val
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Thr	Gln	Gln	Val	Val	Ser	Val	Gly	Ala	Ser	Leu	Ile	Pro	Phe	Leu
			660					665					670	Glu
His	Asp	Asp	Ala	Asn	Arg	Ala	Leu	Met	Gly	Ala	Asn	Met	Gln	Arg
		675					680					685		Gln
Ala	Val	Pro	Thr	Leu	Arg	Ala	Asp	Lys	Pro	Leu	Val	Gly	Thr	Gly
	690					695					700			Met
Glu	Arg	Ala	Val	Ala	Val	Asp	Ser	Gly	Val	Thr	Ala	Val	Ala	Lys
705					710					715				Arg
Gly	Gly	Val	Val	Gln	Tyr	Val	Asp	Ala	Ser	Arg	Ile	Val	Ile	Lys
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Asn	Glu	Asp	Glu	Met	Tyr	Pro	Gly	Glu	Ala	Gly	Ile	Asp	Ile	Tyr
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Leu	Thr	Lys	Tyr	Thr	Arg	Ser	Asn	Gln	Asn	Thr	Cys	Ile	Asn	Gln
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Pro	Cys	Val	Ser	Leu	Gly	Glu	Pro	Val	Glu	Arg	Gly	Asp	Val	Leu
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785					790					795				800
Arg	Val	Ala	Phe	Met	Pro	Trp	Asn	Gly	Tyr	Asn	Phe	Glu	Asp	Ser
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Leu	Val	Ser	Glu	Arg	Val	Val	Gln	Glu	Asp	Arg	Phe	Thr	Thr	Ile
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Ile	Gln	Glu	Leu	Ala	Cys	Val	Ser	Arg	Asp	Thr	Lys	Leu	Gly	Pro
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Glu Ile Thr Ala Asp Ile Pro Asn Val Gly Glu Ala Ala Leu Ser Lys
850 855 860

Leu Asp Glu Ser Gly Ile Val Tyr Ile Gly Ala Glu Val Thr Gly Gly
865 870 875 880

Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Gln Leu Thr
885 890 895

Pro Glu Glu Lys Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Ser Asp
900 905 910

Val Lys Asp Ser Ser Leu Arg Val Pro Asn Gly Val Ser Gly Thr Val
915 920 925

Ile Asp Val Gln Val Phe Thr Arg Asp Gly Val Glu Lys Asp Lys Arg
930 935 940

Ala Leu Glu Ile Glu Glu Met Gln Leu Lys Gln Ala Lys Lys Asp Leu
945 950 955 960

Ser Glu Glu Leu Gln Ile Leu Glu Ala Gly Leu Phe Ser Arg Ile Arg
965 970 975

Ala Val Leu Val Ala Gly Gly Val Glu Ala Glu Lys Leu Asp Lys Leu
980 985 990

Pro Arg Asp Arg Trp Leu Glu Leu Gly Leu Thr Asp Glu Glu Lys Gln
995 1000 1005

Asn Gln Leu Glu Gln Leu Ala Glu Gln Tyr Asp Glu Leu Lys His
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Glu Phe Glu Lys Lys Leu Glu Ala Lys Arg Arg Lys Ile Thr Gln
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Gly Asp Asp Leu Ala Pro Gly Val Leu Lys Ile Val Lys Val Tyr
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Leu Ala Val Lys Arg Arg Ile Gln Pro Gly Asp Lys Met Ala Gly

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Asp Met Pro Tyr Asp Glu Asn Gly Thr Pro Val Asp Ile Val Leu 1085 1090 1095		
Asn Pro Leu Gly Val Pro Ser Arg Met Asn Ile Gly Gln Ile Leu 1100 1105 1110		
Glu Thr His Leu Gly Met Ala Ala Lys Gly Ile Gly Asp Lys Ile 1115 1120 1125		
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Phe Ile Gln Arg Ala Tyr Asp Leu Gly Ala Asp Val Arg Gln Lys 1145 1150 1155		
Val Asp Leu Ser Thr Phe Ser Asp Glu Glu Val Met Arg Leu Ala 1160 1165 1170		
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Gly Ala Lys Glu Ala Glu Ile Lys Glu Leu Leu Lys Leu Gly Asp 1190 1195 1200		
Leu Pro Thr Ser Gly Gln Ile Arg Leu Tyr Asp Gly Arg Thr Gly 1205 1210 1215		
Glu Gln Phe Glu Arg Pro Val Thr Val Gly Tyr Met Tyr Met Leu 1220 1225 1230		
Lys Leu Asn His Leu Val Asp Asp Lys Met His Ala Arg Ser Thr 1235 1240 1245		
Gly Ser Tyr Ser Leu Val Thr Gln Gln Pro Leu Gly Gly Lys Ala 1250 1255 1260		

Gln Phe Gly Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Leu
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Glu Ala Tyr Gly Ala Ala Tyr Thr Leu Gln Glu Met Leu Thr Val
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Lys Ser Asp Asp Val Asn Gly Arg Thr Lys Met Tyr Lys Asn Ile
1295 1300 1305

Val Asp Gly Asn His Gln Met Glu Pro Gly Met Pro Glu Ser Phe
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Asn Val Leu Leu Lys Glu Ile Arg Ser Leu Gly Ile Asn Ile Glu
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Leu Glu Asp Glu
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<211> 4224
<212> DNA
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cagtccatcg gtgaaccggg tacacagctg accatgcgta cgttccacat cgggtggtgcg	2820
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agcaacgtga agtcggttgt gaactccagc ggtaaactgg ttatcacttc ccgtaatact	2940
gaactgaaac tgatcgacga attcggtcgt actaaagaaa gctacaaagt accttacggt	3000
gcgggtactgg cgaaaggcga tggcgaacag gttgctggcg gcgaaaccgt tgcaaactgg	3060
gacccgcaca ccatgccggt tatcaccgaa gtaagcggtt ttgtacgctt tactgacatg	3120
atcgacggcc agaccattac gcgtcagacc gacgaactga ccggtctgtc ttcgctggtg	3180
gttctggatt ccgcagaacg taccgcaggt ggtaaagatc tgcgtccggc actgaaaatc	3240
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ctggcgcgta ttccgcagga atccggcgggt accaaggaca tcaccggtgg tctgccgcgc	3420
gttgcggaac tgttcgaagc acgtcgtccg aaagagccgg caatcctggc tgaaatcagc	3480
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ctgcgtaaag ctaccatcgt taacgcgggt agctccgact tcctggaagg cgaacaggtt	3840
gaatactctc gcgtcaagat cgcaaaccgc gaactggaag cgaacggcaa agtgggtgca	3900
acttactccc gcgatctgct gggatatcacc aaagcgtctc tggcaaccga gtccttcac	3960

tccgcggcat cgttccagga gaccactcgc gtgctgaccg aagcagccgt tgcgggcaaa	4020
cgcgacgaac tgcgcggcct gaaagagaac gttatcgtgg gtcgtctgat cccggcaggt	4080
accggttacg cgtaccacca ggatcgtatg cgtcgccgtg ctgcgggtga agctccggct	4140
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<210> 28
 <211> 1407
 <212> PRT
 <213> Escherichia coli

<400> 28

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Phe	Asp	Ala	Ile	Lys	Ile	Ala	Leu	Ala	Ser	Pro	Asp	Met	Ile	Arg	Ser
			20					25					30		

Trp	Ser	Phe	Gly	Glu	Val	Lys	Lys	Pro	Glu	Thr	Ile	Asn	Tyr	Arg	Thr
		35					40					45			

Phe	Lys	Pro	Glu	Arg	Asp	Gly	Leu	Phe	Cys	Ala	Arg	Ile	Phe	Gly	Pro
	50					55					60				

Val	Lys	Asp	Tyr	Glu	Cys	Leu	Cys	Gly	Lys	Tyr	Lys	Arg	Leu	Lys	His
65					70					75					80

Arg	Gly	Val	Ile	Cys	Glu	Lys	Cys	Gly	Val	Glu	Val	Thr	Gln	Thr	Lys
			85						90					95	

Val	Arg	Arg	Glu	Arg	Met	Gly	His	Ile	Glu	Leu	Ala	Ser	Pro	Thr	Ala
			100					105					110		

His	Ile	Trp	Phe	Leu	Lys	Ser	Leu	Pro	Ser	Arg	Ile	Gly	Leu	Leu	Leu
		115					120					125			

Asp	Met	Pro	Leu	Arg	Asp	Ile	Glu	Arg	Val	Leu	Tyr	Phe	Glu	Ser	Tyr
	130					135					140				

Val Val Ile Glu Gly Gly Met Thr Asn Leu Glu Arg Gln Gln Ile Leu
145 150 155 160

Thr Glu Glu Gln Tyr Leu Asp Ala Leu Glu Glu Phe Gly Asp Glu Phe
165 170 175

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

Asp Leu Glu Gln Glu Cys Glu Gln Leu Arg Glu Glu Leu Asn Glu Thr
195 200 205

Asn Ser Glu Thr Lys Arg Lys Lys Leu Thr Lys Arg Ile Lys Leu Leu
210 215 220

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

Val Leu Pro Val Leu Pro Pro Asp Leu Arg Pro Leu Val Pro Leu Asp
245 250 255

Gly Gly Arg Phe Ala Thr Ser Asp Leu Asn Asp Leu Tyr Arg Arg Val
260 265 270

Ile Asn Arg Asn Asn Arg Leu Lys Arg Leu Leu Asp Leu Ala Ala Pro
275 280 285

Asp Ile Ile Val Arg Asn Glu Lys Arg Met Leu Gln Glu Ala Val Asp
290 295 300

Ala Leu Leu Asp Asn Gly Arg Arg Gly Arg Ala Ile Thr Gly Ser Asn
305 310 315 320

Lys Arg Pro Leu Lys Ser Leu Ala Asp Met Ile Lys Gly Lys Gln Gly
325 330 335

Arg Phe Arg Gln Asn Leu Leu Gly Lys Arg Val Asp Tyr Ser Gly Arg
340 345 350

Ser Val Ile Thr Val Gly Pro Tyr Leu Arg Leu His Gln Cys Gly Leu

355

360

365

Pro Lys Lys Met Ala Leu Glu Leu Phe Lys Pro Phe Ile Tyr Gly Lys
 370 375 380

Leu Glu Leu Arg Gly Leu Ala Thr Thr Ile Lys Ala Ala Lys Lys Met
 385 390 395 400

Val Glu Arg Glu Glu Ala Val Val Trp Asp Ile Leu Asp Glu Val Ile
 405 410 415

Arg Glu His Pro Val Leu Leu Asn Arg Ala Pro Thr Leu His Arg Leu
 420 425 430

Gly Ile Gln Ala Phe Glu Pro Val Leu Ile Glu Gly Lys Ala Ile Gln
 435 440 445

Leu His Pro Leu Val Cys Ala Ala Tyr Asn Ala Asp Phe Asp Gly Asp
 450 455 460

Gln Met Ala Val His Val Pro Leu Thr Leu Glu Ala Gln Leu Glu Ala
 465 470 475 480

Arg Ala Leu Met Met Ser Thr Asn Asn Ile Leu Ser Pro Ala Asn Gly
 485 490 495

Glu Pro Ile Ile Val Pro Ser Gln Asp Val Val Leu Gly Leu Tyr Tyr
 500 505 510

Met Thr Arg Asp Cys Val Asn Ala Lys Gly Glu Gly Met Val Leu Thr
 515 520 525

Gly Pro Lys Glu Ala Glu Arg Leu Tyr Arg Ser Gly Leu Ala Ser Leu
 530 535 540

His Ala Arg Val Lys Val Arg Ile Thr Glu Tyr Glu Lys Asp Ala Asn
 545 550 555 560

Gly Glu Leu Val Ala Lys Thr Ser Leu Lys Asp Thr Thr Val Gly Arg
 565 570 575

Ala Ile Leu Trp Met Ile Val Pro Lys Gly Leu Pro Tyr Ser Ile Val
580 585 590

Asn Gln Ala Leu Gly Lys Lys Ala Ile Ser Lys Met Leu Asn Thr Cys
595 600 605

Tyr Arg Ile Leu Gly Leu Lys Pro Thr Val Ile Phe Ala Asp Gln Ile
610 615 620

Met Tyr Thr Gly Phe Ala Tyr Ala Ala Arg Ser Gly Ala Ser Val Gly
625 630 635 640

Ile Asp Asp Met Val Ile Pro Glu Lys Lys His Glu Ile Ile Ser Glu
645 650 655

Ala Glu Ala Glu Val Ala Glu Ile Gln Glu Gln Phe Gln Ser Gly Leu
660 665 670

Val Thr Ala Gly Glu Arg Tyr Asn Lys Val Ile Asp Ile Trp Ala Ala
675 680 685

Ala Asn Asp Arg Val Ser Lys Ala Met Met Asp Asn Leu Gln Thr Glu
690 695 700

Thr Val Ile Asn Arg Asp Gly Gln Glu Glu Lys Gln Val Ser Phe Asn
705 710 715 720

Ser Ile Tyr Met Met Ala Asp Ser Gly Ala Arg Gly Ser Ala Ala Gln
725 730 735

Ile Arg Gln Leu Ala Gly Met Arg Gly Leu Met Ala Lys Pro Asp Gly
740 745 750

Ser Ile Ile Glu Thr Pro Ile Thr Ala Asn Phe Arg Glu Gly Leu Asn
755 760 765

Val Leu Gln Tyr Phe Ile Ser Thr His Gly Ala Arg Lys Gly Leu Ala
770 775 780

Asp Thr Ala Leu Lys Thr Ala Asn Ser Gly Tyr Leu Thr Arg Arg Leu

785		790		795		800									
Val	Asp	Val	Ala	Gln	Asp	Leu	Val	Val	Thr	Glu	Asp	Asp	Cys	Gly	Thr
				805					810					815	
His	Glu	Gly	Ile	Met	Met	Thr	Pro	Val	Ile	Glu	Gly	Gly	Asp	Val	Lys
			820					825					830		
Glu	Pro	Leu	Arg	Asp	Arg	Val	Leu	Gly	Arg	Val	Thr	Ala	Glu	Asp	Val
		835					840					845			
Leu	Lys	Pro	Gly	Thr	Ala	Asp	Ile	Leu	Val	Pro	Arg	Asn	Thr	Leu	Leu
	850					855					860				
His	Glu	Gln	Trp	Cys	Asp	Leu	Leu	Glu	Glu	Asn	Ser	Val	Asp	Ala	Val
865					870					875					880
Lys	Val	Arg	Ser	Val	Val	Ser	Cys	Asp	Thr	Asp	Phe	Gly	Val	Cys	Ala
				885					890					895	
His	Cys	Tyr	Gly	Arg	Asp	Leu	Ala	Arg	Gly	His	Ile	Ile	Asn	Lys	Gly
			900					905					910		
Glu	Ala	Ile	Gly	Val	Ile	Ala	Ala	Gln	Ser	Ile	Gly	Glu	Pro	Gly	Thr
		915					920					925			
Gln	Leu	Thr	Met	Arg	Thr	Phe	His	Ile	Gly	Gly	Ala	Ala	Ser	Arg	Ala
	930					935					940				
Ala	Ala	Glu	Ser	Ser	Ile	Gln	Val	Lys	Asn	Lys	Gly	Ser	Ile	Lys	Leu
945					950					955					960
Ser	Asn	Val	Lys	Ser	Val	Val	Asn	Ser	Ser	Gly	Lys	Leu	Val	Ile	Thr
				965					970					975	
Ser	Arg	Asn	Thr	Glu	Leu	Lys	Leu	Ile	Asp	Glu	Phe	Gly	Arg	Thr	Lys
			980					985					990		
Glu	Ser	Tyr	Lys	Val	Pro	Tyr	Gly	Ala	Val	Leu	Ala	Lys	Gly	Asp	Gly
		995					1000					1005			

Glu Gln Val Ala Gly Gly Glu Thr Val Ala Asn Trp Asp Pro His
1010 1015 1020

Thr Met Pro Val Ile Thr Glu Val Ser Gly Phe Val Arg Phe Thr
1025 1030 1035

Asp Met Ile Asp Gly Gln Thr Ile Thr Arg Gln Thr Asp Glu Leu
1040 1045 1050

Thr Gly Leu Ser Ser Leu Val Val Leu Asp Ser Ala Glu Arg Thr
1055 1060 1065

Ala Gly Gly Lys Asp Leu Arg Pro Ala Leu Lys Ile Val Asp Ala
1070 1075 1080

Gln Gly Asn Asp Val Leu Ile Pro Gly Thr Asp Met Pro Ala Gln
1085 1090 1095

Tyr Phe Leu Pro Gly Lys Ala Ile Val Gln Leu Glu Asp Gly Val
1100 1105 1110

Gln Ile Ser Ser Gly Asp Thr Leu Ala Arg Ile Pro Gln Glu Ser
1115 1120 1125

Gly Gly Thr Lys Asp Ile Thr Gly Gly Leu Pro Arg Val Ala Asp
1130 1135 1140

Leu Phe Glu Ala Arg Arg Pro Lys Glu Pro Ala Ile Leu Ala Glu
1145 1150 1155

Ile Ser Gly Ile Val Ser Phe Gly Lys Glu Thr Lys Gly Lys Arg
1160 1165 1170

Arg Leu Val Ile Thr Pro Val Asp Gly Ser Asp Pro Tyr Glu Glu
1175 1180 1185

Met Ile Pro Lys Trp Arg Gln Leu Asn Val Phe Glu Gly Glu Arg
1190 1195 1200

Val Glu Arg Gly Asp Val Ile Ser Asp Gly Pro Glu Ala Pro His

1205						1210						1215					
Asp	Ile	Leu	Arg	Leu	Arg	Gly	Val	His	Ala	Val	Thr	Arg	Tyr	Ile			
1220						1225						1230					
Val	Asn	Glu	Val	Gln	Asp	Val	Tyr	Arg	Leu	Gln	Gly	Val	Lys	Ile			
1235						1240						1245					
Asn	Asp	Lys	His	Ile	Glu	Val	Ile	Val	Arg	Gln	Met	Leu	Arg	Lys			
1250						1255						1260					
Ala	Thr	Ile	Val	Asn	Ala	Gly	Ser	Ser	Asp	Phe	Leu	Glu	Gly	Glu			
1265						1270						1275					
Gln	Val	Glu	Tyr	Ser	Arg	Val	Lys	Ile	Ala	Asn	Arg	Glu	Leu	Glu			
1280						1285						1290					
Ala	Asn	Gly	Lys	Val	Gly	Ala	Thr	Tyr	Ser	Arg	Asp	Leu	Leu	Gly			
1295						1300						1305					
Ile	Thr	Lys	Ala	Ser	Leu	Ala	Thr	Glu	Ser	Phe	Ile	Ser	Ala	Ala			
1310						1315						1320					
Ser	Phe	Gln	Glu	Thr	Thr	Arg	Val	Leu	Thr	Glu	Ala	Ala	Val	Ala			
1325						1330						1335					
Gly	Lys	Arg	Asp	Glu	Leu	Arg	Gly	Leu	Lys	Glu	Asn	Val	Ile	Val			
1340						1345						1350					
Gly	Arg	Leu	Ile	Pro	Ala	Gly	Thr	Gly	Tyr	Ala	Tyr	His	Gln	Asp			
1355						1360						1365					
Arg	Met	Arg	Arg	Arg	Ala	Ala	Gly	Glu	Ala	Pro	Ala	Ala	Pro	Gln			
1370						1375						1380					
Val	Thr	Ala	Glu	Asp	Ala	Ser	Ala	Ser	Leu	Ala	Glu	Leu	Leu	Asn			
1385						1390						1395					
Ala	Gly	Leu	Gly	Gly	Ser	Asp	Asn	Glu									
1400						1405											

<210> 29
<211> 720
<212> DNA
<213> Escherichia coli

<400> 29
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gatcgctgc tgactcgtga atctttccat cttatggtag tggatttaac gttacctggt 180
gaagatggct tgtcgatttg ccgacgtctt cgtagtcaga gcaacccgat gccgatcatt 240
atggtgacgg cgaaagggga agaagtggac cgtatcgtag gcctggagat tggcgctgac 300
gactacattc caaaaccgtt taaccgcgt gaactgctgg cccgtatccg tgcggtgctg 360
cgctgcagg cgaacgaact gccaggcgca ccgtcacagg aagaggcggg aattgctttc 420
ggtaagttca aacttaacct cggtagcgcg gaaatgttcc gcgaagacga gccgatgccg 480
ctcaccagcg gtgagtttgc ggtactgaag gactgggtca gccatccgcg tgagccgctc 540
tcccgcgata agctgatgaa ccttgcccgt ggtcgtgaat attccgcaat ggaacgctcc 600
atcgacgtgc agatttcgcg tctgcgccgc atgggtggaag aagatccagc gcatccgctg 660
tacattcaga ccgtctgggg tctgggctac gtctttgtac cggacggctc taaagcatga 720

<210> 30
<211> 239
<212> PRT
<213> Escherichia coli

<400> 30

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

Ser Val Ala Asn Ala Glu Gln Met Asp Arg Leu Leu Thr Arg Glu Ser
35 40 45

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

Ser Ile Cys Arg Arg Leu Arg Ser Gln Ser Asn Pro Met Pro Ile Ile
65 70 75 80

Met Val Thr Ala Lys Gly Glu Glu Val Asp Arg Ile Val Gly Leu Glu
85 90 95

Ile Gly Ala Asp Asp Tyr Ile Pro Lys Pro Phe Asn Pro Arg Glu Leu
100 105 110

Leu Ala Arg Ile Arg Ala Val Leu Arg Arg Gln Ala Asn Glu Leu Pro
115 120 125

Gly Ala Pro Ser Gln Glu Glu Ala Val Ile Ala Phe Gly Lys Phe Lys
130 135 140

Leu Asn Leu Gly Thr Arg Glu Met Phe Arg Glu Asp Glu Pro Met Pro
145 150 155 160

Leu Thr Ser Gly Glu Phe Ala Val Leu Lys Ala Leu Val Ser His Pro
165 170 175

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

Glu Tyr Ser Ala Met Glu Arg Ser Ile Asp Val Gln Ile Ser Arg Leu
195 200 205

Arg Arg Met Val Glu Glu Asp Pro Ala His Pro Arg Tyr Ile Gln Thr
210 215 220

Val Trp Gly Leu Gly Tyr Val Phe Val Pro Asp Gly Ser Lys Ala
225 230 235

<210> 31
<211> 672
<212> DNA
<213> Escherichia coli

<400> 31
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caggatgctg gtcacaggt cgatgacgca gaagatgcc aagaagccga ttattatctc 120

aatgaacata taccggatat tgcgattgtc gatctcggat tgccagacga ggacggctctg 180
tcaactgattc gccgctggcg tagcaacgat gtttcactgc cgattctggt attaaccgcc 240
cgtgaaagct ggacaggacaa agtcgaagta ttaagtgccg gtgctgatga ttatgtgact 300
aaaccgtttc atattgaaga ggtgatggcg cgaatgcagg cattaatgcg gcgtaatagc 360
ggctctggctt cacaggtcat ttcgctcccc ccgtttcagg ttgatctctc tcgccgtgaa 420
ttatctatta atgacgaagt gatcaaactg accgcgttcg aatacactat tatggaaacg 480
ttgatacgca ataatggcaa agtggtcagc aaagattcgt taatgctcca actctatccg 540
gatgcggagc tgcgggaaag ccataccatt gatgtactga tgggacgtct gcgcaaaaaa 600
attcaggcac aatatcccca agaagtgatt accaccgttc gcggccaggg ctatctgttc 660
gaattgctgc ga 672

<210> 32
<211> 223
<212> PRT
<213> Escherichia coli

<400> 32

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

Ala Lys Glu Ala Asp Tyr Tyr Leu Asn Glu His Ile Pro Asp Ile Ala
35 40 45

Ile Val Asp Leu Gly Leu Pro Asp Glu Asp Gly Leu Ser Leu Ile Arg
50 55 60

Arg Trp Arg Ser Asn Asp Val Ser Leu Pro Ile Leu Val Leu Thr Ala
65 70 75 80

Arg Glu Ser Trp Gln Asp Lys Val Glu Val Leu Ser Ala Gly Ala Asp
85 90 95

Asp Tyr Val Thr Lys Pro Phe His Ile Glu Glu Val Met Ala Arg Met

100

105

110

Gln Ala Leu Met Arg Arg Asn Ser Gly Leu Ala Ser Gln Val Ile Ser
 115 120 125

Leu Pro Pro Phe Gln Val Asp Leu Ser Arg Arg Glu Leu Ser Ile Asn
 130 135 140

Asp Glu Val Ile Lys Leu Thr Ala Phe Glu Tyr Thr Ile Met Glu Thr
 145 150 155 160

Leu Ile Arg Asn Asn Gly Lys Val Val Ser Lys Asp Ser Leu Met Leu
 165 170 175

Gln Leu Tyr Pro Asp Ala Glu Leu Arg Glu Ser His Thr Ile Asp Val
 180 185 190

Leu Met Gly Arg Leu Arg Lys Lys Ile Gln Ala Gln Tyr Pro Gln Glu
 195 200 205

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

<210> 33

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer Sequence

<400> 33

ctgtctctta ta