

<110> CJ CHEILJEDANG CORPORATION
 <120> MICROORGANISMS FOR PRODUCING PUTRESCINE OR ORNITHINE AND PROCESS
 FOR PRODUCING PUTRESCINE OR ORNITHINE USING THEM
 <130> OPA16044
 <150> KR10-2015-0090021
 <151> 2015-06-24
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 <170> KopatentIn 2.0
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 <211> 259
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 <213> Corynebacterium glutamicum ATCC13032 SugR
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 Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr
 20 25 30
 Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
 35 40 45
 Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
 50 55 60
 Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
 65 70 75 80
 Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly
 85 90 95
 Gly Leu Phe Leu Asp Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu
 100 105 110
 Ile Ser Glu His Pro Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys
 115 120 125
 Leu Pro Ile Ala Leu Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln
 130 135 140
 Leu Leu Gly Gly Ser Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp
 145 150 155 160
 Thr Ala Leu Arg Thr Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile
 165 170 175
 Gly Thr Asn Ala Leu Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser
 180 185 190
 Gln Glu Ala Ala Met Lys Ser Ala Met Ile Thr Asn Ala His Lys Val
 195 200 205
 Val Val Leu Cys Asp Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser
 210 215 220
 Phe Gly Ala Ile Ser Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala
 225 230 235 240
 Pro Ala Ser Phe Val Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val
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Ile Ala Glu

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<211>      780
<212>      DNA
<213>      Corynebacterium glutamicum ATCC13032 sugR

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gcggtgctag accgcgaggg aattgttcac cgcgttcacg gtggcgcagt agccacccaa      180
tctttccaaa ccacagagtt gagcttggat actcgtttca ggtctgcatc gtcagcaaag      240
tactccattg ccaaggcagc gatgcagttc ctgcccgtg agcatggcgg actgttcctc      300
gatgcgggaa ctactgttac tgctttggcc gatctcattt ctgagcatcc tagctccaag      360
cagtggtcga tcgtgaccaa ctgcctcccc atcgcactta atctggccaa cgccgggctt      420
gatgatgtcc agctgcttgg aggaagcgtt cgcgcgatca cccaggctgt tgtgggtgac      480
actgcgcttc gtactctcgc gctgatgcgt gcggatgtag tgttcatcgg caccaacgcg      540
ttgacgttgg atcacggatt gtctacggcc gattcccaag aggctgccat gaaatctgcg      600
atgatcacca acgcccacaa ggtggtggtg ttgtgtgact ccaccaagat gggcaccgac      660
tacctcgtga gctttggcgc aatcagcgat atcgatgtgg tggtcaccga tgcgggtgca      720
ccagcaagtt tcgttgagca gttgcgagaa cgcgatgtag aagttgtgat tgcagaatga      780

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<212>      PRT
<213>      Corynebacterium glutamicum ATCC13869 SugR

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Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr
  20          25          30
Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
  35          40          45
Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
  50          55          60
Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
  65          70          75          80
Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly
  85          90          95
Gly Leu Phe Leu Asp Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu
 100          105          110
Ile Ser Glu His Pro Ser Ala Lys Gln Trp Ser Ile Val Thr Asn Cys
 115          120          125

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3761553_1.txt

Leu Pro Ile Ala Leu Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln
 130 135 140
 Leu Leu Gly Gly Ser Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp
 145 150 155 160
 Thr Ala Leu Arg Thr Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile
 165 170 175
 Gly Thr Asn Ala Leu Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser
 180 185 190
 Gln Glu Ala Ala Met Lys Ser Ala Met Ile Thr Asn Ala His Lys Val
 195 200 205
 Val Val Leu Cys Asp Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser
 210 215 220
 Phe Gly Ala Ile Ser Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala
 225 230 235 240
 Pro Ala Ser Phe Val Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val
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Ile

<210> 4
 <211> 780
 <212> DNA
 <213> Corynebacterium glutamicum ATCC13869 sugR

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 gcggtgctag accgcgaggg aattgttcac cgcgttcacg gtggcgagc agccacccaa 180
 tctttccaaa ccacagagtt gagcttggat actcgtttca ggtctgcata gtcagcaaag 240
 tactccattg ccaaggcagc gatgcagttc ctgcccgcgt agcatggcgg actgttcctc 300
 gatgcgggaa ctactgttac tgctttggcc gatctcattt ctgagcatcc tagcgccaag 360
 cagtggtcga tcgtgaccaa ctgcctcccc atcgactta atctggccaa cgccgggctt 420
 gatgatgtcc agctacttgg aggaagcgtt cgcgcgatca cccaggctgt tgtgggtgac 480
 actgcgcttc gtactctcgc gctgatgcgt gcggatgtag tgttcatcgg caccaacgcg 540
 ttgacgttgg atcacggatt gtctacggcc gattcccaag aggctgccat gaaatctgcg 600
 atgatcacca acgcccacaa ggtgggtggtg ttgtgtgact ccaccaagat gggcaccgac 660
 tacctcgtga gctttggcgc aatcagcgat atcgatgtgg tggtcaccga tgcgggtgca 720
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<210> 5
 <211> 437
 <212> PRT
 <213> Corynebacterium glutamicum ATCC13032 GluA

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<400> 5
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 His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile Ile Glu Ala Ser Glu
 20 25 30
 Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu Ser Glu Thr Gly Leu
 35 40 45
 Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys
 50 55 60
 Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr
 65 70 75 80
 Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr
 85 90 95
 Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp Glu Leu His Lys Phe
 100 105 110
 Asn Asp Glu Ile Arg His His Thr Leu Leu Asp Glu Asp Phe Lys Ser
 115 120 125
 Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro Met Ala Thr Leu Ala
 130 135 140
 Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro
 145 150 155 160
 Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val Arg Leu Met Ala Lys
 165 170 175
 Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala Arg Lys Gly Ala Pro
 180 185 190
 Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg
 195 200 205
 Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met
 210 215 220
 Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His Ala Asp His Glu Gln
 225 230 235 240
 Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly Ser Ala Gln Ala Asn
 245 250 255
 Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu
 260 265 270
 His Gly Gly Ala Asn Gln Ala Val Leu Glu Met Leu Glu Asp Ile Lys
 275 280 285
 Ser Asn His Gly Gly Asp Ala Thr Glu Phe Met Asn Lys Val Lys Asn
 290 295 300
 Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly His Arg Val Tyr Lys
 305 310 315 320
 Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile
 325 330 335
 Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu
 340 345 350

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Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr
 355 360 365
 Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe
 370 375 380
 Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly
 385 390 395 400
 Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile
 405 410 415
 Asn Arg Pro Arg Gln Val Tyr Thr Gly Asn Glu Ser Arg Lys Leu Val
 420 425 430
 Pro Arg Glu Glu Arg
 435

<210> 6
 <211> 1314
 <212> DNA
 <213> Corynebacterium glutamicum ATCC13032 gltA

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 aagatgctgt ctgagactgg actgatcact ttgacccag gttatgtgag cactggctcc 180
 accgagtcga agatcaccta catcgatggc gatgcgggaa tcctgcgtta ccgcggctat 240
 gacatcgctg atctggctga gaatgccacc ttcaacgagg tttcttacct acttatcaac 300
 ggtgagctac caaccccaga tgagcttcac aagtttaacg acgagattcg ccaccacacc 360
 cttctggacg aggacttcaa gtcccagttc aacgtgttcc cacgcgacgc tcaccaatg 420
 gcaaccttgg cttcctcggt taacattttg tctacctact accaggacca gctgaaccca 480
 ctcgatgagg cacagcttga taaggcaacc gttcgcctca tggcaaagggt tccaatgctg 540
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 aatgcgcgtg agaacttctt gcgcatgatg ttcggttacc caaccgagcc atacgagatc 660
 gaccaatca tgggtcaaggc tctggacaag ctgctcatcc tgcacgctga ccacgagcag 720
 aactgctcca cctccaccgt tcgtatgatc ggttccgcac aggccaacat gtttgtctcc 780
 atcgctggtg gcatcaacgc tctgtccggc cactgcacg gtggcgcaaa ccaggctggt 840
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 aaggtcaaga acaaggaaga cggcgtccgc ctcatgggct tcggacaccg cgtttacaag 960
 aactacgatc cacgtgcagc aatcgtcaag gagaccgcac acgagatcct cgagcacctc 1020
 ggtggcgacg atcttctgga tctggcaatc aagctggaag aaattgcact ggctgatgat 1080
 tacttcatct cccgcaagct ctacccgaac gtagacttct acaccggcct gatctaccgc 1140
 gcaatgggct tcccaactga cttcttcacc gtattgttcg caatcggtcg tctgccagga 1200
 tggatcgctc actaccgcga gcagctcggg gcagcaggca acaagatcaa ccgcccacgc 1260
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<210>      7
<211>     437
<212>     PRT
<213>     Corynebacterium glutamicum ATCC13869 GltA

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His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile Ile Glu Ala Ser Glu
          20          25          30

Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu Ser Glu Thr Gly Leu
          35          40          45

Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys
  50          55          60

Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr
  65          70          75          80

Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr
          85          90          95

Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp Glu Leu His Lys Phe
          100          105          110

Asn Asp Glu Ile Arg His His Thr Leu Leu Asp Glu Asp Phe Lys Ser
  115          120          125

Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro Met Ala Thr Leu Ala
  130          135          140

Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro
  145          150          155          160

Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val Arg Leu Met Ala Lys
          165          170          175

Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala Arg Lys Gly Ala Pro
          180          185          190

Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg
  195          200          205

Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met
  210          215          220

Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His Ala Asp His Glu Gln
  225          230          235          240

Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly Ser Ala Gln Ala Asn
          245          250          255

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

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

Asn Asn His Gly Gly Asp Ala Thr Ala Phe Met Asn Lys Val Lys Asn
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Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly His Arg Val Tyr Lys
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<212>	DNA
<213>	Corynebacterium glutamicum ATCC13869 gltA

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accgagtcga	agatcaccta	catcgatggc	gatgcgggaa	tcctgcgtta	ccgcggctat		240
gacatcgctg	atctggctga	gaatgccacc	ttcaacgagg	tttcttacct	acttatcaac		300
ggtgagctac	caaccccaga	tgagcttcac	aagtttaacg	acgagattcg	ccaccacacc		360
cttctggacg	aggacttcaa	gtcccagttc	aacgtgttcc	cacgcgacgc	tcacccaatg		420
gcaaccttgg	cttcctcggg	taacattttg	tctacctact	accaggatca	gctgaaccca		480
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gctgcgtacg	cacaccgcgc	acgcaagggt	gtcctttaca	tgtaccaga	caactccctc		600
aacgcgcgtg	agaacttcct	gcgcatgatg	ttcggttacc	caaccgagcc	atacgagatc		660
gacccaatca	tgggtcaaggc	tctggacaag	ctgctcatcc	tgcacgctga	ccacgagcag		720
aactgctcca	cctccaccgt	tcgtatgatc	ggttccgcac	aggccaacat	gtttgtctcc		780
atcgctggtg	gcatcaacgc	tctgtccggc	ccactgcacg	gtggcgcaaa	ccaggctggt		840
ctggagatgc	tcgaagacat	caagaacaac	cacggtggcg	acgcaaccgc	gttcatgaac		900
aaggtcaaga	acaaggaaga	cggcgtccgc	ctcatgggct	tcggacaccg	cgtttacaag		960
aactacgatc	cacgtgcagc	aatcgtcaag	gagaccgcac	acgagatcct	cgagcacctc		1020
ggtggcgacg	atcttctgga	tctggcaatc	aagctggaag	aaattgcact	ggctgatgat		1080
tgcttcatct	cccgcaagct	ctacccgaac	gtagactttct	acaccggcct	gatctaccgc		1140

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 tggatcgctc actaccgcca gcagctcggg gcagcaggca acaagatcaa ccgcccacgc 1260
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<210> 9
 <211> 319
 <212> PRT
 <213> Corynebacterium glutamicum ATCC13032 ArgF

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 20 25 30
 Ala Ala Pro Phe Ser Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala
 35 40 45
 Val Leu Phe Asp Lys Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala
 50 55 60
 Gly Ile Ala His Leu Gly Gly His Ala Ile Val Val Asp Ser Gly Ser
 65 70 75 80
 Ser Gln Met Gly Lys Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu
 85 90 95
 Ser Arg Tyr Val Glu Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn
 100 105 110
 Phe His Ala Met Ala Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu
 115 120 125
 Ser Asp Asp Leu His Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile
 130 135 140
 Val Glu Asn Leu Ser Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys
 145 150 155 160
 Lys Ala Val Tyr Leu Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr
 165 170 175
 Met Ile Gly Phe Ala Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro
 180 185 190
 Glu Gly Phe Gln Pro Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg
 195 200 205
 Gly Gln Glu Thr Gly Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu
 210 215 220
 Val Ala Gly Ala Asp Val Val Ile Thr Asp Thr Trp Val Ser Met Gly
 225 230 235 240
 Met Glu Asn Asp Gly Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln
 245 250 255
 Val Asn Asp Glu Val Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu
 260 265 270
 His Cys Leu Pro Ala Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile
 275 280 285

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Asp Gly Pro Ala Ser Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His
 290 295 300

Ala Gln Lys Ala Leu Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
 305 310 315

<210> 10
 <211> 960
 <212> DNA
 <213> Corynebacterium glutamicum ATCC13032 argF

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 ctcgagggac caaagtccgt tgcagttctt tttgataaga cttcaactcg tactcgcttc 180
 tccttcgacg cgggcatcgc tcatttgggt ggacacgcca tcgtcgtgga ttccggtagc 240
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 gaagcaattg tgtggcgcac ctacgcacac agcaatttcc acgcatggc ggagacgtcc 360
 actgtgccgc tgggtgaactc cttgtccgat gatctgcacc catgccagat tctggctgat 420
 ctgcagacta tcgtggaaaa cctcagccct gaagaaggcc cagcaggcct taagggttaag 480
 aaggctgtgt acctgggcga tggcgacaac aacatggcca actcctacat gattggcttt 540
 gccaccgcgg gcatggatat ttccatcatc gtcctgaag ggttccagcc tcgtgcggaa 600
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 agcctcgacg aggttgccgg cgccgatgtt gtcatcaccg atacctgggt atccatgggt 720
 atggaaaacg acggcatcga tcgcaccaca ctttctgttc cttaccaggt caacgatgag 780
 gtcattggcga aagctaacga cggcgccatc ttctgcact gccttcctgc ctaccgtggc 840
 aaagaagtgg cagcctccgt gattgatgga ccagcgtcca aagttttcga tgaagcagaa 900
 aaccgcctcc acgctcagaa agcactgctg gtgtggctgc tggccaacca gccgaggtaa 960

<210> 11
 <211> 319
 <212> PRT
 <213> Corynebacterium glutamicum ATCC13869 ArgF

<400> 11
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 Thr Pro Ala Glu Gln Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys
 20 25 30
 Ala Ala Pro Phe Ser Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala
 35 40 45
 Val Leu Phe Asp Lys Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala
 50 55 60
 Gly Ile Ala His Leu Gly Gly His Ala Ile Val Val Asp Ser Gly Ser
 65 70 75 80

3761553_1.txt

Ser Gln Met Gly Lys₈₅ Gly Glu Thr Leu Gln₉₀ Asp Thr Ala Ala Val₉₅ Leu
 Ser Arg Tyr Val₁₀₀ Glu Ala Ile Val₁₀₅ Trp Arg Thr Tyr Ala His₁₁₀ Ser Asn
 Phe His Ala₁₁₅ Met Ala Glu Thr Ser₁₂₀ Thr Val Pro Leu Val₁₂₅ Asn Ser Leu
 Ser Asp₁₃₀ Asp Leu His Pro Cys₁₃₅ Gln Ile Leu Ala Asp₁₄₀ Leu Gln Thr Ile
 Val₁₄₅ Glu Asn Leu Ser Pro₁₅₀ Glu Glu Gly Pro Ala₁₅₅ Gly Leu Lys Gly Lys₁₆₀
 Lys Ala Val Tyr₁₆₅ Leu Gly Asp Gly Asp₁₇₀ Asn Asn Met Ala Asn Ser₁₇₅ Tyr
 Met Ile Gly Phe₁₈₀ Ala Thr Ala Gly Met₁₈₅ Asp Ile Ser Ile Ile₁₉₀ Ala Pro
 Glu Gly Phe₁₉₅ Gln Pro Arg Ala Glu₂₀₀ Phe Val Glu Arg Ala₂₀₅ Glu Lys Arg
 Gly Gln₂₁₀ Glu Thr Gly Ala Lys₂₁₅ Val Val Val Thr Asp₂₂₀ Ser Leu Asp Glu
 Val₂₂₅ Ala Gly Ala Asp Val₂₃₀ Val Ile Thr Asp Thr₂₃₅ Trp Val Ser Met Gly₂₄₀
 Met Glu Asn Asp Gly₂₄₅ Ile Asp Arg Thr Thr₂₅₀ Pro Phe Val Pro Tyr₂₅₅ Gln
 Val Asn Asp Glu₂₆₀ Val Met Ala Lys Ala₂₆₅ Asn Asp Gly Ala Ile₂₇₀ Phe Leu
 His Cys Leu₂₇₅ Pro Ala Tyr Arg Gly₂₈₀ Lys Glu Val Ala Ala₂₈₅ Ser Val Ile
 Asp Gly₂₉₀ Pro Ala Ser Lys Val₂₉₅ Phe Asp Glu Ala Glu₃₀₀ Asn Arg Leu His
 Ala Gln Lys Ala Leu Leu₃₁₀ Val Trp Leu Leu Ala₃₁₅ His Gln Pro Arg

<210> 12
 <211> 960
 <212> DNA
 <213> Corynebacterium glutamicum ATCC13869 argF

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 ctcgagggaac caaagtccgt tgcagttctt tttgataaga cttcaactcg tactcgcttc 180
 tccttcgacg cgggcatcgc tcatttgggt ggacatgcca tcgtcgtgga ttccggcagc 240
 tcacagatgg gtaagggcga gaccctgcag gacaccgcag ctgtattgtc ccgctacgtg 300
 gaagcaattg tgtggcgcac ctacgcacac agcaatttcc acgccatggc ggagacgtcc 360
 actgtgccac tggatgaactc cttgtccgat gatctgcacc catgccagat tctggctgat 420
 ctgcagacca tcgtggaaaa cctcagccct gaagaaggcc cagcaggcct taagggtaag 480

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ttcgtggagc gcgcggaaaa gcgtggccag gaaaccggcg cgaaggttgt tgtcaccgac      660
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atggaaaacg acggcatcga tcgcaccaca ctttcgttc cctaccaggt caacgatgag      780
gtcatggcga aagctaacga cggcgccatc ttcctgact gccttcctgc ctaccgcggc      840
aaagaagtgg cagcctccgt gattgatgga ccagcgcca aagttttcga tgaagcagaa      900
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<210>      13
<211>      533
<212>      PRT
<213>      Corynebacterium glutamicum ATCC13032 NCgl1221

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<400>      13
Met Ile Leu Gly Val Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn
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Trp Ile Val Asp Thr Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala
          20          25          30
Phe Leu Ile Pro Arg Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg
          35          40          45
Arg Val Glu Ser Ala Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala
          50          55          60
Phe Ala Gly Val Gly Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met
          65          70          75          80
Leu Ala Val Ser Ala Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala
          85          90          95
Ala Ile Pro Ala Thr Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln
          100         105         110
Ser Ile Val Ala Asp Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys
          115         120         125
Gln Phe Gly Val Gly Asp Trp Val Arg Phe Glu Gly Asn Gly Ile Val
          130         135         140
Val Glu Gly Thr Val Ile Glu Ile Thr Met Arg Ala Thr Lys Ile Arg
          145         150         155         160
Thr Ile Ala Gln Glu Thr Val Ile Ile Pro Asn Ser Thr Ala Lys Val
          165         170         175
Cys Ile Asn Asn Ser Asn Asn Trp Ser Arg Ala Val Val Val Ile Pro
          180         185         190
Ile Pro Met Leu Gly Ser Glu Asn Ile Thr Asp Val Ile Ala Arg Ser
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Glu Ala Ala Thr Arg Arg Ala Leu Gly Gln Glu Lys Ile Ala Pro Glu
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3761553_1.txt

Ile Leu Gly Glu Leu Asp Val His Pro Ala Thr Glu Val Thr Pro Pro
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 Thr Val Val Gly Met Pro Trp Met Val Thr Met Arg Phe Leu Val Gln
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 260 265 270
 Ile Ile Ser Glu Phe Trp Glu Glu Tyr Gly Ser Ala Thr Thr Thr Ser
 275 280 285
 Gly Thr Leu Ile Asp Ser Leu His Val Glu His Glu Glu Pro Lys Thr
 290 295 300
 Ser Leu Ile Asp Ala Ser Pro Gln Ala Leu Lys Glu Pro Lys Pro Glu
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 Ala Ala Ala Thr Val Ala Ser Leu Ala Ala Ser Ser Asn Asp Asp Ala
 325 330 335
 Asp Asn Ala Asp Ala Ser Val Ile Asn Ala Gly Asn Pro Glu Lys Glu
 340 345 350
 Leu Asp Ser Asp Val Leu Glu Gln Glu Leu Ser Ser Glu Glu Pro Glu
 355 360 365
 Glu Thr Ala Lys Pro Asp His Ser Leu Arg Gly Phe Phe Arg Thr Asp
 370 375 380
 Tyr Tyr Pro Asn Arg Trp Gln Lys Ile Leu Ser Phe Gly Gly Arg Val
 385 390 395 400
 Arg Met Ser Thr Ser Leu Leu Leu Gly Ala Leu Leu Leu Leu Ser Leu
 405 410 415
 Phe Lys Val Met Thr Val Glu Pro Ser Glu Asn Trp Gln Asn Ser Ser
 420 425 430
 Gly Trp Leu Ser Pro Ser Thr Ala Thr Ser Thr Ala Val Thr Thr Ser
 435 440 445
 Glu Thr Ser Ala Pro Val Ser Thr Pro Ser Met Thr Val Pro Thr Thr
 450 455 460
 Val Glu Glu Thr Pro Thr Met Glu Ser Asn Val Glu Thr Gln Gln Glu
 465 470 475 480
 Thr Ser Thr Pro Ala Thr Ala Thr Pro Gln Arg Ala Asp Thr Ile Glu
 485 490 495
 Pro Thr Glu Glu Ala Thr Ser Gln Glu Glu Thr Thr Ala Ser Gln Thr
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 Gln Ser Pro Ala Val Glu Ala Pro Thr Ala Val Gln Glu Thr Val Ala
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 Pro Thr Ser Thr Pro
 530

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<213> Corynebacterium glutamicum ATCC13032 NCgl1221

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60

3761553_1.txt

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aaccagctcg cgttcgccgg cgttggcggt tatatcgcg aaattgtggc gtttttcatg      240
cttgccgtct ccgcatgca ggcttttggg ttctctctcg cggcgctgc gattccggca      300
accattgctg cagctgcat tggccttggg gcgcatcga ttgttgcgga cttcttggcc      360
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gccacgtcgc aggaggaaac gactgcgtcg cagacgcagt ctccagcagt ggaagcacca     1560
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Trp Ile Val Asp Thr Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala
          20           25           30
Phe Leu Ile Pro Arg Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Gln
          35           40           45

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3761553_1.txt

Arg Val Glu Ser Ala Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala
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 Phe Ala Gly Val Gly Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met
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 Leu Ala Val Ser Ala Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala
 85 90 95
 Ala Ile Pro Ala Thr Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln
 100 105 110
 Ser Ile Val Ala Asp Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys
 115 120 125
 Gln Phe Gly Val Gly Asp Trp Val Arg Phe Glu Gly Asn Gly Ile Val
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 Val Glu Gly Thr Val Ile Glu Ile Thr Met Arg Ala Thr Lys Ile Arg
 145 150 155 160
 Thr Ile Ala Gln Glu Thr Val Ile Ile Pro Asn Ser Thr Ala Lys Val
 165 170 175
 Cys Ile Asn Asn Ser Asn Asn Trp Ser Arg Ala Val Val Val Ile Pro
 180 185 190
 Ile Pro Met Leu Gly Ser Glu Asn Ile Thr Asp Val Ile Ala Arg Ser
 195 200 205
 Glu Ala Ala Thr Arg Arg Ala Leu Gly Gln Glu Lys Ile Ala Pro Glu
 210 215 220
 Ile Leu Gly Glu Leu Asp Val His Pro Ala Thr Glu Val Thr Pro Pro
 225 230 235 240
 Thr Val Val Gly Met Pro Trp Met Val Thr Met Arg Phe Leu Val Gln
 245 250 255
 Val Thr Ala Gly Asn Gln Trp Leu Val Glu Arg Ala Ile Arg Thr Glu
 260 265 270
 Ile Ile Asn Glu Phe Trp Glu Glu Tyr Gly Ser Ala Thr Thr Thr Ser
 275 280 285
 Gly Thr Leu Ile Asp Ser Leu His Val Glu His Glu Glu Pro Lys Thr
 290 295 300
 Ser Leu Ile Asp Ala Ser Pro Gln Ala Leu Lys Glu Pro Lys Pro Glu
 305 310 315 320
 Ala Ala Ala Thr Val Ala Ser Leu Ala Ala Ser Ser Asn Asp Asp Ala
 325 330 335
 Asp Asn Ala Asp Ala Ser Ala Ile Asn Ala Gly Asn Pro Glu Lys Glu
 340 345 350
 Leu Asp Ser Asp Val Leu Glu Gln Glu Leu Ser Ser Glu Glu Pro Glu
 355 360 365
 Glu Thr Ala Lys Pro Asp His Ser Leu Arg Gly Phe Phe Arg Thr Asp
 370 375 380
 Tyr Tyr Pro Asn Arg Trp Gln Lys Ile Leu Ser Phe Gly Gly Arg Val
 385 390 395 400
 Arg Met Ser Thr Ser Leu Leu Leu Gly Ala Leu Leu Leu Leu Ser Leu

3761553_1.txt

405

410

415

Phe Lys Val Met Thr Val Glu Pro Ser Glu Asn Trp Gln Asn Ser Ser
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 Gly Trp Leu Ser Pro Ser Thr Ala Thr Ser Thr Ala Val Thr Thr Ser
 435 440 445
 Glu Thr Ser Ala Pro Ala Ser Thr Pro Ser Met Thr Val Pro Thr Thr
 450 455 460
 Val Glu Glu Thr Pro Thr Met Glu Ser Ser Val Glu Thr Gln Gln Glu
 465 470 475 480
 Thr Ser Thr Pro Ala Thr Ala Thr Pro Gln Arg Ala Asp Thr Ile Glu
 485 490 495
 Pro Thr Glu Glu Ala Thr Ser Gln Glu Glu Thr Thr Ala Ser Gln Thr
 500 505 510
 Gln Ser Pro Ala Val Glu Ala Pro Thr Ala Val Gln Glu Thr Val Ala
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 Pro Thr Ser Thr Pro
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 <213> Corynebacterium glutamicum ATCC13869 NCgl1221

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 ctggccatgc gtattatcaa gcagcgagtg gagtctgcag ccgatgcgga caccactaag 180
 aaccagctcg cgttcgctgg cgttggcggt tatatcgcg aaattgtggc gtttttcatg 240
 cttgccgtct ccgcgatgca ggcttttggg ttctctctcg cgggcgctgc gattccggca 300
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 aacggcatcg ttgttgaagg caccgtcatt gagatcacca tgcgcgcgac caaaattcgc 480
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3761553_1.txt

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gccacgtcgc aggaggaaac gactgcatcg cagacgcagt ctccagcagt ggaagcacca      1560
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<213>      Escherichia coli Spec

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          20          25          30
Val  Ala  Ala  Val  Val  Ile  Thr  Ala  Ala  Asp  Ser  Arg  Ser  Gly  Ile  Leu
          35          40          45
Ala  Leu  Leu  Lys  Arg  Thr  Gly  Phe  His  Leu  Pro  Val  Phe  Leu  Tyr  Ser
 50          55          60
Glu  His  Ala  Val  Glu  Leu  Pro  Ala  Gly  Val  Thr  Ala  Val  Ile  Asn  Gly
 65          70          75          80
Asn  Glu  Gln  Gln  Trp  Leu  Glu  Leu  Glu  Ser  Ala  Ala  Cys  Gln  Tyr  Glu
          85          90          95
Glu  Asn  Leu  Leu  Pro  Pro  Phe  Tyr  Asp  Thr  Leu  Thr  Gln  Tyr  Val  Glu
100          105          110
Met  Gly  Asn  Ser  Thr  Phe  Ala  Cys  Pro  Gly  His  Gln  His  Gly  Ala  Phe
115          120          125
Phe  Lys  Lys  His  Pro  Ala  Gly  Arg  His  Phe  Tyr  Asp  Phe  Phe  Gly  Glu
130          135          140
Asn  Val  Phe  Arg  Ala  Asp  Met  Cys  Asn  Ala  Asp  Val  Lys  Leu  Gly  Asp
145          150          155          160
Leu  Leu  Ile  His  Glu  Gly  Ser  Ala  Lys  Asp  Ala  Gln  Lys  Phe  Ala  Ala
165          170          175
Lys  Val  Phe  His  Ala  Asp  Lys  Thr  Tyr  Phe  Val  Leu  Asn  Gly  Thr  Ser
180          185          190
Ala  Ala  Asn  Lys  Val  Val  Thr  Asn  Ala  Leu  Leu  Thr  Arg  Gly  Asp  Leu
195          200          205
Val  Leu  Phe  Asp  Arg  Asn  Asn  His  Lys  Ser  Asn  His  His  Gly  Ala  Leu
210          215          220

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3761553_1.txt

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 Phe Gly Phe Ile Gly Gly Ile Asp Ala His Cys Phe Asn Glu Glu Tyr
 245 250 255
 Leu Arg Gln Gln Ile Arg Asp Val Ala Pro Glu Lys Ala Asp Leu Pro
 260 265 270
 Arg Pro Tyr Arg Leu Ala Ile Ile Gln Leu Gly Thr Tyr Asp Gly Thr
 275 280 285
 Val Tyr Asn Ala Arg Gln Val Ile Asp Thr Val Gly His Leu Cys Asp
 290 295 300
 Tyr Ile Leu Phe Asp Ser Ala Trp Val Gly Tyr Glu Gln Phe Ile Pro
 305 310 315 320
 Met Met Ala Asp Ser Ser Pro Leu Leu Leu Glu Leu Asn Glu Asn Asp
 325 330 335
 Pro Gly Ile Phe Val Thr Gln Ser Val His Lys Gln Gln Ala Gly Phe
 340 345 350
 Ser Gln Thr Ser Gln Ile His Lys Lys Asp Asn His Ile Arg Gly Gln
 355 360 365
 Ala Arg Phe Cys Pro His Lys Arg Leu Asn Asn Ala Phe Met Leu His
 370 375 380
 Ala Ser Thr Ser Pro Phe Tyr Pro Leu Phe Ala Ala Leu Asp Val Asn
 385 390 395 400
 Ala Lys Ile His Glu Gly Glu Ser Gly Arg Arg Leu Trp Ala Glu Cys
 405 410 415
 Val Glu Ile Gly Ile Glu Ala Arg Lys Ala Ile Leu Ala Arg Cys Lys
 420 425 430
 Leu Phe Arg Pro Phe Ile Pro Pro Val Val Asp Gly Lys Leu Trp Gln
 435 440 445
 Asp Tyr Pro Thr Ser Val Leu Ala Ser Asp Arg Arg Phe Phe Ser Phe
 450 455 460
 Glu Pro Gly Ala Lys Trp His Gly Phe Glu Gly Tyr Ala Ala Asp Gln
 465 470 475 480
 Tyr Phe Val Asp Pro Cys Lys Leu Leu Leu Thr Thr Pro Gly Ile Asp
 485 490 495
 Ala Glu Thr Gly Glu Tyr Ser Asp Phe Gly Val Pro Ala Thr Ile Leu
 500 505 510
 Ala His Tyr Leu Arg Glu Asn Gly Ile Val Pro Glu Lys Cys Asp Leu
 515 520 525
 Asn Ser Ile Leu Phe Leu Leu Thr Pro Ala Glu Ser His Glu Lys Leu
 530 535 540
 Ala Gln Leu Val Ala Met Leu Ala Gln Phe Glu Gln His Ile Glu Asp
 545 550 555 560
 Asp Ser Pro Leu Val Glu Val Leu Pro Ser Val Tyr Asn Lys Tyr Pro
 565 570 575
 Val Arg Tyr Arg Asp Tyr Thr Leu Arg Gln Leu Cys Gln Glu Met His
 580 585 590

3761553_1.txt

Asp Leu Tyr Val Ser Phe Asp Val Lys Asp Leu Gln Lys Ala Met Phe
 595 600 605
 Arg Gln Gln Ser Phe Pro Ser Val Val Met Asn Pro Gln Asp Ala His
 610 615 620
 Ser Ala Tyr Ile Arg Gly Asp Val Glu Leu Val Arg Ile Arg Asp Ala
 625 630 635 640
 Glu Gly Arg Ile Ala Ala Glu Gly Ala Leu Pro Tyr Pro Pro Gly Val
 645 650 655
 Leu Cys Val Val Pro Gly Glu Val Trp Gly Gly Ala Val Gln Arg Tyr
 660 665 670
 Phe Leu Ala Leu Glu Glu Gly Val Asn Leu Leu Pro Gly Phe Ser Pro
 675 680 685
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3761553_1.txt

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 <213> Corynebacterium glutamicum ATCC13032 ArgC

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 20 25 30
 Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
 35 40 45
 Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
 50 55 60
 Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
 65 70 75 80
 Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
 85 90 95
 Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys
 100 105 110
 Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr
 115 120 125
 Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro
 Page 19

3761553_1.txt

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 145 150 155 160
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 165 170 175
 Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser
 180 185 190
 Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
 195 200 205
 Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
 210 215 220
 Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
 225 230 235 240
 Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Gly Ile Leu Thr Thr
 245 250 255
 Ala Thr Ala Pro Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala
 260 265 270
 Val Tyr Glu Glu Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro
 275 280 285
 Glu Gly Ala Gln Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys
 290 295 300
 His Val Gln Val Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr
 305 310 315 320
 Ser Ala Ile Asp Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln
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 ccagaaatgc caggacaccg cgaggctctt cgtggtgcta agcgtgtagc agtgccagga 480
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3761553_1.txt

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gaaaccttcg tgcattgttct tccagaaggt gcacagccac aaaccaagc agttcttggc      900
tccaacatgt gccacgtgca ggtagaaatt gatgaggaag caggcaaagt ccttgttacc      960
tccgcaatcg ataacctcac caagggaact gccggcgccg ctgttcagtg catgaactta     1020
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<212>      PRT
<213>      Corynebacterium glutamicum ATCC13869 ArgC

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Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala Tyr Ala Ser Gly Glu
          20          25          30
Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu
          35          40          45
Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala Asp Arg Val Ile Gln
          50          55          60
Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp Val Val Phe Leu Gly
          65          70          75          80
Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp
          85          90          95
Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala
          100          105          110
Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln Gly Thr Trp Pro Tyr
          115          120          125
Gly Ile Pro Glu Ile Pro Gly His Arg Glu Ala Leu Arg Gly Ala Lys
          130          135          140
Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu
          145          150          155          160
Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro Asp Val Ser Val Val
          165          170          175
Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys Ala Ser Val Ala Leu
          180          185          190
Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly
          195          200          205
Lys His Arg His Thr Pro Glu Ile Ala Gln Asn Leu Gly Glu Val Ser
          210          215          220

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3761553_1.txt

Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val Leu Ala Pro Leu Pro
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 Arg Gly Ile Leu Thr Thr Ala Thr Ala Pro Leu Lys Glu Gly Val Thr
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 Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu Thr
 260 265 270
 Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala Val
 275 280 285
 Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu Ala
 290 295 300
 Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly Thr
 305 310 315 320
 Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp Glu
 325 330 335
 Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro
 340 345

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 <211> 1044
 <212> DNA
 <213> Corynebacterium glutamicum ATCC13869 argC

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 gcatcaaccg caggcagcac gctcggtgaa ttgatgccac acattccgca gttggcggat 180
 cgtgttattc aagacaccac agctgaaact ctagccggtc atgatgtcgt atttctagga 240
 cttccacacg gattctctgc agaaattgca cttcagctcg gaccagatgt cacagtgatt 300
 gactgtgcag ctgactttcg tctgcaaaat gctgcagatt gggagaagtt ctacggctca 360
 gagcaccagg gaacatggcc ttatggcatt ccagaaatac caggacaccg cgaggctctt 420
 cgtggtgcta agcgtgtagc agtgccagga tgtttcccaa ccggtgcaac cttggctctt 480
 cttcctgcgg ttcaagcggg acttatcgag ccagatgttt ccgtagtgtc catcaccggc 540
 gtatcagggtg caggtaagaa agcatctgtt gcaactcttg gctcggaaac catgggttca 600
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 ggcaagtca gcgacaagcc agtcaagggt agcttcaccc cagtgttgc accgttacct 720
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 cgcgcagtat atgaagagtt ctatgcacag gaaaccttcg tgcattgttct tccagaaggt 840
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 gatgaggaag caggcaaagt cttgttacc tccgcaatcg ataacctcac caagggaact 960
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 ccacaggtcg gcgtcgacc ttaa 1044

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<210>      23
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<213>      Corynebacterium glutamicum ATCC13032 ArgJ

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          20          25          30

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

Arg  Val  Phe  Ala  Ala  Pro  Val  Lys  Val  Ser  Arg  Glu  Asn  Val  Ala  Asp
  50          55          60

Gly  Gln  Ile  Arg  Ala  Val  Leu  Tyr  Asn  Ala  Gly  Asn  Ala  Asn  Ala  Cys
  65          70          75          80

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

Ala  Gln  Asn  Leu  Gly  Leu  Glu  Asp  Ser  Asp  Ile  Gly  Val  Cys  Ser  Thr
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Gly  Leu  Ile  Gly  Glu  Leu  Leu  Pro  Met  Asp  Lys  Leu  Asn  Ala  Gly  Ile
          115          120          125

Asp  Gln  Leu  Thr  Ala  Glu  Gly  Ala  Leu  Gly  Asp  Asn  Gly  Ala  Ala  Ala
          130          135          140

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

Phe  Ala  Asp  Gly  Trp  Thr  Val  Gly  Gly  Met  Gly  Lys  Gly  Val  Gly  Met
          165          170          175

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

Ser  Val  Thr  Gln  Glu  Met  Ala  Gln  Ile  Ala  Leu  Ala  Asn  Ala  Thr  Ala
          195          200          205

Val  Thr  Phe  Asp  Thr  Leu  Asp  Ile  Asp  Gly  Ser  Thr  Ser  Thr  Asn  Asp
          210          215          220

Thr  Val  Phe  Leu  Leu  Ala  Ser  Gly  Ala  Ser  Gly  Ile  Thr  Pro  Thr  Gln
          225          230          235          240

Asp  Glu  Leu  Asn  Asp  Ala  Val  Tyr  Ala  Ala  Cys  Ser  Asp  Ile  Ala  Ala
          245          250          255

Lys  Leu  Gln  Ala  Asp  Ala  Glu  Gly  Val  Thr  Lys  Arg  Val  Ala  Val  Thr
          260          265          270

Val  Val  Gly  Thr  Thr  Asn  Asn  Glu  Gln  Ala  Ile  Asn  Ala  Ala  Arg  Thr
          275          280          285

Val  Ala  Arg  Asp  Asn  Leu  Phe  Lys  Cys  Ala  Met  Phe  Gly  Ser  Asp  Pro
          290          295          300

Asn  Trp  Gly  Arg  Val  Leu  Ala  Ala  Val  Gly  Met  Ala  Asp  Ala  Asp  Met
          305          310          315          320

Glu  Pro  Glu  Lys  Ile  Ser  Val  Phe  Phe  Asn  Gly  Gln  Ala  Val  Cys  Leu
          325          330          335

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3761553_1.txt

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 Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala
 355 360 365
 Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser
 370 375 380
 Ala Tyr Ser Ser
 385

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 <212> DNA
 <213> Corynebacterium glutamicum ATCC13032 argJ

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 gcagcggccg tgtttacacg taaccgagtt ttcgcagcgc ctgtgaaggt gagccgagag 180
 aacgttgctg atggccagat cagggctgtt ttgtacaacg ctggtaatgc taatgcgtgt 240
 aatggtctgc agggtgagaa ggatgctcgt gagtctgttt ctcacttagc tcaaaatttg 300
 ggcttgagg attccgatat tgggtgtgtg tccactggtc ttattggtga gttgcttccg 360
 atggataagc tcaatgcagg tattgatcag ctgaccgctg agggcgcttt gggtgacaat 420
 ggtgcagctg ctgccaaggc gatcatgacc actgacacgg tggataagga aaccgtcgtg 480
 tttgctgatg gttggactgt cggcggaatg ggcaagggcg tgggcatgat ggcgccgtct 540
 cttgccacca tgctgggtct cttgaccact gatgcatccg ttactcagga aatggctcag 600
 atcgcgctgg ctaatgctac ggccgttacg tttgacaccc tggatattga tggatcaacc 660
 tccaccaatg acaccgtgtt cctgctggca tctggcgcta gcggaatcac cccaactcag 720
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<210> 25
 <211> 388
 <212> PRT
 <213> Corynebacterium glutamicum ATCC13869 ArgJ

<400> 25
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 Page 24

3761553_1.txt

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Val Asn Gln ₃₅ Gly Pro Glu Phe Ser ₄₀ Ala Ala Ala Val Phe ₄₅ Thr Arg Asn			
Arg Val ₅₀ Phe Ala Ala Pro Val ₅₅ Lys Val Ser Arg Glu ₆₀ Asn Val Ala Asp			
Gly ₆₅ Gln Ile Arg Ala Val ₇₀ Leu Tyr Asn Ala Gly ₇₅ Asn Ala Asn Ala Cys ₈₀			
Asn Gly Leu Gln Gly ₈₅ Glu Lys Asp Ala Arg ₉₀ Glu Ser Val Ser His ₉₅ Leu			
Ala Gln Asn Leu ₁₀₀ Gly Leu Glu Asp Ser ₁₀₅ Asp Ile Gly Val Cys ₁₁₀ Ser Thr			
Gly Leu Ile ₁₁₅ Gly Glu Leu Leu Pro ₁₂₀ Met Asp Lys Leu Asn ₁₂₅ Thr Gly Ile			
Asp Gln ₁₃₀ Leu Thr Ala Glu Gly ₁₃₅ Ala Leu Gly Asp Asn ₁₄₀ Gly Ala Ala Ala			
Ala ₁₄₅ Lys Ala Ile Met Thr ₁₅₀ Thr Asp Thr Val Asp ₁₅₅ Lys Glu Thr Val Val ₁₆₀			
Phe Ala Asp Gly Trp ₁₆₅ Thr Val Gly Gly Met ₁₇₀ Gly Lys Gly Val Gly ₁₇₅ Met			
Met Ala Pro Ser ₁₈₀ Leu Ala Thr Met Leu ₁₈₅ Val Cys Leu Thr Thr ₁₉₀ Asp Ala			
Ser Val Thr ₁₉₅ Gln Glu Met Ala Gln ₂₀₀ Ile Ala Leu Ala Asn ₂₀₅ Ala Thr Ala			
Val Thr ₂₁₀ Phe Asp Thr Leu Asp ₂₁₅ Ile Asp Gly Ser Thr ₂₂₀ Ser Thr Asn Asp			
Thr ₂₂₅ Val Phe Leu Leu Ala ₂₃₀ Ser Gly Ala Ser Gly ₂₃₅ Ile Thr Pro Thr Gln ₂₄₀			
Asp Glu Leu Asn Asp ₂₄₅ Ala Val Tyr Ala Ala ₂₅₀ Cys Ser Asp Ile Ala ₂₅₅ Ala			
Lys Leu Gln Ala ₂₆₀ Asp Ala Glu Gly Val ₂₆₅ Thr Lys Arg Val Ala ₂₇₀ Val Thr			
Val Val Gly ₂₇₅ Thr Thr Asn Asn Glu ₂₈₀ Gln Ala Ile Asn Ala ₂₈₅ Ala Arg Thr			
Val Ala ₂₉₀ Arg Asp Asn Leu Phe ₂₉₅ Lys Cys Ala Met Phe ₃₀₀ Gly Ser Asp Pro			
Asn Trp Gly Arg Val Leu ₃₁₀ Ala Ala Val Gly Met ₃₁₅ Ala Asp Ala Asp Met ₃₂₀			
Glu Pro Glu Lys Ile ₃₂₅ Ser Val Phe Phe Asn ₃₃₀ Asp Gln Ala Val Cys ₃₃₅ Leu			
Asp Ser Thr Gly ₃₄₀ Ala Pro Gly Ala Arg ₃₄₅ Glu Val Asp Leu Ser Gly Ala			
Asp Ile Asp ₃₅₅ Val Arg Ile Asp Leu ₃₆₀ Gly Thr Ser Gly Glu ₃₆₅ Gly Gln Ala			

3761553_1.txt

Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser
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Ala Tyr Ser Ser
 385

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 <211> 1167
 <212> DNA
 <213> Corynebacterium glutamicum ATCC13869 argJ

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 gcagcgggccg tgtttacacg caaccgagtt ttcgcagcgc ctgtgaagggt gagccgggag 180
 aacgttgctg atggccagat cagggctgtt ttgtacaacg ctggtaatgc taatgcgtgt 240
 aatggtctgc aggggtgagaa ggatgctcgt gagtctgttt ctcacttagc tcaaaatttg 300
 ggcttgagg attccgatat tgggtgtgtgt tccactgggtc ttattggtga gttgcttccg 360
 atggataagc tcaatacagg tattgatcag ctgaccgctg agggcgcttt gggtgacaat 420
 ggtgcagctg ctgccaaggc gatcatgacc actgacacgg tggataagga aaccgtcgtg 480
 tttgctgatg gttggactgt cggcggaatg ggcaagggcg tgggcatgat ggcgccgtct 540
 cttgccacca tgctggtctg cttgaccact gatgcatccg ttactcagga aatggctcag 600
 attgcgctgg ctaatgctac ggccgttacg tttgacaccc tggatattga tggatcaacc 660
 tccaccaatg acaccgtgtt cctgctggca tctggcgcta gcggaatcac cccaactcag 720
 gatgaactca acgatgcggt gtacgcagct tgttctgata tcgcagcgaa gcttcaggct 780
 gatgcagagg ggggtgacaa gcgcgttgct gtgacagtgg tgggaaccac caacaacgag 840
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 gtccttggtg ctcgtgaggt ggatctttcc ggcgtgaca ttgatgtccg aattgatttg 1080
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 <212> PRT
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 20 25 30
 Val Val Lys Tyr Gly Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala
 35 40 45

3761553_1.txt

Ala Phe Ala Ala Asp Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro
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Val Val Val His Gly Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg
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Val Gly Leu Gln Gly Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro
85 90 95
Glu Val Met Asp Ile Val Arg Met Val Leu Phe Gly Gln Val Gly Arg
100 105 110
Asp Leu Val Gly Leu Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr
115 120 125
Ser Gly Glu Asp Ala Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn
130 135 140
Ile Asp Gly Val Pro Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn
145 150 155 160
Val Asp Ala Ser Ser Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro
165 170 175
Val Val Ser Thr Ile Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile
180 185 190
Asn Ala Asp Thr Ala Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu
195 200 205
Arg Leu Leu Val Leu Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro
210 215 220
Asp Lys Ser Ser Leu Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala
225 230 235 240
Ile Leu Pro Gly Leu Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys
245 250 255
Leu Asn Ala Val Arg Gly Gly Val Ser Ala Ala His Val Ile Asp Gly
260 265 270
Arg Ile Ala His Ser Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile
275 280 285
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Gly Thr Val Phe Arg Lys Asp Asp Lys Asp Gly Glu Leu
305 310 315

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<211> 954

<212> DNA

<213> Corynebacterium glutamicum ATCC13032 argB

<400> 28

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atgggtggatg atgatctcaa ggctgctttt gctgccgaca tggctcttctt gcgcaccgtg 180

ggcgcaaac cagtgggtgg gcacgggtgg ggacctcaga tttctgagat gctaaaccgt 240

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3761553_1.txt

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<213>      Corynebacterium glutamicum ATCC13869 ArgB

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          20          25          30
Val Val Lys Tyr Gly Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala
          35          40          45
Ala Phe Ala Ala Asp Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro
          50          55          60
Val Val Val His Gly Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg
          65          70          75          80
Val Gly Leu Gln Gly Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro
          85          90          95
Glu Val Met Asp Ile Val Arg Met Val Leu Phe Gly Gln Val Gly Arg
          100          105          110
Asp Leu Val Gly Leu Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr
          115          120          125
Ser Gly Glu Asp Ala Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn
          130          135          140
Ile Asp Gly Val Pro Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn
          145          150          155          160
Val Asp Ala Ser Ser Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro
          165          170          175
Val Val Ser Thr Ile Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile
          180          185          190
Asn Ala Asp Thr Ala Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu
          195          200          205

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3761553_1.txt

Arg Leu Leu Val Leu Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro
 210 215 220
 Asp Lys Ser Ser Leu Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala
 225 230 235 240
 Ile Leu Pro Gly Leu Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys
 245 250 255
 Leu Asn Ala Val Arg Gly Gly Val Ser Ala Ala His Val Ile Asp Gly
 260 265 270
 Arg Ile Ala His Ser Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile
 275 280 285
 Gly Thr Met Val Leu Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu
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<210> 30
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 cgtgggggag taagcgctgc tcatgtcatt gacggccgca tcgcgcactc ggtgttgctg 840
 gagcttttga ccatgggtgg aattggcacg atgggtgctgc cggatgtttt tgatcgggag 900
 aattatccgg aaggcaccgt ttttagaaaa gacgacaagg atggggaact gtaa 954

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 <211> 391
 <212> PRT
 <213> Corynebacterium glutamicum ATCC13032 ArgD

<400> 31

3761553_1.txt

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 Asp Gln Gly₃₅ Asn Val Tyr Ile Asp₄₀ Leu Leu Ala Gly Ile₄₅ Ala Val Asn
 Ala Leu₅₀ Gly His Ala His Pro₅₅ Ala Ile Ile Glu Ala₆₀ Val Thr Asn Gln
 Ile₆₅ Gly Gln Leu Gly His₇₀ Val Ser Asn Leu Phe₇₅ Ala Ser Arg Pro Val₈₀
 Val Glu Val Ala Glu₈₅ Glu Leu Ile Lys Arg₉₀ Phe Ser Leu Asp Asp₉₅ Ala
 Thr Leu Ala Ala₁₀₀ Gln Thr Arg Val Phe₁₀₅ Phe Cys Asn Ser Gly₁₁₀ Ala Glu
 Ala Asn Glu₁₁₅ Ala Ala Phe Lys Ile₁₂₀ Ala Arg Leu Thr Gly₁₂₅ Arg Ser Arg
 Ile Leu₁₃₀ Ala Ala Val His Gly₁₃₅ Phe His Gly Arg Thr₁₄₀ Met Gly Ser Leu
 Ala Leu Thr Gly Gln Pro₁₅₀ Asp Lys Arg Glu Ala₁₅₅ Phe Leu Pro Met Pro₁₆₀
 Ser Gly Val Glu Phe₁₆₅ Tyr Pro Tyr Gly Asp₁₇₀ Thr Asp Tyr Leu Arg₁₇₅ Lys
 Met Val Glu Thr₁₈₀ Asn Pro Thr Asp Val₁₈₅ Ala Ala Ile Phe Leu₁₉₀ Glu Pro
 Ile Gln Gly₁₉₅ Glu Thr Gly Val₂₀₀ Val Pro Ala Pro Glu Gly₂₀₅ Phe Leu Lys
 Ala Val₂₁₀ Arg Glu Leu Cys Asp₂₁₅ Glu Tyr Gly Ile Leu₂₂₀ Met Ile Thr Asp
 Glu Val₂₂₅ Gln Thr Gly Val₂₃₀ Gly Arg Thr Gly Asp₂₃₅ Phe Phe Ala His Gln₂₄₀
 His Asp Gly Val₂₄₅ Val Pro Asp Val Val Thr₂₅₀ Met Ala Lys Gly Leu₂₅₅ Gly
 Gly Gly Leu Pro₂₆₀ Ile Gly Ala Cys Leu₂₆₅ Ala Thr Gly Arg Ala₂₇₀ Ala Glu
 Leu Met Thr₂₇₅ Pro Gly Lys His Gly₂₈₀ Thr Thr Phe Gly Gly₂₈₅ Asn Pro Val
 Ala Cys₂₉₀ Ala Ala Ala Lys Ala₂₉₅ Val Leu Ser Val Val₃₀₀ Asp Asp Ala Phe
 Cys₃₀₅ Ala Glu Val Ala Arg₃₁₀ Lys Gly Glu Leu Phe₃₁₅ Lys Glu Leu Leu Ala₃₂₀
 Lys Val Asp Gly Val₃₂₅ Val Asp Val Arg Gly₃₃₀ Arg Gly Leu Met Leu₃₃₅ Gly
 Val Val Leu Glu₃₄₀ Arg Asp Val Ala Lys₃₄₅ Gln Ala Val Leu Asp₃₅₀ Gly Phe
 Lys His Gly₃₅₅ Val Ile Leu Asn Ala₃₆₀ Pro Ala Asp Asn Ile₃₆₅ Ile Arg Leu

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Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
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Ala Ile Ala Glu Thr Ile Ala
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 <213> Corynebacterium glutamicum ATCC13032 argD

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 ttgctcgcg gcatcgagc caacgcgttg ggccacgccc acccggcgat catcgaggcg 180
 gtcaccaacc agatcggcca acttggtcac gtctcaaact tgttcgcatc caggcccgtc 240
 gtcgaggtcg ccgaggagct catcaagcgt ttttcgcttg acgacgccac cctcgccgag 300
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 gcacgcttga ctggctgctc ccggattctg gctgcagttc atggttttcca cggccgcacc 420
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 agcgggtgtg agttctaccc ttacggcgac accgattact tgcgcaaat ggtagaaacc 540
 aaccaacgg atgtggctgc tatcttcctc gagccaatcc aggggtgaaac gggcgttggt 600
 ccagcacctg aaggattcct caaggcagtg cgcgagctgt gcgatgagta cggcatcttg 660
 atgatcaccg atgaagtcca gactggcggt ggccgtaccg gcgatttctt tgcacatcag 720
 cacgatggcg ttgttccga tgtggtgacc atggccaagg gacttggcgg cggcttctcc 780
 atcggtgctt gtttggccac tggccgtgca gctgaattga tgacccagg caagcacggc 840
 accactttcg gtggcaacc agttgcttgt gcagctgcca aggcagtgt gtctgttgtc 900
 gatgacgctt tctgctgaga agttgccgc aagggcgagc tgttcaagga acttcttgcc 960
 aaggttgacg gcgtttaga cgtccgtggc aggggcttga tgttgggcgt ggtgctggag 1020
 cgcgacgtcg caaagcaagc tgttcttgat ggttttaagc acggcgttat tttgaatgca 1080
 ccggcggaaca acattatccg tttgacccg ccgctggtga tcaccgacga agaaatcgca 1140
 gacgcagtcaggctattgc cgagacaatc gcataa 1176

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 <213> Corynebacterium glutamicum ATCC13869 ArgD

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 Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30

Asp Gln Gly Lys Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
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      35              40              45
Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
   50              55              60
Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
   65              70              75              80
Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
              85              90              95
Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
              100              105              110
Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
              115              120              125
Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
              130              135              140
Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
              145              150              155              160
Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
              165              170              175
Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
              180              185              190
Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
              195              200              205
Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
              210              215              220
Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
              225              230              235              240
His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
              245              250              255
Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
              260              265              270
Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
              275              280              285
Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
              290              295              300
Cys Ala Glu Val Thr Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
              305              310              315              320
Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
              325              330              335
Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
              340              345              350
Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
              355              360              365
Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
              370              375              380
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 ttgctcgcg gcatcgcagt caacgcgttg ggccacgccc acccggcgat catcgaggcg 180
 gtcaccaacc agatcggcca acttggtcac gtctcaaact tgttcgcatc caggcccgtc 240
 gtcgaggtcg ccgaggagct catcaagcgt ttttcgcttg acgacgccac cctcgcccg 300
 caaaccggg ttttcttctg caactcgggc gccgaagcaa acgaggctgc tttcaagatt 360
 gcacgcttga ctggtcgttc ccgattctg gctgcagttc atggtttcca cggccgcacc 420
 atgggttccc tcgcgctgac tggccagcca gacaagcgtg aagcattcct gccaatgcca 480
 agcgggtgtg agttctaccc ttacggcgac accgattact tgcgcaaaat ggtagaaacc 540
 aaccaacgg atgtggctgc tatcttcctc gagccaatcc agggtgaaac gggcgttggt 600
 ccagcacctg aaggattcct caaggcagtg cgcgagctgt gcgatgagta cggcatcttg 660
 atgatcaccg atgaagtcca gactggcggt ggccgtaccg gcgatttctt tgcacatcag 720
 cacgatggcg ttgttcccga tgtggtgacc atggccaagg gacttggcg cggcttccc 780
 atcggtgctt gtttggccac tggccgtgca gctgaattga tgacccagg caagcacggc 840
 accactttcg gtggcaacc agttgcttgt gcagctgcca aggcagtgt gtctgttgtc 900
 gatgacgctt tctgcgaga agttaccgc aagggcgagc tgttcaagga acttcttgcc 960
 aaggttgacg gcgtttaga cgtccgtggc aggggcttga tgttggcggt ggtgctggag 1020
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 ccggcggaca acattatccg tttgaccccg ccgctggtga tcaccgacga agaaatcgca 1140
 gacgcagtca aggctattgc cgagacaatc gcataa 1176

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 <213> Corynebacterium glutamicum ATCC13032 NCg11469
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 Val Asp Val Leu Val Glu Ala Phe Ala Asn Asp Pro Ala Phe Leu Arg
 20 25 30
 Trp Ile Pro Gln Pro Asp Pro Gly Ser Ala Lys Leu Arg Ala Leu Phe
 35 40 45
 Glu Leu Gln Ile Glu Lys Gln Tyr Ala Val Ala Gly Asn Ile Asp Val
 50 55 60
 Ala Arg Asp Ser Glu Gly Glu Ile Val Gly Val Ala Leu Trp Asp Arg
 65 70 75 80

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Pro Asp Gly Asn His Ser Ala Lys Asp Gln Ala Ala Met Leu Pro Arg
85 90 95
Leu Val Ser Ile Phe Gly Ile Lys Ala Ala Gln Val Ala Trp Thr Asp
100 105 110
Leu Ser Ser Ala Arg Phe His Pro Lys Phe Pro His Trp Tyr Leu Tyr
115 120 125
Thr Val Ala Thr Ser Ser Ser Ala Arg Gly Thr Gly Val Gly Ser Ala
130 135 140
Leu Leu Asn His Gly Ile Ala Arg Ala Gly Asp Glu Ala Ile Tyr Leu
145 150 155 160
Glu Ala Thr Ser Thr Arg Ala Ala Gln Leu Tyr Asn Arg Leu Gly Phe
165 170 175
Val Pro Leu Gly Tyr Ile Pro Ser Asp Asp Asp Gly Thr Pro Glu Leu
180 185 190
Ala Met Trp Lys Pro Pro Ala Met Pro Thr Val
195 200

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tcagcaaagc ttcgagcact tttcgaactg cagattgaga agcagtatgc agtggcggga 180
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gttggcagtg cgcttcttaa tcacggaatc gtcgcgcggt gtgatgaagc tatctatttg 480
gaggcgacgt cgactcgtgc ggctcaacta tataaccgtc tgggatttgt gcccttgggt 540
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<213> Corynebacterium glutamicum ATCC13869 NCgl1469

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20 25 30
Trp Ile Pro Gln Pro Asp Pro Gly Ser Ala Lys Leu Arg Ala Leu Phe
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35 40 45
 Glu Leu Gln Ile Glu Lys Gln Tyr Ala Val Ala Gly Asn Ile Asp Val
 50 55 60
 Ala Arg Asp Ser Glu Gly Glu Ile Val Gly Val Ala Leu Trp Asp Arg
 65 70 75 80
 Pro Asp Gly Asn His Ser Ala Lys Asp Gln Ala Ala Ile Leu Pro Arg
 85 90 95
 Leu Val Ser Ile Phe Gly Ile Lys Ala Ala Gln Val Ala Trp Thr Asp
 100 105 110
 Leu Ser Ser Ala Arg Phe His Pro Lys Phe Pro His Trp Tyr Leu Tyr
 115 120 125
 Thr Val Ala Thr Ser Ser Ser Ala Arg Gly Thr Gly Val Gly Ser Ala
 130 135 140
 Leu Leu Asn His Gly Ile Ala Arg Ala Gly Asp Glu Ala Ile Tyr Leu
 145 150 155 160
 Glu Ala Thr Ser Thr Arg Ala Ala Gln Leu Tyr Asn Arg Leu Gly Phe
 165 170 175
 Val Pro Leu Gly Tyr Ile Pro Ser Asp Asp Asp Gly Thr Pro Glu Leu
 180 185 190
 Ala Met Trp Lys Pro Pro Ala Met Pro Thr Val
 195 200

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 tcagcaaagc ttcgagcact tttcgaactg cagattgaga agcagtatgc agtggcgggg 180
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 ccaactgttt aa 612

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 Asp Asn Ser₃₅ Ile Leu Tyr Thr Ala₄₀ Leu Pro Leu Leu Arg₄₅ Glu Gln Leu
 Ala Ala₅₀ Thr Glu Thr Gln Ala₅₅ Leu Trp Ile Ile Asn₆₀ Ala Tyr Pro Leu
 Leu₆₅ Met Ala Gly Leu₇₀ Leu Gly Thr Gly₇₅ Thr Leu Gly Asp Lys Ile₈₀
 Gly His Arg Arg Met₈₅ Phe Leu Met Gly₉₀ Leu Ser Ile Phe Gly Ile₉₅ Ala
 Ser Leu Gly Ala₁₀₀ Ala Phe Ala Pro Thr₁₀₅ Ala Trp Ala Leu Val₁₁₀ Ala Ala
 Arg Ala Phe₁₁₅ Leu Gly Ile Gly Ala₁₂₀ Ala Thr Met Met Pro Ala Thr Leu
 Ala Leu₁₃₀ Ile Arg Ile Thr Phe₁₃₅ Glu Asp Glu Arg Glu₁₄₀ Arg Asn Thr Ala
 Ile₁₄₅ Gly Ile Trp Gly Ser₁₅₀ Val Ala Ile Leu Gly₁₅₅ Ala Ala Ala Gly Pro₁₆₀
 Ile Ile Gly Gly Ala₁₆₅ Leu Leu Glu Phe Phe₁₇₀ Trp Trp Gly Ser Val₁₇₅ Phe
 Leu Ile Asn Val₁₈₀ Pro Val Ala Val Ile₁₈₅ Ala Leu Ile Ala Thr₁₉₀ Leu Phe
 Val Ala Pro₁₉₅ Ala Asn Ile Ala Asn₂₀₀ Pro Ser Lys His Trp₂₀₅ Asp Phe Leu
 Ser Ser₂₁₀ Phe Tyr Ala Leu Leu₂₁₅ Thr Leu Ala Gly Leu₂₂₀ Ile Ile Thr Ile
 Lys₂₂₅ Glu Ser Val Asn Thr₂₃₀ Ala Arg His Met Pro₂₃₅ Leu Leu Leu Gly Ala₂₄₀
 Val Ile Met Leu Ile₂₄₅ Ile Gly Ala Val Leu₂₅₀ Phe Ser Ser Arg Gln₂₅₅ Lys
 Lys Ile Glu Glu₂₆₀ Pro Leu Leu Asp Leu₂₆₅ Ser Leu Phe Arg Asn₂₇₀ Arg Leu
 Phe Leu Gly₂₇₅ Gly Val Val Ala Ala₂₈₀ Gly Met Ala Met Phe₂₈₅ Thr Val Ser
 Gly Leu₂₉₀ Glu Met Thr Thr Ser₂₉₅ Gln Arg Phe Gln Leu₃₀₀ Ser Val Gly Phe
 Thr₃₀₅ Pro Leu Glu Ala Gly₃₁₀ Leu Leu Met Ile Pro₃₁₅ Ala Ala Leu Gly Ser₃₂₀
 Phe Pro Met Ser Ile₃₂₅ Ile Gly Gly Ala Asn₃₃₀ Leu His Arg Trp Gly₃₃₅ Phe
 Lys Pro Leu Ile₃₄₀ Ser Gly Gly Phe Ala₃₄₅ Ala Thr Ala Val Gly₃₅₀ Ile Ala
 Leu Cys Ile₃₅₅ Trp Gly Ala Thr His₃₆₀ Thr Asp Gly Leu Pro₃₆₅ Phe Phe Ile

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 Ser Ser Thr Ala Ile Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met
 385 390 395 400
 Ala Ser Ser Ile Glu Glu Val Ser Tyr Glu Phe Gly Thr Leu Leu Ser
 405 410 415
 Val Ala Ile Leu Gly Ser Leu Phe Pro Phe Phe Tyr Ser Leu His Ala
 420 425 430
 Pro Ala Glu Val Ala Asp Asn Phe Ser Ala Gly Val His His Ala Ile
 435 440 445
 Asp Gly Asp Ala Ala Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val
 450 455 460
 Leu Ile Ile Ala Leu Val Cys Ala Val Ala Ala Ala Leu Ile Ser Ser
 465 470 475 480
 Tyr Leu Phe Arg Gly Asn Pro Lys Gly Ala Asn Asn Ala His
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 cgcaacactg caattggtat ttggggttcc gtggcaattc ttggcgctgc ggcaggcccc 480
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 ccgtctaagc attgggattt cttgtcgtcg ttctatgcgc tgctcacact tgctgggttg 660
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Asp Asn Ser Ile Leu Tyr Thr Ala Leu Pro Leu Leu Arg Glu Gln Leu
35 40 45
Ala Ala Thr Glu Thr Gln Ala Leu Trp Ile Ile Asn Ala Tyr Pro Leu
50 55 60
Leu Met Ala Gly Leu Leu Leu Gly Thr Gly Thr Leu Gly Asp Lys Ile
65 70 75 80
Gly His Arg Arg Met Phe Leu Met Gly Leu Ser Ile Phe Gly Ile Ala
85 90 95
Ser Leu Gly Ala Ala Phe Ala Pro Thr Ala Trp Ala Leu Val Ala Ala
100 105 110
Arg Ala Phe Leu Gly Ile Gly Ala Ala Thr Met Met Pro Ala Thr Leu
115 120 125
Ala Leu Ile Arg Ile Thr Phe Glu Asp Glu Arg Glu Arg Asn Thr Ala
130 135 140
Ile Gly Ile Trp Gly Ser Val Ala Ile Leu Gly Ala Ala Ala Gly Pro
145 150 155 160
Ile Ile Gly Gly Ala Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe
165 170 175
Leu Ile Asn Val Pro Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe
180 185 190
Val Ala Pro Ala Asn Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu
195 200 205
Ser Ser Phe Tyr Ala Leu Leu Thr Leu Ala Gly Leu Ile Val Thr Ile
210 215 220
Lys Glu Ser Val Asn Thr Ala Arg His Leu Pro Leu Leu Val Gly Ala
225 230 235 240
Ile Ile Leu Leu Ile Ile Gly Ala Val Leu Phe Ser Ser Arg Gln Lys
245 250 255

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 275 280 285
 Gly Leu Glu Met Thr Thr Ser Gln Arg Phe Gln Leu Ser Val Gly Phe
 290 295 300
 Thr Pro Leu Glu Ala Gly Leu Leu Met Ile Pro Ala Ala Leu Gly Ser
 305 310 315 320
 Phe Pro Met Ser Ile Ile Gly Gly Ala Asn Leu His Arg Trp Gly Phe
 325 330 335
 Lys Pro Leu Ile Ser Gly Gly Phe Leu Ala Thr Ala Val Gly Ile Ala
 340 345 350
 Leu Cys Ile Trp Gly Ala Thr His Thr Asp Gly Leu Pro Phe Phe Ile
 355 360 365
 Ala Gly Leu Phe Phe Met Gly Ala Gly Ala Gly Ser Val Met Ser Val
 370 375 380
 Ser Ser Thr Ala Ile Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met
 385 390 395 400
 Ala Ser Ser Ile Glu Glu Val Ser Tyr Glu Phe Gly Thr Leu Leu Ser
 405 410 415
 Val Ala Ile Leu Gly Ser Leu Phe Pro Phe Phe Tyr Ser Leu His Ala
 420 425 430
 Pro Ala Glu Val Ala Asp Asn Phe Ser Ala Gly Val His His Ala Ile
 435 440 445
 Tyr Gly Asp Ala Ala Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val
 450 455 460
 Leu Ile Ile Ala Leu Val Cys Ala Val Ala Ala Leu Ile Ser Ser
 465 470 475 480
 Tyr Leu Phe Arg Gly Asn Pro Lys Gly Ala Asn Asn Ala His
 485 490

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 <213> Corynebacterium glutamicum ATCC13869 NCgl2522

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 gcatatcccc tgctcatggc gggctcttct ttgggtaccg gcactttggg tgacaaaatc 240
 ggccaccgcc ggatgttcct catgggcttg agcattttcg gaatcgcttc acttggcgct 300
 gcgtttgctc caactgcgtg ggctcttggt gctgagagag ctttccttgg catcggtgctg 360
 gcgacgatga tgcccgaac cttggctctg atccgcatta cgtttgaaga tgaacgcgaa 420
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3761553_1.txt

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3761553_1.txt

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