

eof-seq1.txt

SEQUENCE LISTING

<110> Evonik Degussa GmbH

<120> Verfahren zur Herstellung von L-Aminosäuren unter Verwendung
verbesserter Stämme der Familie Enterobacteriaceae

<130> 2007P00111

<160> 20

<170> PatentIn version 3.3

<210> 1

<211> 1509

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1509)

<223> glpK Kodierregion

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Ser Arg Ala Val Val Met Asp His Asp Ala Asn Ile Ile Ser Val Ser	
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cag cgc gaa ttt gag caa atc tac cca aaa cca ggt tgg gta gaa cac	144
Gln Arg Glu Phe Glu Gln Ile Tyr Pro Lys Pro Gly Trp Val Glu His	
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gac cca atg gaa atc tgg gcc acc caa agc tcc acg ctg gta gaa gtg	192
Asp Pro Met Glu Ile Trp Ala Thr Gln Ser Ser Thr Leu Val Glu Val	
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ctg gcg aaa gcc gat atc agt tcc gat caa att gca gct atc ggt att	240
Leu Ala Lys Ala Asp Ile Ser Ser Asp Gln Ile Ala Ala Ile Gly Ile	
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acg aac cag cgt gaa acc act att gtc tgg gaa aaa gaa acc ggc aag	288
Thr Asn Gln Arg Glu Thr Thr Ile Val Trp Glu Lys Glu Thr Gly Lys	
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cct atc tat aac gcc att gtc tgg cag tgc cgt cgt acc gca gaa atc	336
Pro Ile Tyr Asn Ala Ile Val Trp Gln Cys Arg Arg Thr Ala Glu Ile	
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tgc gag cat tta aaa cgt gac ggt tta gaa gat tat atc cgc agc aat	384
Cys Glu His Leu Lys Arg Asp Gly Leu Glu Asp Tyr Ile Arg Ser Asn	
115 120 125	
acc ggt ctg gtg att gac ccg tac ttt tct ggc acc aaa gtg aag tgg	432
Thr Gly Leu Val Ile Asp Pro Tyr Phe Ser Gly Thr Lys Val Lys Trp	
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Ile Leu Asp His Val Glu Gly Ser Arg Glu Arg Ala Arg Arg Gly Glu	
145 150 155 160	
ttg ctg ttt ggt acg gtt gat acg tgg ctt atc tgg aaa atg act cag	528
Leu Leu Phe Gly Thr Val Asp Thr Trp Leu Ile Trp Lys Met Thr Gln	
165 170 175	

eolf-seql.txt

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Phe	Asn	Ile	His	Thr	Leu	Asp	Trp	Asp	Asp	Lys	Met	Leu	Glu	Val	Leu	
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Tyr	Gly	Gln	Thr	Asn	Ile	Gly	Gly	Lys	Gly	Gly	Thr	Arg	Ile	Pro	Ile	
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eo1f-seq1.txt

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 Ser Gly Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Leu Cys
 245 250 255
 Val Lys Glu Gly Met Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Met
 260 265 270
 Leu Met Asn Thr Gly Glu Lys Ala Val Lys Ser Glu Asn Gly Leu Leu
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 Thr Thr Ile Ala Cys Gly Pro Thr Gly Glu Val Asn Tyr Ala Leu Glu
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 Gly Ala Val Phe Met Ala Gly Ala Ser Ile Gln Trp Leu Arg Asp Glu
 305 310 315 320
 Met Lys Leu Ile Asn Asp Ala Tyr Asp Ser Glu Tyr Phe Ala Thr Lys
 325 330 335
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 370 375 380
 Ile Ala Tyr Gln Thr Arg Asp Val Leu Glu Ala Met Gln Ala Asp Ser
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 Asn Phe Leu Met Gln Phe Gln Ser Asp Ile Leu Gly Thr Arg Val Glu
 420 425 430
 Arg Pro Glu Val Arg Glu Val Thr Ala Leu Gly Ala Ala Tyr Leu Ala
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 Gly Leu Ala Val Gly Phe Trp Gln Asn Leu Asp Glu Leu Gln Glu Lys
 450 455 460

eof-seq1.txt

Ala Val Ile Glu Arg Glu Phe Arg Pro Gly Ile Glu Thr Thr Glu Arg
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Trp Glu Glu His Asp Glu
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20 25 30	
cag cgt gaa ttt gag caa att tat cct aag cca ggc tgg gta gaa cac	144
Gln Arg Glu Phe Glu Gln Ile Tyr Pro Lys Pro Gly Trp Val Glu His	
35 40 45	
gac ccg atg gaa att tgg gcg tcc caa agc tca acg ctg gta gaa gtg	192
Asp Pro Met Glu Ile Trp Ala Ser Gln Ser Ser Thr Leu Val Glu Val	
50 55 60	
ctg gct aag gcc gat atc agt tcc gat cag att gcc gct atc ggt atc	240
Leu Ala Lys Ala Asp Ile Ser Ser Asp Gln Ile Ala Ala Ile Gly Ile	
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acc aac caa cgt gaa acc gcg atc gtc tgg gaa cgt gaa acc ggc aaa	288
Thr Asn Gln Arg Glu Thr Ala Ile Val Trp Glu Arg Glu Thr Gly Lys	
85 90 95	
ccg ata tac aac gct att gtc tgg cag tgc cgt cgt acc gcc gat att	336
Pro Ile Tyr Asn Ala Ile Val Trp Gln Cys Arg Arg Thr Ala Asp Ile	
100 105 110	
tgc gaa cag ctt aaa cgc gac ggc ctg gaa gat tac atc cgc gac aat	384
Cys Glu Gln Leu Lys Arg Asp Gly Leu Glu Asp Tyr Ile Arg Asp Asn	
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Thr Gly Leu Val Val Asp Pro Tyr Phe Ser Gly Thr Lys Val Lys Trp	
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Ile Leu Asp His Val Glu Gly Ser Arg Glu Arg Ala Lys Arg Gly Glu	
145 150 155 160	
ctg ctg ttc ggt acg gtg gat acc tgg ctt atc tgg aag atg acg cag	528
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165 170 175	

eolf-seql.txt

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gat	atc	cca	cgc	gcg	atg	ctg	ccc	cag	gta	cgt	aag	tcc	tcc	gaa	gtc	672
Asp	Ile	Pro	Arg	Ala	Met	Leu	Pro	Gln	Val	Arg	Lys	Ser	Ser	Glu	Val	
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gta	aag	gaa	gga	atg	gca	aag	aat	acc	tac	ggc	acc	ggc	tgc	ttt	atg	816
Val	Lys	Glu	Gly	Met	Ala	Lys	Asn	Thr	Tyr	Gly	Thr	Gly	Cys	Phe	Met	
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Asn	Phe	Leu	Met	Gln	Phe	Gln	Ser	Asp	Ile	Leu	Gly	Thr	Arg	Val	Glu	
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Arg	Pro	Glu	Val	Arg	Glu	Val	Thr	Ala	Leu	Gly	Ala	Ala	Tyr	Leu	Ala	
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eolf-seql.txt

Gly	Leu	Ala	Val	Gly	Tyr	Trp	Gln	Asn	Leu	Asp	Glu	Leu	Gln	Glu	Lys		
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aac	tac	cgt	tac	agc	ggc	tgg	aag	aaa	gcg	ggt	aaa	cgc	gca	atg	gcg	1488	
Asn	Tyr	Arg	Tyr	Ser	Gly	Trp	Lys	Lys	Ala	Val	Lys	Arg	Ala	Met	Ala		
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tgg	gaa	gag	cac	gac	aag	taa										1509	
Trp	Glu	Glu	His	Asp	Lys												
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Cys	Glu	Gln	Leu	Lys	Arg	Asp	Gly	Leu	Glu	Asp	Tyr	Ile	Arg	Asp	Asn		
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eo1f-seq1.txt

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 Ala Gly Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Leu Cys
 245 250 255
 Val Lys Glu Gly Met Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Met
 260 265 270
 Leu Met Asn Thr Gly Glu Lys Ala Val Lys Ser Glu Asn Gly Leu Leu
 275 280 285
 Ile Thr Ile Ala Cys Gly Pro Ser Gly Glu Val Asn Tyr Ala Leu Glu
 290 295 300
 Gly Ala Val Phe Met Ala Gly Ala Ser Ile Gln Trp Leu Arg Asp Glu
 305 310 315 320
 Met Lys Leu Ile Ser Asp Ala Phe Asp Ser Glu Tyr Phe Ala Thr Lys
 325 330 335
 Val Lys Asp Thr Asn Gly Val Tyr Val Val Pro Ala Phe Thr Gly Leu
 340 345 350
 Gly Ala Pro Tyr Trp Asp Pro Tyr Ala Arg Gly Ala Ile Phe Gly Leu
 355 360 365
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 370 375 380
 Ile Ala Tyr Gln Thr Arg Asp Val Leu Glu Ala Met Gln Ala Asp Ser
 385 390 395 400
 Gly Ile Arg Leu His Ala Leu Arg Val Asp Gly Gly Ala Val Ala Asn
 405 410 415
 Asn Phe Leu Met Gln Phe Gln Ser Asp Ile Leu Gly Thr Arg Val Glu
 420 425 430
 Arg Pro Glu Val Arg Glu Val Thr Ala Leu Gly Ala Ala Tyr Leu Ala
 435 440 445
 Gly Leu Ala Val Gly Tyr Trp Gln Asn Leu Asp Glu Leu Gln Glu Lys
 450 455 460

eof-seq1.txt

Ala Val Ile Glu Arg Glu Phe Arg Pro Gly Ile Glu Thr Thr Glu Arg
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Ser Arg Ala Val Val Met Asp His Asp Ala Asn Ile Ile Ser Val Ser	
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cag cgc gaa ttt gag caa atc tac cca aaa cca ggt tgg gta gaa cac	144
Gln Arg Glu Phe Glu Gln Ile Tyr Pro Lys Pro Gly Trp Val Glu His	
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gac cca atg gaa atc tgg gcc acc caa agc tcc acg ctg gta gaa gtg	192
Asp Pro Met Glu Ile Trp Ala Thr Gln Ser Ser Thr Leu Val Glu Val	
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Leu Ala Lys Ala Asp Ile Ser Ser Asp Gln Ile Ala Ala Ile Gly Ile	
65 70 75 80	
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Thr Asn Gln Arg Glu Thr Thr Ile Val Trp Glu Lys Glu Thr Gly Lys	
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cct atc tat aac gcc att gtc tgg cag tgc cgt cgt acc gca gaa atc	336
Pro Ile Tyr Asn Ala Ile Val Trp Gln Cys Arg Arg Thr Ala Glu Ile	
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Cys Glu His Leu Lys Arg Asp Gly Leu Glu Asp Tyr Ile Arg Ser Asn	
115 120 125	
acc ggt ctg gtg att gac ccg tac ttt tct ggc acc aaa gtg aag tgg	432
Thr Gly Leu Val Ile Asp Pro Tyr Phe Ser Gly Thr Lys Val Lys Trp	
130 135 140	
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Ile Leu Asp His Val Glu Gly Ser His Glu Arg Ala Arg Arg Gly Glu	
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ttg ctg ttt ggt acg gtt gat acg tgg ctt atc tgg aaa atg act cag	528
Leu Leu Phe Gly Thr Val Asp Thr Trp Leu Ile Trp Lys Met Thr Gln	
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eolf-seql.txt

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Phe	Asn	Ile	His	Thr	Leu	Asp	Trp	Asp	Asp	Lys	Met	Leu	Glu	Val	Leu	
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Thr	Thr	Ile	Ala	Cys	Gly	Pro	Thr	Gly	Glu	Val	Asn	Tyr	Ala	Leu	Glu	
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Arg	Pro	Glu	Val	Arg	Glu	Val	Thr	Ala	Leu	Gly	Ala	Ala	Tyr	Leu	Ala	
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eolf-seql.txt

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Thr	Gly	Leu	Val	Ile	Asp	Pro	Tyr	Phe	Ser	Gly	Thr	Lys	Val	Lys	Trp	
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eo1f-seq1.txt

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 225 230 235 240
 Ser Gly Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Leu Cys
 245 250 255
 Val Lys Glu Gly Met Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Met
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 Leu Met Asn Thr Gly Glu Lys Ala Val Lys Ser Glu Asn Gly Leu Leu
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 Thr Thr Ile Ala Cys Gly Pro Thr Gly Glu Val Asn Tyr Ala Leu Glu
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 Gly Ala Val Phe Met Ala Gly Ala Ser Ile Gln Trp Leu Arg Asp Glu
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 Met Lys Leu Ile Asn Asp Ala Tyr Asp Ser Glu Tyr Phe Ala Thr Lys
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 Thr Arg Gly Val Asn Ala Asn His Ile Ile Arg Ala Thr Leu Glu Ser
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 Ile Ala Tyr Gln Thr Arg Asp Val Leu Glu Ala Met Gln Ala Asp Ser
 385 390 395 400
 Gly Ile Arg Leu His Ala Leu Arg Val Asp Gly Gly Ala Val Ala Asn
 405 410 415
 Asn Phe Leu Met Gln Phe Gln Ser Asp Ile Leu Gly Thr Arg Val Glu
 420 425 430
 Arg Pro Glu Val Arg Glu Val Thr Ala Leu Gly Ala Ala Tyr Leu Ala
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 Gly Leu Ala Val Gly Phe Trp Gln Asn Leu Asp Glu Leu Gln Glu Lys
 450 455 460

eof-seq1.txt

Ala Val Ile Glu Arg Glu Phe Arg Pro Gly Ile Glu Thr Thr Glu Arg
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Met Thr Glu
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aaa aaa tat atc gtt gcg ctc gac cag ggc acc acc agc tcc gcg gcg 165
Lys Lys Tyr Ile Val Ala Leu Asp Gln Gly Thr Thr Ser Ser Arg Ala
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Val Val Met Asp His Asp Ala Asn Ile Ile Ser Val Ser Gln Arg Glu
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ttt gag caa atc tac cca aaa cca ggt tgg gta gaa cac gac cca atg 261
Phe Glu Gln Ile Tyr Pro Lys Pro Gly Trp Val Glu His Asp Pro Met
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gaa atc tgg gcc acc caa agc tcc acg ctg gta gaa gtg ctg gcg aaa 309
Glu Ile Trp Ala Thr Gln Ser Ser Thr Leu Val Glu Val Leu Ala Lys
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gcc gat atc agt tcc gat caa att gca gct atc ggt att acg aac cag 357
Ala Asp Ile Ser Ser Asp Gln Ile Ala Ala Ile Gly Ile Thr Asn Gln
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cgt gaa acc act att gtc tgg gaa aaa gaa acc ggc aag cct atc tat 405
Arg Glu Thr Thr Ile Val Trp Glu Lys Glu Thr Gly Lys Pro Ile Tyr
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aac gcc att gtc tgg cag tgc cgt cgt acc gca gaa atc tgc gag cat 453
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135 140 145

cat gtg gaa ggc tct cgc gag cgt gca cgt cgt ggt gaa ttg ctg ttt 597
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Page 13

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cat His 180	gtg Val	acc Thr	gat Asp	tac Tyr	acc Thr 185	aac Asn	gcc Ala	tct Ser	cgt Arg	acc Thr 190	atg Met	ttg Leu	ttc Phe	aac Asn	atc Ile 195	693
cat His	acc Thr	ctg Leu	gac Asp	tgg Trp 200	gac Asp	gac Asp	aaa Lys	atg Met	ctg Leu 205	gaa Glu	gtg Val	ctg Leu	gat Asp	att Ile 210	ccg Pro	741
cgc Arg	gag Glu	atg Met	ctg Leu 215	cca Pro	gaa Glu	gtg Val	cgt Arg	cgt Arg 220	tct Ser	tcc Ser	gaa Glu	gta Val	tac Tyr 225	ggg Gly	cag Gln	789
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gcc Ala	ggt Gly 245	gac Asp	cag Gln	cag Gln	gcc Ala	gcg Ala 250	ctg Leu	ttt Phe	ggt Gly	cag Gln	ttg Leu 255	tgc Cys	gtg Val	aaa Lys	gaa Glu	885
ggg Gly 260	atg Met	gcg Ala	aag Lys	aac Asn	acc Thr 265	tat Tyr	ggc Gly	act Thr	ggc Gly	tgc Cys 270	ttt Phe	atg Met	ctg Leu	atg Met	aac Asn 275	933
act Thr	ggc Gly	gag Glu	aaa Lys	gcg Ala 280	gtg Val	aaa Lys	tca Ser	gaa Glu	aac Asn 285	ggc Gly	ctg Leu	ctg Leu	acc Thr	acc Thr 290	atc Ile	981
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ctg Leu	cac His 405	gcc Ala	ctg Leu	cgc Arg	gtg Val 410	gat Asp	ggg Gly	ggc Gly	gca Ala	gta Val	gca Ala 415	aac Asn	aat Asn	ttc Phe	ctg Leu	1365
atg Met 420	cag Gln	ttc Phe	cag Gln	tcc Ser	gat Asp 425	att Ile	ctc Leu	ggc Gly	acc Thr	cgc Arg 430	gtt Val	gag Glu	cgc Arg	ccg Pro	gaa Glu 435	1413

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Asp Pro Met Glu Ile Trp Ala Thr Gln Ser Ser Thr Leu Val Glu Val 50 55 60
Leu Ala Lys Ala Asp Ile Ser Ser Asp Gln Ile Ala Ala Ile Gly Ile 65 70 75 80
Thr Asn Gln Arg Glu Thr Thr Ile Val Trp Glu Lys Glu Thr Gly Lys 85 90 95

eo1f-seq1.txt

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130 135 140

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165 170 175

Gly Arg Val His Val Thr Asp Tyr Thr Asn Ala Ser Arg Thr Met Leu
180 185 190

Phe Asn Ile His Thr Leu Asp Trp Asp Asp Lys Met Leu Glu Val Leu
195 200 205

Asp Ile Pro Arg Glu Met Leu Pro Glu Val Arg Arg Ser Ser Glu Val
210 215 220

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Ser Gly Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Leu Cys
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Met Lys Leu Ile Asn Asp Ala Tyr Asp Ser Glu Tyr Phe Ala Thr Lys
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eof-seq1.txt

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eof-seq1.txt

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 cgattacacc aacgcctctc gtaccatggt gttcaacatc cataccctgg actgggacga 60
 caaaatgctg gaagtgtctg atattccgcg cgagatgctg ccagaagtgc gtcgttcttc 120
 cgaagtatac ggtcagacta acattggcgg caaaggcggc acgcgtattc caatctccgg 180
 gatcgccggt gaccagcagg ccgcgctggt tggtcagttg tgcgtgaaag aagggatggc 240
 gaagaacacc tatggcactg gctgctttat gctgatgaac actggcgaga aagcggtgaa 300
 atcagaaaac ggcctgctga ccaccatcgc ctgcggcccg actggcgaag tgaactatgc 360
 gttggaaggt gcggtgttta tggcaggcgc atccattcag tggctgcgcg atgaaatgaa 420
 gttgattaac gacgcctacg attccgaata tttcgccacc aaagtgcaaa acaccaatgg 480
 tgtgtatgtg gttccggcat ttaccgggct ggggtgcgccg tactgggacc cgtatgcgcg 540
 cggggcgatt ttcggtctga ctcgtggggt gaacgctaac cacattatac gcgcgacgct 600
 ggagtctatt gcttatcaga cgcgtgacgt gctggaagcg atgcaggccg actctggtat 660
 ccgtctgcac gccctgcgcg tggatggtgg cgcagtagca aacaatttcc tgatgcagtt 720

eof-seq1.txt

```

ccagtccgat attctcgata cccgcgttga gcgctccgaa gtgcgcgaag tcaccgcatt    780
gggtgcggcc tatctcgag gcctggcggt tggcttctgg cagaacctcg acgagctgca    840
agagaaagcg gtgattgagc gcgagttccg tccaggcatc gaaaccactg agcgtaatta    900
ccgttacgca ggctggaaaa aagcggttaa acgcgcgatg gcgtgggaag aacacgacga    960
ataatgtaaa tgccgaatga agcgtttatg ccgcatccgg tagtcccgaa acgtgcgggg   1020
gcaacccgc acacatcaat aatccctccc ttccctgtg ctacacttcg cgccattcct   1080
tactgcttag agtttgctat gagacgagaa cttgccatcg aattttcccg cgtcaccgaa   1140
tcagcggcgc tggctggcta caaatggta ggacgcggcg ataaaaacac cgcggaaggc   1200
gcggcggtaa acgccatgcg tattatgctc aaccaggta acattgacgg caccatcgtc   1260
attggtgaag gtgaaatcga cgaagcaccg atgctctaca ttggtgaaaa agtcggtact   1320
ggtcgcggcg acgcggtaga tattgctgtt gatccgattg aaggcacgcg catgacggcg   1380
atgggccagg ctaacgcgct ggcggtgctg gcagtaggcg ataaaggctg cttcctcaat   1440
gcgccggata tgtatatgga gaagctgatt gtcgggc                                1477

```

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<210> 14
<211> 29
<212> DNA
<213> artificial sequence

```

```

<220>
<223> primer with SalI recognition site

```

```

<220>
<221> primer
<222> (1)..(29)
<223> glpK_1

```

```

<400> 14
cggtcgacat gactacggga caattaaac                                29

```

```

<210> 15
<211> 40
<212> DNA
<213> artificial sequence

```

```

<220>
<223> "gene SOEing"-primer

```

```

<220>
<221> primer
<222> (1)..(40)
<223> glpK_7_SOEing

```

```

<400> 15
gaattcgcg gccgcctttg ccatcaatgt tagtctgacc                                40

```

```

<210> 16
<211> 40
<212> DNA
<213> artificial sequence

```

eolf-seql.txt

```

<220>
<223> "gene SOEing"-primer

<220>
<221> primer
<222> (1)..(40)
<223> glpK_8_SOEing

<400> 16
cattgatggc aaaggcggca cgcgaattcc aatctccggg          40

<210> 17
<211> 28
<212> DNA
<213> artificial sequence

<220>
<223> primer with salI recognition site

<220>
<221> primer
<222> (1)..(28)
<223> glpFK_2

<400> 17
cggtcgactt attcgtcgtg ttcttccc          28

<210> 18
<211> 1546
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (30)..(1538)
<223> glpK kodierregion

<220>
<221> mutation
<222> (721)..(722)
<223> transitions gc -> at

<400> 18
cggtcgacat gactacggga caattaaac atg act gaa aaa aaa tat atc gtt          53
                                Met Thr Glu Lys Lys Tyr Ile Val
                                1                                5

gcg ctc gac cag ggc acc acc agc tcc cgc gcg gtc gta atg gat cac          101
Ala Leu Asp Gln Gly Thr Thr Ser Ser Arg Ala Val Val Met Asp His
10                                15                                20

gat gcc aat atc att agc gtg tcg cag cgc gaa ttt gag caa atc tac          149
Asp Ala Asn Ile Ile Ser Val Ser Gln Arg Glu Phe Glu Gln Ile Tyr
25                                30                                35                                40

cca aaa cca ggt tgg gta gaa cac gac cca atg gaa atc tgg gcc acc          197
Pro Lys Pro Gly Trp Val Glu His Asp Pro Met Glu Ile Trp Ala Thr
45                                50                                55

caa agc tcc acg ctg gta gaa gtg ctg gcg aaa gcc gat atc agt tcc          245
Gln Ser Ser Thr Leu Val Glu Val Leu Ala Lys Ala Asp Ile Ser Ser
60                                65                                70

gat caa att gca gct atc ggt att acg aac cag cgt gaa acc act att          293

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eolf-seql.txt

Asp	Gln	Ile	Ala	Ala	Ile	Gly	Ile	Thr	Asn	Gln	Arg	Glu	Thr	Thr	Ile	
		75					80					85				
gtc	tgg	gaa	aaa	gaa	acc	ggc	aag	cct	atc	tat	aac	gcc	att	gtc	tgg	341
Val	Trp	Glu	Lys	Glu	Thr	Gly	Lys	Pro	Ile	Tyr	Asn	Ala	Ile	Val	Trp	
	90					95					100					
cag	tgc	cgt	cgt	acc	gca	gaa	atc	tgc	gag	cat	tta	aaa	cgt	gac	ggt	389
Gln	Cys	Arg	Arg	Thr	Ala	Glu	Ile	Cys	Glu	His	Leu	Lys	Arg	Asp	Gly	
105					110					115					120	
tta	gaa	gat	tat	atc	cgc	agc	aat	acc	ggg	ctg	gtg	att	gac	ccg	tac	437
Leu	Glu	Asp	Tyr	Ile	Arg	Ser	Asn	Thr	Gly	Leu	Val	Ile	Asp	Pro	Tyr	
				125					130					135		
ttt	tct	ggc	acc	aaa	gtg	aag	tgg	atc	ctc	gac	cat	gtg	gaa	ggc	tct	485
Phe	Ser	Gly	Thr	Lys	Val	Lys	Trp	Ile	Leu	Asp	His	Val	Glu	Gly	Ser	
			140					145					150			
cgc	gag	cgt	gca	cgt	cgt	ggg	gaa	ttg	ctg	ttt	ggg	acg	gtt	gat	acg	533
Arg	Glu	Arg	Ala	Arg	Arg	Gly	Glu	Leu	Leu	Phe	Gly	Thr	Val	Asp	Thr	
		155					160					165				
tgg	ctt	atc	tgg	aaa	atg	act	cag	ggc	cgt	gtc	cat	gtg	acc	gat	tac	581
Trp	Leu	Ile	Trp	Lys	Met	Thr	Gln	Gly	Arg	Val	His	Val	Thr	Asp	Tyr	
	170					175					180					
acc	aac	gcc	tct	cgt	acc	atg	ttg	ttc	aac	atc	cat	acc	ctg	gac	tgg	629
Thr	Asn	Ala	Ser	Arg	Thr	Met	Leu	Phe	Asn	Ile	His	Thr	Leu	Asp	Trp	
185					190					195					200	
gac	gac	aaa	atg	ctg	gaa	gtg	ctg	gat	att	ccg	cgc	gag	atg	ctg	cca	677
Asp	Asp	Lys	Met	Leu	Glu	Val	Leu	Asp	Ile	Pro	Arg	Glu	Met	Leu	Pro	
				205					210					215		
gaa	gtg	cgt	cgt	tct	tcc	gaa	gta	tac	ggg	cag	act	aac	att	gat	ggc	725
Glu	Val	Arg	Arg	Ser	Ser	Glu	Val	Tyr	Gly	Gln	Thr	Asn	Ile	Asp	Gly	
			220					225					230			
aaa	ggc	ggc	acg	cga	att	cca	atc	tcc	ggg	atc	gcc	ggg	gac	cag	cag	773
Lys	Gly	Gly	Thr	Arg	Ile	Pro	Ile	Ser	Gly	Ile	Ala	Gly	Asp	Gln	Gln	
		235					240					245				
gcc	gcg	ctg	ttt	ggg	cag	ttg	tgc	gtg	aaa	gaa	ggg	atg	gcg	aag	aac	821
Ala	Ala	Leu	Phe	Gly	Gln	Leu	Cys	Val	Lys	Glu	Gly	Met	Ala	Lys	Asn	
	250					255					260					
acc	tat	ggc	act	ggc	tgc	ttt	atg	ctg	atg	aac	act	ggc	gag	aaa	gcg	869
Thr	Tyr	Gly	Thr	Gly	Cys	Phe	Met	Leu	Met	Asn	Thr	Gly	Glu	Lys	Ala	
265				270						275					280	
gtg	aaa	tca	gaa	aac	ggc	ctg	ctg	acc	acc	atc	gcc	tgc	ggc	ccg	act	917
Val	Lys	Ser	Glu	Asn	Gly	Leu	Leu	Thr	Thr	Ile	Ala	Cys	Gly	Pro	Thr	
				285					290					295		
ggc	gaa	gtg	aac	tat	gcg	ttg	gaa	ggg	gcg	gtg	ttt	atg	gca	ggc	gca	965
Gly	Glu	Val	Asn	Tyr	Ala	Leu	Glu	Gly	Ala	Val	Phe	Met	Ala	Gly	Ala	
			300					305					310			
tcc	att	cag	tgg	ctg	cgc	gat	gaa	atg	aag	ttg	att	aac	gac	gcc	tac	1013
Ser	Ile	Gln	Trp	Leu	Arg	Asp	Glu	Met	Lys	Leu	Ile	Asn	Asp	Ala	Tyr	
		315					320					325				
gat	tcc	gaa	tat	ttc	gcc	acc	aaa	gtg	caa	aac	acc	aat	ggg	gtg	tat	1061
Asp	Ser	Glu	Tyr	Phe	Ala	Thr	Lys	Val	Gln	Asn	Thr	Asn	Gly	Val	Tyr	
	330					335					340					
gtg	gtt	ccg	gca	ttt	acc	ggg	ctg	ggg	gcg	ccg	tac	tgg	gac	ccg	tat	1109
Val	Val	Pro	Ala	Phe	Thr	Gly	Leu	Gly	Ala	Pro	Tyr	Trp	Asp	Pro	Tyr	

eolf-seq1.txt
355

345		350		360	
gcg cgc ggg gcg att ttc ggt ctg act cgt ggg gtg aac gct aac cac					1157
Ala Arg Gly Ala Ile Phe Gly Leu Thr Arg Gly Val Asn Ala Asn His					
		365		370	
att ata cgc ggc acg ctg gag tct att gct tat cag acg cgt gac gtg					1205
Ile Ile Arg Ala Thr Leu Glu Ser Ile Ala Tyr Gln Thr Arg Asp Val					
		380		385	
ctg gaa ggc atg cag gcc gac tct ggt atc cgt ctg cac gcc ctg cgc					1253
Leu Glu Ala Met Gln Ala Asp Ser Gly Ile Arg Leu His Ala Leu Arg					
		395		400	
gtg gat ggt ggc gca gta gca aac aat ttc ctg atg cag ttc cag tcc					1301
Val Asp Gly Gly Ala Val Ala Asn Asn Phe Leu Met Gln Phe Gln Ser					
		410		415	
gat att ctc ggc acc cgc gtt gag cgc ccg gaa gtg cgc gaa gtc acc					1349
Asp Ile Leu Gly Thr Arg Val Glu Arg Pro Glu Val Arg Glu Val Thr					
		425		430	
gca ttg ggt ggc gcc tat ctc gca ggc ctg gcg gtt ggc ttc tgg cag					1397
Ala Leu Gly Ala Ala Tyr Leu Ala Gly Leu Ala Val Gly Phe Trp Gln					
		445		450	
aac ctc gac gag ctg caa gag aaa gcg gtg att gag cgc gag ttc cgt					1445
Asn Leu Asp Glu Leu Gln Glu Lys Ala Val Ile Glu Arg Glu Phe Arg					
		460		465	
cca ggc atc gaa acc act gag cgt aat tac cgt tac gca ggc tgg aaa					1493
Pro Gly Ile Glu Thr Thr Glu Arg Asn Tyr Arg Tyr Ala Gly Trp Lys					
		475		480	
aaa gcg gtt aaa cgc gcg atg gcg tgg gaa gaa cac gac gaa taa					1538
Lys Ala Val Lys Arg Ala Met Ala Trp Glu Glu His Asp Glu					
		490		495	
gtcgaccg					1546

<210> 19
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 <212> PRT
 <213> Escherichia coli
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Ser Arg Ala Val Val Met Asp His Asp Ala Asn Ile Ile Ser Val Ser	
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Gln Arg Glu Phe Glu Gln Ile Tyr Pro Lys Pro Gly Trp Val Glu His	
35 40 45	
Asp Pro Met Glu Ile Trp Ala Thr Gln Ser Ser Thr Leu Val Glu Val	
50 55 60	
Leu Ala Lys Ala Asp Ile Ser Ser Asp Gln Ile Ala Ala Ile Gly Ile	
65 70 75 80	
Thr Asn Gln Arg Glu Thr Thr Ile Val Trp Glu Lys Glu Thr Gly Lys	

eo1f-seq1.txt

85

90

95

Pro Ile Tyr Asn Ala Ile Val Trp Gln Cys Arg Arg Thr Ala Glu Ile
100 105 110

Cys Glu His Leu Lys Arg Asp Gly Leu Glu Asp Tyr Ile Arg Ser Asn
115 120 125

Thr Gly Leu Val Ile Asp Pro Tyr Phe Ser Gly Thr Lys Val Lys Trp
130 135 140

Ile Leu Asp His Val Glu Gly Ser Arg Glu Arg Ala Arg Arg Gly Glu
145 150 155 160

Leu Leu Phe Gly Thr Val Asp Thr Trp Leu Ile Trp Lys Met Thr Gln
165 170 175

Gly Arg Val His Val Thr Asp Tyr Thr Asn Ala Ser Arg Thr Met Leu
180 185 190

Phe Asn Ile His Thr Leu Asp Trp Asp Asp Lys Met Leu Glu Val Leu
195 200 205

Asp Ile Pro Arg Glu Met Leu Pro Glu Val Arg Arg Ser Ser Glu Val
210 215 220

Tyr Gly Gln Thr Asn Ile Asp Gly Lys Gly Gly Thr Arg Ile Pro Ile
225 230 235 240

Ser Gly Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Leu Cys
245 250 255

Val Lys Glu Gly Met Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Met
260 265 270

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

Thr Thr Ile Ala Cys Gly Pro Thr Gly Glu Val Asn Tyr Ala Leu Glu
290 295 300

Gly Ala Val Phe Met Ala Gly Ala Ser Ile Gln Trp Leu Arg Asp Glu
305 310 315 320

Met Lys Leu Ile Asn Asp Ala Tyr Asp Ser Glu Tyr Phe Ala Thr Lys
325 330 335

Val Gln Asn Thr Asn Gly Val Tyr Val Val Pro Ala Phe Thr Gly Leu
340 345 350

Gly Ala Pro Tyr Trp Asp Pro Tyr Ala Arg Gly Ala Ile Phe Gly Leu
355 360 365

eof-seq1.txt

Thr Arg Gly Val Asn Ala Asn His Ile Ile Arg Ala Thr Leu Glu Ser
370 375 380

Ile Ala Tyr Gln Thr Arg Asp Val Leu Glu Ala Met Gln Ala Asp Ser
385 390 395 400

Gly Ile Arg Leu His Ala Leu Arg Val Asp Gly Gly Ala Val Ala Asn
405 410 415

Asn Phe Leu Met Gln Phe Gln Ser Asp Ile Leu Gly Thr Arg Val Glu
420 425 430

Arg Pro Glu Val Arg Glu Val Thr Ala Leu Gly Ala Ala Tyr Leu Ala
435 440 445

Gly Leu Ala Val Gly Phe Trp Gln Asn Leu Asp Glu Leu Gln Glu Lys
450 455 460

Ala Val Ile Glu Arg Glu Phe Arg Pro Gly Ile Glu Thr Thr Glu Arg
465 470 475 480

Asn Tyr Arg Tyr Ala Gly Trp Lys Lys Ala Val Lys Arg Ala Met Ala
485 490 495

Trp Glu Glu His Asp Glu
500

<210> 20
<211> 502
<212> PRT
<213> Escherichia coli

<400> 20

Met Thr Glu Lys Lys Tyr Ile Val Ala Leu Asp Gln Gly Thr Thr Ser
1 5 10 15

Ser Arg Ala Val Val Met Asp His Asp Ala Asn Ile Ile Ser Val Ser
20 25 30

Gln Arg Glu Phe Glu Gln Ile Tyr Pro Lys Pro Gly Trp Val Glu His
35 40 45

Asp Pro Met Glu Ile Trp Ala Thr Gln Ser Ser Thr Leu Val Glu Val
50 55 60

Leu Ala Lys Ala Asp Ile Ser Ser Asp Gln Ile Ala Ala Ile Gly Ile
65 70 75 80

Thr Asn Gln Arg Glu Thr Thr Ile Val Trp Glu Lys Glu Thr Gly Lys
85 90 95

eo1f-seq1.txt

Pro Ile Tyr Asn Ala Ile Val Trp Gln Cys Arg Arg Thr Ala Glu Ile
100 105 110

Cys Glu His Leu Lys Arg Asp Gly Leu Glu Asp Tyr Ile Arg Ser Asn
115 120 125

Thr Gly Leu Val Ile Asp Pro Tyr Phe Ser Gly Thr Lys Val Lys Trp
130 135 140

Ile Leu Asp His Val Glu Gly Ser Arg Glu Arg Ala Arg Arg Gly Glu
145 150 155 160

Leu Leu Phe Gly Thr Val Asp Thr Trp Leu Ile Trp Lys Met Thr Gln
165 170 175

Gly Arg Val His Val Thr Asp Tyr Thr Asn Ala Ser Arg Thr Met Leu
180 185 190

Phe Asn Ile His Thr Leu Asp Trp Asp Asp Lys Met Leu Glu Val Leu
195 200 205

Asp Ile Pro Arg Glu Met Leu Pro Glu Val Arg Arg Ser Ser Glu Val
210 215 220

Tyr Gly Gln Thr Asn Ile Gly Gly Lys Gly Gly Thr Ser Ile Pro Ile
225 230 235 240

Ser Gly Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Leu Cys
245 250 255

Val Lys Glu Gly Met Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Met
260 265 270

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

Thr Thr Ile Ala Cys Gly Pro Thr Gly Glu Val Asn Tyr Ala Leu Glu
290 295 300

Gly Ala Val Phe Met Ala Gly Ala Ser Ile Gln Trp Leu Arg Asp Glu
305 310 315 320

Met Lys Leu Ile Asn Asp Ala Tyr Asp Ser Glu Tyr Phe Ala Thr Lys
325 330 335

Val Gln Asn Thr Asn Gly Val Tyr Val Val Pro Ala Phe Thr Gly Leu
340 345 350

Gly Ala Pro Tyr Trp Asp Pro Tyr Ala Arg Gly Ala Ile Phe Gly Leu
355 360 365

Thr Arg Gly Val Asn Ala Asn His Ile Ile Arg Ala Thr Leu Glu Ser

[illegible]