

<110> CJ CHEILJEDANG CORPORATION
 <120> MICROORGANISMS FOR PRODUCING PUTRESCINE OR ORNITHINE AND PROCESS
 FOR PRODUCING PUTRESCINE OR ORNITHINE USING THEM
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 <150> KR10-2015-0102624
 <151> 2015-07-20
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 <170> KopatentIn 2.0
 <210> 1
 <211> 443
 <212> PRT
 <213> E.coli N-acetylglutamate synthase
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 20 25 30
 Gly Gly Glu Ala Ile Glu His Glu Asn Phe Ser Ser Ile Val Asn Asp
 35 40 45
 Ile Gly Leu Leu His Ser Leu Gly Ile Arg Leu Val Val Val Tyr Gly
 50 55 60
 Ala Arg Pro Gln Ile Asp Ala Asn Leu Ala Ala His His His Glu Pro
 65 70 75 80
 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
 165 170 175
 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
 210 215 220
 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
 275 280 285
 Gln Ile Val Met Glu Ser Ala Glu Gln Ile Arg Arg Ala Thr Ile Asn
 290 295 300
 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
 340 345 350
 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
 420 425 430
 Arg Lys Ser Lys Val Leu Met Ala Asp Leu Gly
 435 440

<210> 2
 <211> 1332
 <212> DNA
 <213> E.coli N-acetylglutamate synthase

<400> 2
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 aatttctcca gtatcgtaa tgatatcggg ttgttgaca gcctcggcat ccgtctggtg 180
 gtggtctatg gcgcacgtcc gcagatcgac gcaaactctg ctgcgcatca ccacgaaccg 240
 ctgtatcaca agaataacg tgtgaccgac gccaaaacac tggaactggt gaagcaggct 300
 gcgggaacat tgcaactgga tattactgct cgcctgtcga tgagtctcaa taacacgccg 360
 ctgcagggcg cgcatatcaa cgtcgtcagt ggcaatttta ttattgccca gccgctgggc 420
 gtcgatgacg gcgtggatta ctgccatagc gggcgtatcc ggcggattga tgaagacgcg 480
 atccatcgtc aactggacag cgggtgcaata gtgctaattg ggccggtcgc tgtttcagtc 540
 actggcgaga gctttaacct gacctcgga gagattgccca ctcaactggc catcaaactg 600
 aaagctgaaa agatgattgg ttttgcctc tcccagggcg tcactaatga cgacggtgat 660
 attgtctccg aacttttccc taacgaagcg caagcgcggg tagaagcca ggaagagaaa 720
 ggcgattaca actccggtac ggtgcgcttt ttgcgtggcg cagtgaaagc ctgccgcagc 780

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gcaacaatca acgatattgg cggatttctg gagttgattc gcccactgga gcagcaaggt      960
attctggtac gccgttctcg cgagcagctg gagatggaaa tcgacaaatt caccattatt    1020
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
ctgcccgaga gcaaaaagca gttgtacaac taccagcgta aatccaaagt gttgatggcg    1320
gatttagggt aa      1332

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<210>      3
<211>     408
<212>     PRT
<213>     E.coli Acetylornithine deacetylase

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Gln Ser Lys Ala Gly Val Arg Gln Val Pro Ser Thr Glu Gly Gln Trp
          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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210 215 220
 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
 370 375 380
 Val Thr Leu Glu Gly Met Glu Lys Ala Val Gln Val Ile Val Arg Ile
 385 390 395 400
 Ala Glu Leu Thr Ala Gln Arg Lys
 405

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

<400> 4
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 ggggtgagac aggttcccag cacggaaggc caatggaagt tattgcatct gctgaaagag 120
 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
 ccgcatgggtg atattcgcgt cgcctttacc ccggatgaag aagtgggcaa aggggcgaaa 540
 cattttgatg ttgacgcctt cgatgccgcg tgggcttaca ctgttgatgg tgggtggcgta 600
 ggcgaaactg agtttgaaaa cttcaacgcc gcgtcgggtca atatcaaat tgctcggtaac 660
 aatgttcatc cgggcacggc gaaaggagt atggtaaatt cgctgtcgct ggcggcacgt 720

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attcatgcgg aagttccggc ggatgaaagc ccggaatga cagaaggcta tgaaggtttc      780
tatcatctgg cgagcatgaa aggcaccgtt gaacggggccg atatgcacta catcatccgt      840
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 gtgccgaac ctgttctactg gcggttacia ctatcatggt     1140
aagcatgagt ttgtgactct ggaaggtatg gaaaaagcgg tgcaggtgat cgtccgtatt     1200
gccgagttaa cggcgcaacg gaagtaa                                           1227

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<210>      5
<211>     859
<212>      PRT
<213>      Corynebacterium glutamicum ATCC 13032 pta-ackA

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<400>      5
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Phe Asp Gly Phe Asp Leu Glu Glu Val Ala Ala Asp Leu Gly Val Arg
 20          25          30
Leu Thr Tyr Leu Pro Asp Glu Glu Leu Glu Val Ser Lys Val Leu Ala
 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

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Ser Lys Ser Val Thr Ile Asp Glu Ala Arg Glu Ile Met Lys Asp Ile
 225 230 235 240
 Ser 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
 450 455 460
 Leu Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu
 465 470 475 480
 Val Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu
 485 490 495
 Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Ile Glu
 500 505 510
 Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly
 515 520 525
 Leu Asn Leu Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser
 530 535 540
 Gln Leu Glu Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile
 545 550 555 560
 Leu Phe Ser Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu Met Ile
 565 570 575
 Arg Asp Leu Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn Val Asp
 580 585 590

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Gly Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His Val Ala
 595 600 605
 Val Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala Ala Leu
 610 615 620
 Tyr Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg Arg Tyr
 625 630 635 640
 Gly Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val Val Glu
 645 650 655
 Ile Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe His Leu
 660 665 670
 Gly Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala Val Asp
 675 680 685
 Thr Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly Thr Arg
 690 695 700
 Ser Gly Asp Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg Thr Ala
 705 710 715 720
 Gly Met Ser Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys Ser Gly
 725 730 735
 Val Lys Gly Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg Glu Met
 740 745 750
 Ile Asp Asn Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile Tyr Ile
 755 760 765
 His Gln Leu Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu Gly Arg
 770 775 780
 Val Asp Thr Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala Gln Phe
 785 790 795 800
 Val Arg Glu Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile Glu Ile
 805 810 815
 Asp Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu Ile Ser
 820 825 830
 Thr Asp Ala Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu
 835 840 845
 Leu Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala
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 <212> DNA
 <213> Corynebacterium glutamicum ATCC 13032 pta-ackA

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 ctagaagtat ccaaagttct cgcggcggac ctctcgctg aggggccagc tctcatcatc 180
 ggtgtaggaa acacgttttt cgacgccag gtcgccgctg ccctcggcgt cccagtgcta 240
 ctgctggtag acaagcaagg caagcacgtt gctcttgctc gcaccaggt aaacaatgcc 300

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tggctgtca	agcgcgcacg	cgagagcac	tcccacattg	tgctgccaga	aggtgacgac	480
gaccgcatct	tgatggctgc	ccaccagctg	cttgatcaag	acatctgtga	catcacgata	540
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gactgtgctg	ttaacccgaa	cccaactgct	gaacagcttg	gtgaaatcgc	cgttgtgtca	960
gaaaaaactg	cagcacaatt	tggcattgat	cctcgcgtag	ccatcttgtc	ctactccact	1020
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ccaccgaaga	catcaacacc	atcaccttcc	acctgggcaa	cggcgcatcc	atggctgctg	2040
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tgggtacccg	aagcgggtgac	attgatccag	gtatcgtctt	ccacctttcc	cgcaccgctg	2160
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 acgcattgcc aaacgatggt cctcgattga tttccaccga tgcctccaag gtgaaggtgt 2520
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 <211> 859
 <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

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275 280 285
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 290 295 300
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 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
 450 455 460
 Leu Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu
 465 470 475 480
 Val Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu
 485 490 495
 Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Val Glu
 500 505 510
 Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly
 515 520 525
 Leu Asn Leu Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser
 530 535 540
 Gln Leu Glu Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile
 545 550 555 560
 Leu Phe Ser Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu Met Ile
 565 570 575
 Arg Asp Leu Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn Val Asp
 580 585 590
 Gly Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His Val Ala
 595 600 605
 Val Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala Ala Leu
 610 615 620
 Tyr Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg Arg Tyr
 625 630 635 640

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Gly Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val Val Glu
 645 650 655
 Ile Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe His Leu
 660 665 670
 Gly Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala Val Asp
 675 680 685
 Thr Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly Thr Arg
 690 695 700
 Ser Gly Asp Ile Asp Pro Gly Val Val Phe His Leu Ser Arg Thr Ala
 705 710 715 720
 Gly Met Ser Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys Ser Gly
 725 730 735
 Val Lys Gly Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg Glu Met
 740 745 750
 Ile Asp Asn Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile Tyr Ile
 755 760 765
 His Gln Leu Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu Gly Arg
 770 775 780
 Val Asp Thr Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala Gln Phe
 785 790 795 800
 Val Arg Glu Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile Glu Ile
 805 810 815
 Asp Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu Ile Ser
 820 825 830
 Thr Asp Ala Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu
 835 840 845
 Leu Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala
 850 855

<210> 8
 <211> 2580
 <212> DNA
 <213> Corynebacterium glutamicum ATCC 13869 pta-ackA

<400> 8
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 gatttggaag aagtagcagc agaccttgga gttcggctca ccgacctgcc cgacgaagaa 120
 ctagaagtat ccaaagttct cgcggcggac ctctcgctg aggggccagc tctcatcatc 180
 ggtgtaggaa acacgttttt cgacgccag gtcgccgctg ccctcggcgt cccagtgcta 240
 ctgctggtag acaagcaagg caagcacgtt gctcttgctc gcacccaggt aaacaatgcc 300
 ggcgcagttg ttgcagcagc atttaccgct gaacaagagc caatgccgga taagctgcgc 360
 aaggctgtgc gcaaccacag caacctcgaa ccagtcatga gcgccgaact ctttgaaaac 420
 tggctgtca agcgcgcacg cgagagcac tcccacattg tgctgccaga aggtgacgac 480
 gaccgatct tgatggctgc ccaccagctg cttgatcaag acatctgtga catcacgac 540
 ctgggcgatc cagtacagat caaggagcgc gctaccgaac ttggcctgca ccttaacact 600

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gcatacctgg	tcaatccgct	gacagatcct	cgcttgagg	aattcgccga	acaattcgcg	660
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tgctacttcg	gcaccatgat	ggtccacaac	ggcgacgccg	acggaatggt	atccggtgca	780
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
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cgactcaacc	cagaactatg	cgtcgatgga	ccacttcagt	tcgacgccgc	cgtcgacccg	1140
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ggcatgagca	tcgatgagat	cgataatctg	ctgaacaaaa	agtcgggtgt	aaagggactt	2220
tccggagtca	atgatttccg	tgaactgcgg	gaaatgatcg	acaacaatga	tcaagatgcc	2280
tggtccgcgt	acaacattta	catacaccaa	ctccgccgct	acctcggttc	ctacatggtg	2340
gcactgggac	gggtagacac	catcgtgttc	accgccggtg	ttggtgaaaa	tgcccagttt	2400
gtccgtgagg	atgccttggc	aggtttggaa	atgtacggca	tcgaaatcga	tccggagcgc	2460
aacgcactgc	caaacgatgg	tcctagattg	atttccaccg	atgcctccaa	ggtgaagggtg	2520
tttgttattc	caactaatga	agagttggct	atcgctaggt	acgcggtgaa	gttcgcttag	2580

2580

<210> 9
 <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
tgccttgacc gccatctgca agaaaacggc gatcgtagcg ccatcatctg ggaaggcgac 300
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
cgactggtga tcacttccga cgaaggtgtg cgtgccgggc gcagtattcc gctgaagaaa 600
aacgttgatg acgcgctgaa aaacccgaac gtcaccagcg tagagcatgt ggtggtactg 660
aagcgtagtg gcgggaaaat tgactggcag gaagggcgcg acctgtggtg gcacgacctg 720
gttgagcaag cgagcgatca gcaccaggcg gaagagatga acgccgaaga tccgctgttt 780
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gaaggtagcc tggtaatcac cgactcctgg ccgggtcagg cgcgtagct gtttgcgat 1440
cacgaacgtt ttgaacagac ctacttctcc accttcaaaa atatgtattt cagcggcgac 1500
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aagattgccg aagccgccgt agtaggtatt ccgcacaata ttaaagggtca ggcgatctac 1680
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ctgcttgaag agaagcaggc tatcgcgatg ccatcgtaa 1959

<210> 11
 <211> 37
 <212> DNA
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 <220>
 <223> PlysC-argA-F

 <400> 11
 gaaaggtgca caaatatggt aaaggaacgt aaaaccg 37

 <210> 12
 <211> 34
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 <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
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 <210> 14
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PlysC-R

 <400> 14
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 <210> 15
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 <212> DNA
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 <220>
 <223> PlysC-argE-F

 <400> 15
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 <210> 16
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<212> DNA
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 <223> Tn-argE-RXh
 <400> 16
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 <210> 17
 <211> 38
 <212> DNA
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 <223> Pro-pta-FX
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 <210> 18
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 <223> Pro-pta-RX

<400> 21
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<210> 22
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<220>
 <223> Pta-ackA-R

<400> 22
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 <223> 13869_pta-PlysC-R

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<210> 24
 <211> 33
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<220>
 <223> PlysC-acS-F

<400> 24
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<210> 25
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 <212> DNA
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<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
 Met Thr Ser Glu Thr Leu Gln Ala Gln Ala Pro Thr Lys Thr Gln Arg
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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
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 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> 27
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 <212> DNA
 <213> Corynebacterium glutamicum ATCC 13032 putrescine exporter

<400> 27
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 ctccctctgc tgcgtgaaca gctcgcagcc accgaaaccc aagcggttgat gatcatcaac 180
 gcatatcccc tgctcatggc gggccttctt ttgggtaccg gcactttggg tgacaaaatc 240
 ggccaccgcc ggatgttctt catgggcttg agcattttcg gaatcgcttc acttggtgct 300
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 cgcaacactg caattggtat ttgggggttc gtggcaattc ttggcgctgc ggcaggcccc 480
 atcattggtg gtgcgctggt ggaattcttc tgggtggggt cggttttcct cattaacgtt 540
 ccggtggctg ttatcgctgt gatcgctacg ctttttgtgg cgccggccaa tatcgcgaa 600
 ccgtctaagc attgggattt cttgtcgtcg ttctatgcgc tgctcacact tgctgggttg 660
 atcatcacga tcaaggaatc tgtgaatact gcacgccata tgcctcttct tttgggtgca 720
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 agtgggtggt ttgctgccac tgccgttggc atcgccctgt gtatttgggg cgcgactcat 1080
 actgatggtt tgccgttttt catcgcggtt ctattcttca tgggcgcggg tgctgggttcg 1140

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gtaatgtctg tgtcttccac tgcgattatc ggttccgcgc cgggtgcgtaa ggctggcatg 1200
gcgtcgtcga tcgaagaggt ctcttatgag ttcggcacgc tgttgtctgt cgcgattttg 1260
ggtagcttgt tcccattctt ctactcgtg catgccccgg cagaggttgc ggataacttc 1320
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tacattaacg tgttgatcat tgccctagta tgcgcagtag cggctgctct gatcagcagt 1440
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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 ctttctgatc ggtgtagaca actcaatcct ctacaccgca 120
 ctccccctgc tgcgtgaaca actcgcagcc actgaaaccc aagcgttgtg 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 ggtaaacact gcacgtcatc 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
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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>	Met	Ser	Pro	Thr	Val	Leu	Pro	Ala	Thr	Gln	Ala	Asp	Phe	Pro	Lys	Ile
1			31		5					10					15	
Val	Asp	Val		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
Page 24

20	25	30
Leu Gly His ₃₅ Pro Ala Tyr Ala Ser ₄₀ Gly Glu Leu Glu Ile ₄₅ Gly Ala Leu		
Thr Ala ₅₀ Ala Ser Thr Ala Gly ₅₅ Ser Thr Leu Gly Glu ₆₀ Leu Met Pro His		
Ile ₆₅ Pro Gln Leu Ala Asp ₇₀ Arg Val Ile Gln Asp ₇₅ Thr Thr Ala Glu Thr ₈₀		
Leu Ala Gly His Asp ₈₅ Val Val Phe Leu Gly ₉₀ Leu Pro His Gly Phe ₉₅ Ser		
Ala Glu Ile Ala ₁₀₀ Leu Gln Leu Gly Pro ₁₀₅ Asp Val Thr Val Ile ₁₁₀ Asp Cys		
Ala Ala Asp ₁₁₅ Phe Arg Leu Gln Asn ₁₂₀ Ala Ala Asp Trp Glu ₁₂₅ Lys Phe Tyr		
Gly Ser ₁₃₀ Glu His Gln Gly Thr ₁₃₅ Trp Pro Tyr Gly Ile ₁₄₀ Pro Glu Met Pro		
Gly ₁₄₅ His Arg Glu Ala Leu ₁₅₀ Arg Gly Ala Lys Arg ₁₅₅ Val Ala Val Pro Gly ₁₆₀		
Cys Phe Pro Thr Gly ₁₆₅ Ala Thr Leu Ala Leu ₁₇₀ Leu Pro Ala Val Gln Ala ₁₇₅		
Gly Leu Ile Glu ₁₈₀ Pro Asp Val Ser Val ₁₈₅ Val Ser Ile Thr Gly ₁₉₀ Val Ser		
Gly Ala Gly ₁₉₅ Lys Lys Ala Ser Val ₂₀₀ Ala Leu Leu Gly Ser ₂₀₅ Glu Thr Met		
Gly Ser ₂₁₀ Leu Lys Ala Tyr Asn ₂₁₅ Thr Ser Gly Lys His ₂₂₀ Arg His Thr Pro		
Glu Ile Ala Gln Asn ₂₃₀ Leu Gly Glu Val Ser Asp ₂₃₅ Lys Pro Val Lys Val ₂₄₀		
Ser Phe Thr Pro Val ₂₄₅ Leu Ala Pro Leu Pro ₂₅₀ Arg Gly Ile Leu Thr ₂₅₅ Thr		
Ala Thr Ala Pro ₂₆₀ Leu Lys Glu Gly Val ₂₆₅ Thr Ala Glu Gln Ala ₂₇₀ Arg Ala		
Val Tyr Glu ₂₇₅ Glu Phe Tyr Ala Gln ₂₈₀ Glu Thr Phe Val His ₂₈₅ Val Leu Pro		
Glu Gly ₂₉₀ Ala Gln Pro Gln Thr ₂₉₅ Gln Ala Val Leu Gly ₃₀₀ Ser Asn Met Cys		
His Val Gln Val Glu Ile ₃₁₀ Asp Glu Glu Ala Gly ₃₁₅ Lys Val Leu Val Thr ₃₂₀		
Ser Ala Ile Asp Asn ₃₂₅ Leu Thr Lys Gly Thr ₃₃₀ Ala Gly Ala Ala Val ₃₃₅ Gln		
Cys Met Asn ₃₄₀ Leu Ser Val Gly Phe Asp ₃₄₅ Glu Ala Ala Gly Leu ₃₅₀ Pro Gln		
Val Gly Val ₃₅₅ Ala Pro		

<210> 33
 <211> 388

3774219_1.txt

<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
 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
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 Arg Gln Gln Ser Phe Pro Ser Val Val Met Asn Pro Gln Asp Ala His
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 Ser Ala Tyr Ile Arg Gly Asp Val Glu Leu Val Arg Ile Arg Asp Ala
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 Glu Gly Arg Ile Ala Ala Glu Gly Ala Leu Pro Tyr Pro Pro Gly Val
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 Leu Cys Val Val Pro Gly Glu Val Trp Gly Gly Ala Val Gln Arg Tyr
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