

<110> CJ CHEILJEDANG CORPORATION
 <120> MICROORGANISMS FOR PRODUCING PUTRESCINE OR ORNITHINE AND PROCESS
 FOR PRODUCING PUTRESCINE OR ORNITHINE USING THEM
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 <151> 2015-07-20
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 <211> 443
 <212> PRT
 <213> E.coli N-acetylglutamate synthase
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 35 40 45
 Ile Gly Leu Leu His Ser Leu Gly Ile Arg Leu Val Val Val Tyr Gly
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 Ala Arg Pro Gln Ile Asp Ala Asn Leu Ala Ala His His His Glu Pro
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 Leu Tyr His Lys Asn Ile Arg Val Thr Asp Ala Lys Thr Leu Glu Leu
 85 90 95
 Val Lys Gln Ala Ala Gly Thr Leu Gln Leu Asp Ile Thr Ala Arg Leu
 100 105 110
 Ser Met Ser Leu Asn Asn Thr Pro Leu Gln Gly Ala His Ile Asn Val
 115 120 125
 Val Ser Gly Asn Phe Ile Ile Ala Gln Pro Leu Gly Val Asp Asp Gly
 130 135 140
 Val Asp Tyr Cys His Ser Gly Arg Ile Arg Arg Ile Asp Glu Asp Ala
 145 150 155 160
 Ile His Arg Gln Leu Asp Ser Gly Ala Ile Val Leu Met Gly Pro Val
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 Ala Val Ser Val Thr Gly Glu Ser Phe Asn Leu Thr Ser Glu Glu Ile
 180 185 190
 Ala Thr Gln Leu Ala Ile Lys Leu Lys Ala Glu Lys Met Ile Gly Phe
 195 200 205
 Cys Ser Ser Gln Gly Val Thr Asn Asp Asp Gly Asp Ile Val Ser Glu
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 Leu Phe Pro Asn Glu Ala Gln Ala Arg Val Glu Ala Gln Glu Glu Lys
 225 230 235 240
 Gly Asp Tyr Asn Ser Gly Thr Val Arg Phe Leu Arg Gly Ala Val Lys
 245 250 255

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Ala Cys Arg Ser Gly Val Arg Arg Cys His Leu Ile Ser Tyr Gln Glu
 260 265 270
 Asp Gly Ala Leu Leu Gln Glu Leu Phe Ser Arg Asp Gly Ile Gly Thr
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 Gln Ile Val Met Glu Ser Ala Glu Gln Ile Arg Arg Ala Thr Ile Asn
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 Asp Ile Gly Gly Ile Leu Glu Leu Ile Arg Pro Leu Glu Gln Gln Gly
 305 310 315 320
 Ile Leu Val Arg Arg Ser Arg Glu Gln Leu Glu Met Glu Ile Asp Lys
 325 330 335
 Phe Thr Ile Ile Gln Arg Asp Asn Thr Thr Ile Ala Cys Ala Ala Leu
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 Tyr Pro Phe Pro Glu Glu Lys Ile Gly Glu Met Ala Cys Val Ala Val
 355 360 365
 His Pro Asp Tyr Arg Ser Ser Ser Arg Gly Glu Val Leu Leu Glu Arg
 370 375 380
 Ile Ala Ala Gln Ala Lys Gln Ser Gly Leu Ser Lys Leu Phe Val Leu
 385 390 395 400
 Thr Thr Arg Ser Ile His Trp Phe Gln Glu Arg Gly Phe Thr Pro Val
 405 410 415
 Asp Ile Asp Leu Leu Pro Glu Ser Lys Lys Gln Leu Tyr Asn Tyr Gln
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 Arg Lys Ser Lys Val Leu Met Ala Asp Leu Gly
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<210> 2
 <211> 1332
 <212> DNA
 <213> E.coli N-acetylglutamate synthase

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 aatttctcca gtatcgtaa tgatatcggg ttgttgaca gcctcggcat ccgtctggtg 180
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gcaacaatca acgatattgg cggatttctg gagttgattc gcccactgga gcagcaaggt      960
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cagcgcgata acacgactat tgcctgcgcc gcgctctatc cgttcccgga agagaagatt    1080
ggggaaatgg cctgtgtggc agttcacccg gattaccgca gttcatcaag gggatgaagtt    1140
ctgctggaac gcattgccgc tcaggcgaag cagagcggct taagcaaatt gtttgtgctg    1200
accacgcgca gtattcactg gttccaggaa cgtggattta cccagtgga tattgattta    1260
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<210>      3
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<212>     PRT
<213>     E.coli Acetylornithine deacetylase

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

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210 215
Gly Thr Ala Lys Gly Val Met Val Asn Ala Leu Ser Leu Ala Ala Arg
225 230 235 240
Ile His Ala Glu Val Pro Ala Asp Glu Ser Pro Glu Met Thr Glu Gly
245 250 255
Tyr Glu Gly Phe Tyr His Leu Ala Ser Met Lys Gly Thr Val Glu Arg
260 265 270
Ala Asp Met His Tyr Ile Ile Arg Asp Phe Asp Arg Lys Gln Phe Glu
275 280 285
Ala Arg Lys Arg Lys Met Met Glu Ile Ala Lys Lys Val Gly Lys Gly
290 295 300
Leu His Pro Asp Cys Tyr Ile Glu Leu Val Ile Glu Asp Ser Tyr Tyr
305 310 315 320
Asn Met Arg Glu Lys Val Val Glu His Pro His Ile Leu Asp Ile Ala
325 330 335
Gln Gln Ala Met Arg Asp Cys Asp Ile Glu Pro Glu Leu Lys Pro Ile
340 345 350
Arg Gly Gly Thr Asp Gly Ala Gln Leu Ser Phe Met Gly Leu Pro Cys
355 360 365
Pro Asn Leu Phe Thr Gly Gly Tyr Asn Tyr His Gly Lys His Glu Phe
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Val Thr Leu Glu Gly Met Glu Lys Ala Val Gln Val Ile Val Arg Ile
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Ala Glu Leu Thr Ala Gln Arg Lys
405

<210> 4
<211> 1227
<212> DNA
<213> E.coli Acetylornithine deacetylase

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cagctcgaag agatggggct tatcaatgtg accttaagtg agaagggcac tttgatggcg 180
acgttaccgg ctaacgtccc tggcgatatc ccggcgattg gctttatttc tcatgtggat 240
acctcaccgg attgcagcgg caaaaatgtg aatccgcaaa ttgttgaaaa ctatcgcggt 300
ggcgatattg cgctgggtat cggcgatgaa gttttatcac cggttatgtt cccggtgctg 360
catcagctac tgggtcagac gctgattacc accgatggta aaaccttggt aggtgccgat 420
gacaaagcag gtattgcaga aatcatgacc gcgctggcgg tattgcaaca gaaaaaatt 480
ccgcatggtg atattcgcg cgcctttacc ccggatgaag aagtgggcaa aggggcgaaa 540
cattttgatg ttgacgcctt cgatgccgc tgggcttaca ctgttgatgg tgggtggcgta 600
ggcgaactgg agtttgaaaa cttcaacgcc gcgtcgggtca atatcaaat tgctcggtaac 660
aatgttcatc cgggcacggc gaaaggagt atggtaaagt cgctgtcgct ggcggcacgt 720

OPA16079_Draft Amendment to the sequence listing (clean)

attcatgcgg aagttccggc ggatgaaagc ccggaatga cagaaggcta tgaaggtttc 780
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 gatttcgacc gtaaacagtt tgaagcgcgt aaacgtaaaa tgatggagat cgccaaaaaa 900
 gtgggcaaag ggttacatcc tgattgctac attgaactgg tgattgaaga cagttactac 960
 aatatgcgcg agaaagtggg tgagcatccg catattctcg atatcgcca gcaggcgatg 1020
 cgcgattgcg atattgaacc ggaactgaaa ccgatccgcg gtggtaccga cggcgcgcag 1080
 ttgtcgttta tgggattacc gtgcccgaac ctgttctactg gcggttataa ctatcatggt 1140
 aagcatgagt ttgtgactct ggaaggtatg gaaaaagcgg tgcaggtgat cgtccgtatt 1200
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<210> 5
 <211> 858
 <212> PRT
 <213> Corynebacterium glutamicum ATCC 13032 pta-ackA

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

OPA16079_Draft Amendment to the sequence listing (clean)

Ser 225	Lys	Ser	Val	Thr	Ile 230	Asp	Glu	Ala	Arg	Glu 235	Ile	Met	Lys	Asp	Ile 240
Ser	Tyr	Phe	Gly	Thr 245	Met	Met	Val	His	Asn 250	Gly	Asp	Ala	Asp	Gly	Met 255
Val	Ser	Gly	Ala 260	Ala	Asn	Thr	Thr	Ala 265	His	Thr	Ile	Lys	Pro 270	Ser	Phe
Gln	Ile	Ile 275	Lys	Thr	Val	Pro	Glu 280	Ala	Ser	Val	Val	Ser 285	Ser	Ile	Phe
Leu	Met 290	Val	Leu	Arg	Gly	Arg 295	Leu	Trp	Ala	Phe	Gly 300	Asp	Cys	Ala	Val
Asn 305	Pro	Asn	Pro	Thr	Ala 310	Glu	Gln	Leu	Gly	Glu 315	Ile	Ala	Val	Val	Ser 320
Ala	Lys	Thr	Ala	Ala 325	Gln	Phe	Gly	Ile	Asp 330	Pro	Arg	Val	Ala	Ile 335	Leu
Ser	Tyr	Ser	Thr 340	Gly	Asn	Ser	Gly	Gly 345	Gly	Ser	Asp	Val	Asp 350	Arg	Ala
Ile	Asp	Ala 355	Leu	Ala	Glu	Ala	Arg 360	Arg	Leu	Asn	Pro	Glu 365	Leu	Cys	Val
Asp	Gly 370	Pro	Leu	Gln	Phe	Asp 375	Ala	Ala	Val	Asp	Pro 380	Gly	Val	Ala	Arg
Lys 385	Lys	Met	Pro	Asp	Ser 390	Asp	Val	Ala	Gly	Gln 395	Ala	Asn	Val	Phe	Ile 400
Phe	Pro	Asp	Leu	Glu 405	Ala	Gly	Asn	Ile	Gly 410	Tyr	Lys	Thr	Ala	Gln 415	Arg
Thr	Gly	His	Ala 420	Leu	Ala	Val	Gly 425	Pro	Ile	Leu	Gln	Gly 430	Leu	Asn	Lys
Pro	Val	Asn 435	Asp	Leu	Ser	Arg	Gly 440	Ala	Thr	Val	Pro	Asp 445	Ile	Val	Asn
Thr	Val 450	Ala	Ile	Thr	Ala	Ile 455	Gln	Ala	Gly	Gly 460	Arg	Ser	Met	Ala	Leu
Ala 465	Leu	Val	Leu	Asn	Ser 470	Gly	Ser	Ser	Ser	Ile 475	Lys	Phe	Gln	Leu	Val 480
Asn	Pro	Glu	Asn	Ser 485	Ala	Ile	Asp	Glu	Pro 490	Tyr	Val	Ser	Gly	Leu 495	Val
Glu	Gln	Ile	Gly 500	Glu	Pro	Asn	Gly	Arg 505	Ile	Val	Leu	Lys	Ile 510	Glu	Gly
Glu	Lys	Tyr 515	Thr	Leu	Glu	Thr	Pro 520	Ile	Ala	Asp	His	Ser 525	Glu	Gly	Leu
Asn	Leu 530	Ala	Phe	Asp	Leu	Met 535	Asp	Gln	His	Asn	Cys 540	Gly	Pro	Ser	Gln
Leu 545	Glu	Ile	Thr	Ala	Val 550	Gly	His	Arg	Val	Val 555	His	Gly	Gly	Ile	Leu 560
Phe	Ser	Ala	Pro	Glu 565	Leu	Ile	Thr	Asp	Glu 570	Ile	Val	Glu	Met	Ile 575	Arg
Asp	Leu	Ile	Pro 580	Leu	Ala	Pro	Leu	His 585	Asn	Pro	Ala	Asn	Val 590	Asp	Gly

OPA16079_Draft Amendment to the sequence listing (clean)

Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His Val Ala Val
595 600 605

Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala Ala Leu Tyr
610 615 620

Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg Arg Tyr Gly
625 630 635 640

Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val Val Glu Ile
645 650 655

Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe His Leu Gly
660 665 670

Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala Val Asp Thr
675 680 685

Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly Thr Arg Ser
690 695 700

Gly Asp Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg Thr Ala Gly
705 710 715 720

Met Ser Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys Ser Gly Val
725 730 735

Lys Gly Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg Glu Met Ile
740 745 750

Asp Asn Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile Tyr Ile His
755 760 765

Gln Leu Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu Gly Arg Val
770 775 780

Asp Thr Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala Gln Phe Val
785 790 795 800

Arg Glu Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile Glu Ile Asp
805 810 815

Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu Ile Ser Thr
820 825 830

Asp Ala Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu
835 840 845

Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala
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<211> 2579
<212> DNA
<213> Corynebacterium glutamicum ATCC 13032 pta-ackA

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ccggtgttaa	tgatttccgt	gaactgcggg	aatgatcgga	caacaatgat	caagatgcct	2280
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OPA16079_Draft Amendment to the sequence listing (clean)

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 acgcattgcc aaacgatggt cctcgattga tttccaccga tgcctccaag gtgaagggtg 2520
 ttgttattcc aactaatgaa gagttagcta tcgctaggta cgcggtgaag ttcgcttag 2579

<210> 7
 <211> 858
 <212> PRT
 <213> Corynebacterium glutamicum ATCC 13869 pta-ackA

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

275 280 285
 Leu Met Val Leu Arg Gly Arg Leu Trp Ala Phe Gly Asp Cys Ala Val
 290 295 300
 Asn Pro Asn Pro Thr Ala Glu Gln Leu Gly Glu Ile Ala Val Val Ser
 305 310 315 320
 Ala Lys Thr Ala Ala Gln Phe Gly Ile Asp Pro Arg Val Ala Ile Leu
 325 330 335
 Ser Tyr Ser Thr Gly Asn Ser Gly Gly Gly Ser Asp Val Asp Arg Ala
 340 345 350
 Ile Asp Ala Leu Ala Glu Ala Arg Arg Leu Asn Pro Glu Leu Cys Val
 355 360 365
 Asp Gly Pro Leu Gln Phe Asp Ala Ala Val Asp Pro Gly Val Ala Arg
 370 375 380
 Lys Lys Met Pro Asp Ser Asp Val Ala Gly Gln Ala Asn Val Phe Ile
 385 390 395 400
 Phe Pro Asp Leu Glu Ala Gly Asn Ile Gly Tyr Lys Thr Ala Gln Arg
 405 410 415
 Thr Gly His Ala Leu Ala Val Gly Pro Ile Leu Gln Gly Leu Asn Lys
 420 425 430
 Pro Val Asn Asp Leu Ser Arg Gly Ala Thr Val Pro Asp Ile Val Asn
 435 440 445
 Thr Val Ala Ile Thr Ala Ile Gln Ala Gly Gly Arg Ser Met Ala Leu
 450 455 460
 Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu Val
 465 470 475 480
 Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu Val
 485 490 495
 Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Val Glu Gly
 500 505 510
 Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly Leu
 515 520 525
 Asn Leu Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser Gln
 530 535 540
 Leu Glu Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile Leu
 545 550 555 560
 Phe Ser Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu Met Ile Arg
 565 570 575
 Asp Leu Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn Val Asp Gly
 580 585 590
 Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His Val Ala Val
 595 600 605
 Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala Ala Leu Tyr
 610 615 620
 Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg Arg Tyr Gly
 625 630 635 640

OPA16079_Draft Amendment to the sequence listing (clean)

Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val Val Glu Ile
645 650 655

Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe His Leu Gly
660 665 670

Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala Val Asp Thr
675 680 685

Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly Thr Arg Ser
690 695 700

Gly Asp Ile Asp Pro Gly Val Val Phe His Leu Ser Arg Thr Ala Gly
705 710 715 720

Met Ser Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys Ser Gly Val
725 730 735

Lys Gly Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg Glu Met Ile
740 745 750

Asp Asn Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile Tyr Ile His
755 760 765

Gln Leu Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu Gly Arg Val
770 775 780

Asp Thr Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala Gln Phe Val
785 790 795 800

Arg Glu Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile Glu Ile Asp
805 810 815

Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu Ile Ser Thr
820 825 830

Asp Ala Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu
835 840 845

Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala
850 855

<210> 8
<211> 2579
<212> DNA
<213> Corynebacterium glutamicum ATCC 13869 pta-ackA

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ctagaagtat ccaaagttct cgcggcggac ctctcgctg aggggccagc tctcatcatc 180
ggtgtaggaa acacgttttt cgacgcccag gtcgccgctg ccctcggcgt cccagtgcta 240
ctgctggtag acaagcaagg caagcacgtt gctcttgctc gcacccaggt aaacaatgcc 300
ggcgagttg ttgcagcagc atttaccgct gaacaagagc caatgccgga taagctgcgc 360
aaggctgtgc gcaaccacag caacctcgaa ccagtcata ggcgcgaact ctttgaaaac 420
tggctgtca agcgcgcacg cgcagagcac tcccacattg tgctgccaga aggtgacgac 480
gaccgatct tgatggctgc ccaccagctg cttgatcaag acatctgtga catcacgatc 540
ctgggcgatc cagtacagat caaggagcgc gctaccgaac ttggcctgca ccttaacact 600

OPA16079_Draft Amendment to the sequence listing (clean)

gcataacctgg tcaatccgct gacagatcct cgcctggagg aattcgccga acaattcgcg	660
gagctgcgca agtcaaagag cgtcactatc gatgaagccc gcgaaatcat gaaggatatt	720
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gcaaacacca ccgcacacac cattaagcca agcttccaga tcatcaaaac tgttccagaa	840
gcatccgtcg tttcttccat cttcctcatg gtgctgcgcg ggcgactgtg ggcattcggc	900
gactgtgctg ttaacccgaa cccaactgct gaacagcttg gtgaaatcgc cgttgtgtca	960
gcaaaaactg cagcacaatt tggcattgat cctcgcgtag ccatcttgtc ctactccact	1020
ggcaactccg gcggaggctc agatgtggat cgcgccatcg acgctcttgc agaagcacgc	1080
cgactcaacc cagaactatg cgtcgatgga ccacttcagt tcgacgccgc cgtcgacccg	1140
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ttccctgacc tggaagccgg aaacatcggc taaaaaactg cacaacgcac cggtcacgcc	1260
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tcaaccccga aaactctgcc atcgacgagc catatgtttc tggctcttggt gagcagattg	1500
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ccatcgcaga tcaactccga ggcctaaacc tggcgttcga tctcatggac cagcacaact	1620
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ccaccgaaga catcaacacc atcaccttcc acctgggcaa cggcgcaccc atggctgctg	2040
ttcaaggcgg ccgtgcggta gatacttcca tgggtatgac acctctcgcg ggacttgtca	2100
tgggtacccg aagcgggtgac attgatccag gtgtcgtttt ccatctctca cgcaccgctg	2160
gcatgagcat cgatgagatc gataatctgc tgaacaaaaa gtcgggtgta aagggacttt	2220
ccggagtcaa tgatttccgt gaactgcggg aaatgatcga caacaatgat caagatgcct	2280
ggtccgcgta caacatttac atacaccaac tccgccgcta cctcggttcc tacatggtgg	2340
cactgggacg ggtagacacc atcgtgttca ccgccggtgt tggtgaaaat gccagtttg	2400
tccgtgagga tgccttggca ggtttggaaa tgtacggcat cgaaatcgat ccggagcgca	2460
acgcactgcc aaacgatggt cctagattga tttccaccga tgcctccaag gtgaagggtg	2520
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 <211> 652
 <212> PRT
 <213> E.coli acetyl-CoA synthetase

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

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Leu Ala Cys Gly Ala Thr Thr Leu Met Phe Glu Gly Val Pro Asn Trp
 325 330 335
 Pro Thr Pro Ala Arg Met Ala Gln Val Val Asp Lys His Gln Val Asn
 340 345 350
 Ile Leu Tyr Thr Ala Pro Thr Ala Ile Arg Ala Leu Met Ala Glu Gly
 355 360 365
 Asp Lys Ala Ile Glu Gly Thr Asp Arg Ser Ser Leu Arg Ile Leu Gly
 370 375 380
 Ser Val Gly Glu Pro Ile Asn Pro Glu Ala Trp Glu Trp Tyr Trp Lys
 385 390 395 400
 Lys Ile Gly Asn Glu Lys Cys Pro Val Val Asp Thr Trp Trp Gln Thr
 405 410 415
 Glu Thr Gly Gly Phe Met Ile Thr Pro Leu Pro Gly Ala Thr Glu Leu
 420 425 430
 Lys Ala Gly Ser Ala Thr Arg Pro Phe Phe Gly Val Gln Pro Ala Leu
 435 440 445
 Val Asp Asn Glu Gly Asn Pro Leu Glu Gly Ala Thr Glu Gly Ser Leu
 450 455 460
 Val Ile Thr Asp Ser Trp Pro Gly Gln Ala Arg Thr Leu Phe Gly Asp
 465 470 475 480
 His Glu Arg Phe Glu Gln Thr Tyr Phe Ser Thr Phe Lys Asn Met Tyr
 485 490 495
 Phe Ser Gly Asp Gly Ala Arg Arg Asp Glu Asp Gly Tyr Tyr Trp Ile
 500 505 510
 Thr Gly Arg Val Asp Asp Val Leu Asn Val Ser Gly His Arg Leu Gly
 515 520 525
 Thr Ala Glu Ile Glu Ser Ala Leu Val Ala His Pro Lys Ile Ala Glu
 530 535 540
 Ala Ala Val Val Gly Ile Pro His Asn Ile Lys Gly Gln Ala Ile Tyr
 545 550 555 560
 Ala Tyr Val Thr Leu Asn His Gly Glu Glu Pro Ser Pro Glu Leu Tyr
 565 570 575
 Ala Glu Val Arg Asn Trp Val Arg Lys Glu Ile Gly Pro Leu Ala Thr
 580 585 590
 Pro Asp Val Leu His Trp Thr Asp Ser Leu Pro Lys Thr Arg Ser Gly
 595 600 605
 Lys Ile Met Arg Arg Ile Leu Arg Lys Ile Ala Ala Gly Asp Thr Ser
 610 615 620
 Asn Leu Gly Asp Thr Ser Thr Leu Ala Asp Pro Gly Val Val Glu Lys
 625 630 635 640
 Leu Leu Glu Glu Lys Gln Ala Ile Ala Met Pro Ser
 645 650

<210> 10
 <211> 1959
 <212> DNA
 <213> E.coli acetyl-CoA synthetase

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gaacagggaa aaattcttga ctggatcaaa ccttaccaga aggtgaaaaa cacctccttt 180
gcccccggtat atgtgtccat taaatgggtac gaggacggca cgctgaatct ggcggcaaac 240
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gacgccagcc agagcaaaca tatcagctat aaagagctgc accgcgacgt ctgccgcttc 360
gccaataccc tgctcgagct gggcattaaa aaaggtgatg tgggtggcgat ttatatgccg 420
atggtgccgg aagccgcggt tgcatgctg gcctgcgccc gcattggcgc ggtgcattcg 480
gtgattttcg gcggcttctc gccggaagcc gttgccgggc gcattattga ttccaactca 540
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aacgttgatg acgcgctgaa aaacccgaac gtcaccagcg tagagcatgt ggtggtactg 660
aagcgactg gcgggaaaat tgactggcag gaagggcgcg acctgtggtg gcacgacctg 720
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cacgaacgtt ttgaacagac ctacttctcc accttcaaaa atatgtattt cagcggcgac 1500
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gcctacgtca cgcttaatca cggggaggaa ccgtcaccag aactgtacgc agaagtcgcg 1740
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tccctgccta aaacccgctc cggcaaaatt atgcgccgta ttctgcgcaa aattgcggcg 1860
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<210> 11
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PlysC-argA-F

<400> 11
 gaaaggtgca caaatatggt aaaggaacgt aaaaccg

37

<210> 12
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Tn-argA-RXh

<400> 12
 gccactagt ctcgagcatg cggcgttgat ttg

34

<210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Tn-PlysC-FXh

<400> 13
 gaatgagttc ctcgagccga tgctagggcg aaaa

34

<210> 14
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PlysC-R

<400> 14
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36

<210> 15
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PlysC-argE-F

<400> 15
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35

<210> 16
 <211> 36

<212> DNA
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 <223> Tn-argE-RXh
 <400> 16
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 <211> 38
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Pro-pta-FX
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 <223> PlysC-pta-ackA-F
 <400> 20
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 <212> DNA
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<220>
 <223> Pro-pta-RX

<400> 21
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<210> 22
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Pta-ackA-R

<400> 22
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<210> 23
 <211> 43
 <212> DNA
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 <223> 13869_pta-PlysC-R

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<210> 24
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PlysC-acS-F

<400> 24
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<210> 25
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Tn-acS-RXh

<400> 25
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<210> 26
 <211> 494
 <212> PRT
 <213> Corynebacterium glutamicum ATCC 13032 putrescine exporter

<400> 26
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Trp Ala Phe Leu₂₀ Ala Val Ile Ser Gly₂₅ Gly Leu Phe Leu Ile₃₀ Gly Val
 Asp Asn Ser₃₅ Ile Leu Tyr Thr Ala₄₀ Leu Pro Leu Leu Arg₄₅ Glu Gln Leu
 Ala Ala Thr Glu Thr Gln Ala₅₅ Leu Trp Ile Ile Asn₆₀ Ala Tyr Pro Leu
 Leu₆₅ Met Ala Gly Leu₇₀ Leu Leu Gly Thr Gly Thr₇₅ Leu Gly Asp Lys Ile₈₀
 Gly His Arg Arg Met₈₅ Phe Leu Met Gly Leu₉₀ 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 Gln Lys₂₅₅
 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 Phe 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 Gly Phe₃₃₅
 Lys Pro Leu Ile₃₄₀ Ser Gly Gly Phe Ala₃₄₅ Ala Thr Ala Val Gly Ile Ala₃₅₀
 Leu Cys Ile₃₅₅ Trp Gly Ala Thr His₃₆₀ Thr Asp Gly Leu Pro₃₆₅ Phe Phe Ile
 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
 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 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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 <212> DNA
 <213> Corynebacterium glutamicum ATCC 13032 putrescine exporter

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 cgcaacactg caattggtat ttgggggttc gtggcaattc ttggcgctgc ggcaggcccc 480
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 ccgtctaagc attgggattt cttgtcgtcg ttctatgcgc tgctcacact tgctgggttg 660
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<210> 28
<211> 494
<212> PRT
<213> Corynebacterium glutamicum ATCC 13869 putrescine exporter

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20 25 30
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
Lys Ile Glu Glu Pro Leu Leu Asp Leu Ser Leu Phe Arg Asn Arg Leu

260 265 270
 Phe Leu Gly Gly Val Val Ala Ala Gly Met Ala Met Phe Thr Val Ser
 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

<210> 29

<211> 1485

<212> DNA

<213> Corynebacterium glutamicum ATCC 13869 putrescine exporter

<400> 29

atgatttcag aaactttgca ggcgcaagcg cctacgaaaa cccaacgttg ggctttcctc 60
 gctgttatca gcggtggtct ctttctgata ggtgtagaca actcaatcct ctacaccgca 120
 ctccccctgc tgcgtgaaca actcgcagcc actgaaaccc aagcgtttgtg gatcatcaac 180
 gcatatcccc tgctcatggc gggctcttctt ttgggtaccg gcactttggg tgacaaaatc 240
 ggccaccgcc ggatgttcct catgggcttg agcattttcg gaatcgcttc acttggcgct 300
 gcgtttgctc caactgcgtg ggctcttggt gctgcgagag ctttccttgg catcggtgcg 360
 gcgacgatga tgcccgaac cttggctctg atccgcatta cgtttgaaga tgaacgcgaa 420
 cggaacaccg cgattggcat ttggggttct gtggcaattc ttggcgcggc ggcaggtccg 480
 atcattgggtg gtgcgctggt ggaattcttc tgggtggggtt cggttttcct cattaacgtt 540

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ccggtggctg ttatcgcgtt gatcgctacg ctttttgtgg cgccggccaa tatcgcgaat      600
ccgtccaagc actgggattt cttatcctcg ttctatgcat tgcttaccct tgcaggtttg      660
attgtcacca tcaaagaatc ggtaaact gacgctatc tgccactgct tgtaggtgcc      720
atcatcttgc ttatcattgg tgcggtgttg tttagcagtc gtcagaagaa gatcgaggag      780
ccacttctag atctgtcgtt gttccgtaat cgccttttct taggcggtgt ggttgctgcg      840
ggcatggcga tgtttactgt gtccggtttg gaaatgacta cctcgcagcg tttccagttg      900
tctgtgggtt tctctccact tgaggctggg ttgctcatga tcccagctgc attgggtagc      960
ttcccgatgt ctattatcgg tggtgcaaac ttgcatcgtt ggggcttcaa accgctgac      1020
agtgggtggt tccttgccac ggcagtcggc atcgccctgt gtatttgggg cgcgactcat      1080
actgatggtt tgccgttttt catcgcgggt ctgttcttca tgggcgcggg tgctggttcg      1140
gtaatgtctg tgtcttcac tgcgattatc gggtccgcgc cgggtgcgtaa ggctggcatg      1200
gcgtcgtcga tcgaagaggt ctcttatgag ttcggcacgc tgttgtctgt cgcgattttg      1260
ggtagcttgt tccattctt ctactcgtg catgccccgg cagaggttgc ggataacttc      1320
tcggcggggtg ttcaccacgc gatttatggc gatgcggcgc gtgcatcttt ggacaccgca      1380
tacattaacg tgttgatcat tgccctagta tgcgcagtag cggctgctct gatcagcagt      1440
taccttttcc gcggaaatcc gaaggagacc aataatgcgc actag                        1485

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<210>      30
<211>      203
<212>      PRT
<213>      Corynebacterium glutamicum ATCC 13032 acetyltransferase

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<400>      30
Met Ser Pro Thr Val Leu Pro Ala Thr Gln Ala Asp Phe Pro Lys Ile
  1           5           10           15
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
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

<210> 31
 <211> 203
 <212> PRT
 <213> Corynebacterium glutamicum ATCC 13869 acetyltransferase

<400> 31
 Met Ser Pro Thr Val Leu Pro Ala Thr Gln Ala Asp Phe Pro Lys Ile
 1 5 10 15
 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
 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

<210> 32
 <211> 357
 <212> PRT
 <213> Acetyl gamma glutamyl phosphate reductase (ArgC)

<400> 32
 Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala
 1 5 10 15
 Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu

```

      20                               25                               30
Leu Gly His35 Pro Ala Tyr Ala Ser40 Gly Glu Leu Glu Ile45 Gly Ala Leu
Thr Ala50 Ala Ser Thr Ala Gly55 Ser Thr Leu Gly Glu60 Leu Met Pro His
Ile65 Pro Gln Leu Ala Asp70 Arg Val Ile Gln Asp75 Thr Thr Ala Glu Thr80
Leu Ala Gly His Asp85 Val Val Phe Leu Gly90 Leu Pro His Gly Phe95 Ser
Ala Glu Ile Ala100 Leu Gln Leu Gly Pro105 Asp Val Thr Val Ile110 Asp Cys
Ala Ala Asp115 Phe Arg Leu Gln Asn120 Ala Ala Asp Trp Glu125 Lys Phe Tyr
Gly Ser130 Glu His Gln Gly Thr135 Trp Pro Tyr Gly Ile140 Pro Glu Met Pro
Gly145 His Arg Glu Ala Leu150 Arg Gly Ala Lys Arg155 Val Ala Val Pro Gly160
Cys Phe Pro Thr Gly165 Ala Thr Leu Ala Leu170 Leu Pro Ala Val Gln Ala175
Gly Leu Ile Glu180 Pro Asp Val Ser Val185 Val Ser Ile Thr Gly190 Val Ser
Gly Ala Gly195 Lys Lys Ala Ser Val200 Ala Leu Leu Gly Ser205 Glu Thr Met
Gly Ser210 Leu Lys Ala Tyr Asn215 Thr Ser Gly Lys His220 Arg His Thr Pro
Glu Ile Ala Gln Asn230 Leu Gly Glu Val Ser Asp235 Lys Pro Val Lys Val240
Ser Phe Thr Pro Val245 Leu Ala Pro Leu Pro250 Arg Gly Ile Leu Thr255 Thr
Ala Thr Ala Pro260 Leu Lys Glu Gly Val265 Thr Ala Glu Gln Ala270 Arg Ala
Val Tyr Glu275 Glu Phe Tyr Ala Gln280 Glu Thr Phe Val His285 Val Leu Pro
Glu Gly290 Ala Gln Pro Gln Thr295 Gln Ala Val Leu Gly300 Ser Asn Met Cys
His Val Gln Val Glu Ile310 Asp Glu Glu Ala Gly315 Lys Val Leu Val Thr320
Ser Ala Ile Asp Asn325 Leu Thr Lys Gly Thr330 Ala Gly Ala Ala Val335 Gln
Cys Met Asn340 Leu Ser Val Gly Phe Asp345 Glu Ala Ala Gly Leu350 Pro Gln
Val Gly Val Ala Pro
      355

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<210> 33
 <211> 388

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<212> PRT
 <213> Acetyl glutamate synthase or Ornithine acetyl transferase (ArgJ)

<400> 33
 Met Ala Glu Lys Gly Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala
 1 5 10 15
 Thr Thr Ala Gly Ile Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val
 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
 100 105 110
 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
 Asp Ser Thr Gly Ala Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala

340 345 350
 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

<210> 34
 <211> 317
 <212> PRT
 <213> Acetyl glutamate kinase (ArgB)

<400> 34
 Met Asn Asp Leu Ile Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val
 1 5 10 15
 Leu Ala Glu Ala Leu Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val
 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
 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

3774219_1.txt

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
 290 295 300
 Gly Thr Val Phe Arg Lys Asp Asp Lys Asp Gly Glu Leu
 305 310 315

 <210> 35
 <211> 391
 <212> PRT
 <213> Acetyl ornithine aminotransferase (ArgD)

 <400> 35
 Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
 1 5 10 15
 Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30
 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 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

3774219_1.txt

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 Ala 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
 Ala Ile Ala Glu Thr Ile Ala
 385 390

<210> 36
 <211> 319
 <212> PRT
 <213> Ornithine carbamoyl transferase (argF)

<400> 36
 Met Thr Ser Gln Pro Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu
 1 5 10 15
 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
 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

3774219_1.txt

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
 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> 37
 <211> 533
 <212> PRT
 <213> Glutamate expoter (NCgl1221)

<400> 37
 Met Ile Leu Gly Val Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn
 1 5 10 15
 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
 195 200 205

3774219_1.txt

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 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
 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 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
 500 505 510
 Gln Ser Pro Ala Val Glu Ala Pro Thr Ala Val Gln Glu Thr Val Ala
 515 520 525
 Pro Thr Ser Thr Pro
 530

<210> 38
 <211> 711
 <212> PRT

<213> Ornithine decarboxylase (ODC)

<400> 38

Met Lys Ser Met Asn Ile Ala Ala Ser Ser Glu Leu Val Ser Arg Leu
 1 5 10 15
 Ser Ser His Arg Arg Val Val Ala Leu Gly Asp Thr Asp Phe Thr Asp
 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
 Ile Gln Ala Gly Ala Thr Pro Val Tyr Leu Glu Ala Ser Arg Asn Pro
 225 230 235 240
 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

3774219_1.txt

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
 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
 Glu Leu Gln Gly Val Tyr Ser Glu Thr Asp Ala Asp Gly Val Lys Arg
 690 695 700
 Leu Tyr Gly Tyr Val Leu Lys

705

710

<210> 39
<211> 289
<212> DNA
<213> Artificial Sequence

<220>
<223> lysCP1 promoter

<400> 39
ccgatgctag ggcgaaaagc acggcgagca gattgctttg cacttgattc agggtagttg 60
actaaagagt tgctcgcgaa gtagcacctg tcacttttgt ctcaaattatt aaatcgaata 120
tcaatatatg gtctgtttat tggaacgcgt cccagtggct gagacgcata cgctaaagcc 180
ccaggaaccc tgtgcagaaa gaaaacactc ctctggctag gtagacacag tttattgtgg 240
tagagttgag cgggtaactg tcagcacgta gatcgaaagg tgcacaaag 289