

SEQUENZPROTOKOLL

<110> Evonik-Degussa GmbH

<120> Verfahren zur Herstellung von L-Aminosäuren

<130> 200800120 DE

<160> 21

<170> PatentIn version 3.3

<210> 1

<211> 669

<212> DNA

<213> Corynebacterium glutamicum ATCC13032

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<222> (1)..(666)

<223> amtR-Gen

<220>

<221> misc_feature

<222> (8)..(8)

<223> Nukleobase G

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Gly Lys Asn Pro Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe	
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Thr Arg Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala	
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gtg gga atc cgc caa gcc tcg ctg tat tat cac ttc ccg tcc aag acg	192
Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr	
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gaa atc ttc ctc acc ctg ctg aaa tct act gtc gag ccg tcc act gtg	240
Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val	
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ctc gcc gaa gac tta agc acc ctg gac gcc gga cct gag atg cgc ctc	288
Leu Ala Glu Asp Leu Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu	
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Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp	
100 105 110	

aac gtc ggt cgc ctg tac caa ctc ccc atc gtt ggt tct gaa gag ttc	384
Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe	
115 120 125	

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His	Ile	Thr	Met	Ser	Val	Ile	Glu	Met	Arg	Arg	Asn	Asp	Gly	Lys	Ile	
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cca	agc	ccg	ctt	tcc	gca	gac	agc	ctc	ccg	gag	acc	gca	att	atg	ctt	576
Pro	Ser	Pro	Leu	Ser	Ala	Asp	Ser	Leu	Pro	Glu	Thr	Ala	Ile	Met	Leu	
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Ala	Asp	Ala	Ser	Leu	Ala	Val	Leu	Gly	Ala	Pro	Leu	Pro	Ala	Asp	Arg	
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Thr	Arg	Gln	Gly	Phe	Ala	Thr	Thr	Ser	Thr	His	Gln	Ile	Ala	Asp	Ala
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115

120

125

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Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu
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Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr
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Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val
65 70 75 80

Leu Ala Glu Asp Leu Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu
85 90 95

Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp
100 105 110

Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe
115 120 125

Ala Glu Tyr His Ser Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp
130 135 140

Leu Ala Thr Glu Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe
145 150 155 160

His Ile Thr Met Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile
165 170 175

Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu
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 Gly Lys Asn Pro Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe
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 Thr Arg Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala
 35 40 45
 gtg gga atc cgc caa gcc tcg ctg tat tat cac ttc ccg tcc aag acg 192
 Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr
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 ctc gcc gaa gac tta agc acc ctg gac gcc gga cct gag atg cgc ctc 288
 Leu Ala Glu Asp Leu Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu
 85 90 95
 tgg gca atc gtt gcc tcc gaa gtg cgt ctg ctg ctg tcc acc aag tgg 336
 Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp
 100 105 110
 aac gtc ggt cgc ctg tac caa ctc ccc atc gtt ggt tct gaa gag ttc 384
 Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe
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 gcc gag tac cac agc cag cgc gaa gcc ctc acc aac gtc ttc cgc gac 432

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

His Ile Thr Met Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile
165 170 175

Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu
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Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg Gln	
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ctg ctg aaa tct act gtc gag ccg tcc act gtg ctc gcc gaa gac tta	1255
Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp Leu	
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agc acc ctg gac gcc gga cct gag atg cgc ctc tgg gca atc gtt gcc	1303
Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val Ala	
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Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu Ile	
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Glu Leu Ile Lys Gln Ala Asp Ala Lys	
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aattcctcag gcacgctgcc aagaagttta ggaaccataa caagtgtgaa atccgtggac	2226
ttcaccatct ccacgtcagc caaaaagtgt ggatcgctcg gccctacggt tctcacaatg	2286
gttcgttttag gatccaaccc cgatttctta atgttctctg aggcgacctc acggtctacc	2346
tcccctgccc catcttccaa atcaatgatg accatatcgg ccttcgatgc tgcttttgga	2406
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atgtactcat taatacgcga aaaggcagac cttatggtct gccttcaagc gaaatcttta	2526
aaaacttttag tgagcgaagt gtcgcgcacc agtcaggtag atggtcacgc cagccttggt	2586
ggctgcctca atgacctcgt tgtcgcgaat ggatccacca ggctgcacaa cagcagtgat	2646
gccagcctca gcgagaacct caa	2669

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 <212> PRT
 <213> Corynebacterium glutamicum

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Gly Lys Asn Pro Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe
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Thr Arg Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala
35 40 45

Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr
50 55 60

Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val
65 70 75 80

Leu Ala Glu Asp Leu Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu
85 90 95

Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp
100 105 110

Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe
115 120 125

Ala Glu Tyr His Ser Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp
130 135 140

Leu Ala Thr Glu Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe
145 150 155 160

His Ile Thr Met Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile
165 170 175

Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu
180 185 190

Ala Asp Ala Ser Leu Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg
195 200 205

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

<210> 10

<211> 672

<212> DNA

<213> Corynebacterium efficiens

<220>

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<223> amtR-Gen

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Gly Lys Asn Pro Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe	
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acc cgc cag ggt ttc gcc acc acc tcc acg cac cag atc gcc gat gcc	144
Thr Arg Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala	
35 40 45	

gtg ggt atc cgg cag gcc tcc ctg tac tac cac ttc ccg tcc aag acg	192
Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr	
50 55 60	

gag atc ttc ctc acc ctg ctg aaa tcc acc gtc gag cca tcc atg gtg	240
Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Met Val	
65 70 75 80	

ttg gcc ggc gac ctg gcc aat ctc gag gcc tcc ccg gag ctg cgc ctg	288
Leu Ala Gly Asp Leu Ala Asn Leu Glu Ala Ser Pro Glu Leu Arg Leu	
85 90 95	

tgg gca ctg gtg gcg gcc gag gtg cgt cta ctg ctg tcg acg aag tgg	336
Trp Ala Leu Val Ala Ala Glu Val Arg Leu Leu Leu Ser Thr Lys Trp	
100 105 110	

aat gtc ggt cgt ctc tat caa ctg ccg atc gtg gcc tcc gag gag ttc	384
Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Ala Ser Glu Glu Phe	
115 120 125	

gag gag tac cac acg cag cgt gcc acc ctg acg gat acc ttc cgc agc	432
Glu Glu Tyr His Thr Gln Arg Ala Thr Leu Thr Asp Thr Phe Arg Ser	
130 135 140	

ctg gcc acg gag atc gtc ggt gag gat gac ccc cgt gcg gaa ctc ccg	480
Leu Ala Thr Glu Ile Val Gly Glu Asp Asp Pro Arg Ala Glu Leu Pro	
145 150 155 160	

ttc cac atc acg atg tcc gcc atc gag atg cgc cgc aat gac ggc aag	528
Phe His Ile Thr Met Ser Ala Ile Glu Met Arg Arg Asn Asp Gly Lys	
165 170 175	

gtt ccc agc ccc ctg tcg gag gac agc ctc ccg gac acc gcc gtc atg	576
Val Pro Ser Pro Leu Ser Glu Asp Ser Leu Pro Asp Thr Ala Val Met	
180 185 190	

ctt gcc gac gcc gcc ctc gcc gtc ctg ggg gcc gac ctg ccc ggg gac	624
Leu Ala Asp Ala Ala Leu Ala Val Leu Gly Ala Asp Leu Pro Gly Asp	
195 200 205	

cgg gtg gag cgc acc ctg gaa ctg ctc agg cag gct gac gcg aaa taa 672
 Arg Val Glu Arg Thr Leu Glu Leu Leu Arg Gln Ala Asp Ala Lys
 210 215 220

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 <213> Corynebacterium efficiens

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Gly Lys Asn Pro Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe
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Thr Arg Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala
 35 40 45

Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr
 50 55 60

Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Met Val
 65 70 75 80

Leu Ala Gly Asp Leu Ala Asn Leu Glu Ala Ser Pro Glu Leu Arg Leu
 85 90 95

Trp Ala Leu Val Ala Ala Glu Val Arg Leu Leu Leu Ser Thr Lys Trp
 100 105 110

Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Ala Ser Glu Glu Phe
 115 120 125

Glu Glu Tyr His Thr Gln Arg Ala Thr Leu Thr Asp Thr Phe Arg Ser
 130 135 140

Leu Ala Thr Glu Ile Val Gly Glu Asp Asp Pro Arg Ala Glu Leu Pro
 145 150 155 160

Phe His Ile Thr Met Ser Ala Ile Glu Met Arg Arg Asn Asp Gly Lys
 165 170 175

Val Pro Ser Pro Leu Ser Glu Asp Ser Leu Pro Asp Thr Ala Val Met
 180 185 190

Leu Ala Asp Ala Ala Leu Ala Val Leu Gly Ala Asp Leu Pro Gly Asp

195

200

205

Arg Val Glu Arg Thr Leu Glu Leu Leu Arg Gln Ala Asp Ala Lys
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 <222> (1)..(1263)
 <223> lysC-Wildtyp-Gen

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 Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
 20 25 30
 gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat 144
 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45
 gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt 192
 Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60
 gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc 240
 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80
 gtc gcc atg gct att gag tcc ctt ggc gca gaa gcc caa tct ttc acg 288
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95
 ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc 336
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110
 att gtt gat gtc act cca ggt cgt gtg cgt gaa gca ctc gat gag ggc 384
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125
 aag atc tgc att gtt gct ggt ttc cag ggt gtt aat aaa gaa acc cgc 432
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140
 gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg 480
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160
 ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt 528
 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val

165										170					175					
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Asp	Gly	Val	Tyr	Thr	Ala	Asp	Pro	Arg	Ile	Val	Pro	Asn	Ala	Gln	Lys					
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ctg	gaa	aag	ctc	agc	ttc	gaa	gaa	atg	ctg	gaa	ctt	gct	gct	ggt	ggc	624				
Leu	Glu	Lys	Leu	Ser	Phe	Glu	Glu	Met	Leu	Glu	Leu	Ala	Ala	Val	Gly					
		195						200						205						
tcc	aag	att	ttg	gtg	ctg	cgc	agt	ggt	gaa	tac	gct	cgt	gca	ttc	aat	672				
Ser	Lys	Ile	Leu	Val	Leu	Arg	Ser	Val	Glu	Tyr	Ala	Arg	Ala	Phe	Asn					
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att	gcc	ggc	tct	atg	gag	gat	att	cct	gtg	gaa	gaa	gca	gtc	ctt	acc	768				
Ile	Ala	Gly	Ser	Met	Glu	Asp	Ile	Pro	Val	Glu	Glu	Ala	Val	Leu	Thr					
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ggt	gtc	gca	acc	gac	aag	tcc	gaa	gcc	aaa	gta	acc	ggt	ctg	ggt	att	816				
Gly	Val	Ala	Thr	Asp	Lys	Ser	Glu	Ala	Lys	Val	Thr	Val	Leu	Gly	Ile					
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tcc	gat	aag	cca	ggc	gag	gct	gcg	aag	ggt	ttc	cgt	gcg	ttg	gct	gat	864				
Ser	Asp	Lys	Pro	Gly	Glu	Ala	Ala	Lys	Val	Phe	Arg	Ala	Leu	Ala	Asp					
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gca	gaa	atc	aac	att	gac	atg	ggt	ctg	cag	aac	gtc	tct	tct	gta	gaa	912				
Ala	Glu	Ile	Asn	Ile	Asp	Met	Val	Leu	Gln	Asn	Val	Ser	Ser	Val	Glu					
	290					295					300									
gac	ggc	acc	acc	gac	atc	acc	ttc	acc	tgc	cct	cgt	tcc	gac	ggc	cgc	960				
Asp	Gly	Thr	Thr	Asp	Ile	Thr	Phe	Thr	Cys	Pro	Arg	Ser	Asp	Gly	Arg					
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cgc	gcg	atg	gag	atc	ttg	aag	aag	ctt	cag	ggt	cag	ggc	aac	tgg	acc	1008				
Arg	Ala	Met	Glu	Ile	Leu	Lys	Lys	Leu	Gln	Val	Gln	Gly	Asn	Trp	Thr					
			325						330					335						
aat	gtg	ctt	tac	gac	gac	cag	gtc	ggc	aaa	gtc	tcc	ctc	gtg	ggt	gct	1056				
Asn	Val	Leu	Tyr	Asp	Asp	Gln	Val	Gly	Lys	Val	Ser	Leu	Val	Gly	Ala					
			340					345					350							
ggc	atg	aag	tct	cac	cca	ggt	ggt	acc	gca	gag	ttc	atg	gaa	gct	ctg	1104				
Gly	Met	Lys	Ser	His	Pro	Gly	Val	Thr	Ala	Glu	Phe	Met	Glu	Ala	Leu					
		355					360					365								
cgc	gat	gtc	aac	gtg	aac	atc	gaa	ttg	att	tcc	acc	tct	gag	att	cgt	1152				
Arg	Asp	Val	Asn	Val	Asn	Ile	Glu	Leu	Ile	Ser	Thr	Ser	Glu	Ile	Arg					
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att	tcc	gtg	ctg	atc	cgt	gaa	gat	gat	ctg	gat	gct	gct	gca	cgt	gca	1200				
Ile	Ser	Val	Leu	Ile	Arg	Glu	Asp	Asp	Leu	Asp	Ala	Ala	Ala	Arg	Ala					
	385				390				395						400					
ttg	cat	gag	cag	ttc	cag	ctg	ggc	ggc	gaa	gac	gaa	gcc	gtc	ggt	tat	1248				
Leu	His	Glu	Gln	Phe	Gln	Leu	Gly	Gly	Glu	Asp	Glu	Ala	Val	Val	Tyr					
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Ala Gly Thr Gly Arg
420

1266

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<213> Corynebacterium glutamicum

<400> 13

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20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

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

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

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

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

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

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

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

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

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

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

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
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<213> Corynebacterium glutamicum

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<210> 15
<211> 28
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<213> Corynebacterium glutamicum

<220>
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<213> Corynebacterium glutamicum

<220>
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Gly Lys Asn Pro Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe
20 25 30

acc cat caa ggc ttc gca aca acc tcc acg cat caa atc gct gat gcc 144
Thr His Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala
35 40 45

gtg gga atc cgc caa gcc tcg ctg tat tat cac ttc ccg tct aag acg 192
Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr
50 55 60

gaa atc ttc ctc acc ctc ctg aaa tct acc gtc gag ccg tcc act gtg 240
Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val
65 70 75 80

ctc gcc gaa gac tta agc atc ctg gat gca gga cct gag atg cgc ctc 288
Leu Ala Glu Asp Leu Ser Ile Leu Asp Ala Gly Pro Glu Met Arg Leu
85 90 95

tgg gca atc gtt gcc tcc gaa gtg cgt ctg ctg ctg tcc acc aag tgg 336
Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp
100 105 110

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aac gtc ggt cgc ctg tac caa ctc ccc atc gtt ggt tct gaa gag ttc	384
Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe	
115 120 125	

gcc gag tac cac agc cag cgc gaa gcc ctc acc aac gtc ttc cgc gac	432
Ala Glu Tyr His Ser Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp	
130 135 140	

ctc gcc acc gaa atc gtc ggt gac gac ccc cgc gca gaa ctc ccc ttc	480
Leu Ala Thr Glu Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe	
145 150 155 160	

cac atc acc atg tcg gtg atc gaa atg cgt cgc aac gac ggc aag att	528
His Ile Thr Met Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile	
165 170 175	

cca agc ccg ctt tcc gca gac agc ctc ccg gag acc gca att atg ctt	576
Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu	
180 185 190	

gcc gac gcc tcc ctc gcc gtc ctc ggc gcg tcg ctg ccc gcc gac cgg	624
Ala Asp Ala Ser Leu Ala Val Leu Gly Ala Ser Leu Pro Ala Asp Arg	
195 200 205	

gtc gaa aaa acg ctt gaa cta atc aag cag gct gac gcg aaa taa	669
Val Glu Lys Thr Leu Glu Leu Ile Lys Gln Ala Asp Ala Lys	
210 215 220	

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 <213> Corynebacterium glutamicum ATCC14067
 <400> 21

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35 40 45	

Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr	
50 55 60	

Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val	
65 70 75 80	

Leu Ala Glu Asp Leu Ser Ile Leu Asp Ala Gly Pro Glu Met Arg Leu	
85 90 95	

Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp	
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100

105

110

Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe
115 120 125

Ala Glu Tyr His Ser Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp
130 135 140

Leu Ala Thr Glu Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe
145 150 155 160

His Ile Thr Met Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile
165 170 175

Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu
180 185 190

Ala Asp Ala Ser Leu Ala Val Leu Gly Ala Ser Leu Pro Ala Asp Arg
195 200 205

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