

<110> CJ CheilJedang Corporation
 <120> MICROORGANISMS FOR PRODUCING PUTRESCINE AND PROCESS FOR PRODUCING PUTRESCINE BY USING THEM
 <130> OPA21055
 <150> KR 10-2020-0101894
 <151> 2020-08-13
 <160> 30
 <170> KoPatentIn 3.0
 <210> 1
 <211> 335
 <212> PRT
 <213> Unknown
 <220>
 <223> C. glutamicum GNAT family N-acetyltransferase

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

Pro Ala Gln Lys Val Ile Asp Ala Asp Pro Gln Lys Trp Val Met Gly
 165 170 175
 Pro Glu Ile Leu Val Met Thr Lys Ser Leu Asp His Val Glu Ser His
 180 185 190
 Glu Leu Pro Gly Gly Leu Glu Phe Ser Val Asp Lys Gln Pro Asp Gln
 195 200 205
 Glu Trp Leu Gly Met Tyr His Phe Arg Gly Gln Ala Leu Pro Ala His
 210 215 220
 Ala Leu Glu Leu Leu Arg Thr Gln Ile Glu Gly Arg Met Gly Phe Gly
 225 230 235 240
 Arg Leu Thr Thr Pro Ala Gly Gln Thr Val Ala Ile Thr Arg Ala Thr
 245 250 255
 Ile Thr Ala Ala Glu Glu Arg Ile Phe Leu Gly Tyr Ser Ala Val Glu
 260 265 270
 Val Asp Pro Ala Phe Arg Arg Gln Gly Leu Gly Thr Ala Leu Gly Ser
 275 280 285
 Arg Ile Gln Glu Trp Gly Ala Glu Gln His Ala Gln Glu Ala Tyr Leu
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 Gln Val Val Ala His Asn Glu Ala Gly Ile Gly Leu Tyr Gln Lys Leu
 305 310 315 320
 Gly Phe Ser Glu His His Arg His Arg Tyr Ala Glu Arg Lys Phe
 325 330 335

<210> 2
 <211> 1008
 <212> DNA
 <213> Unknown

<220>
 <223> C. glutamicum GNAT family N-acetyltransferase(Ncgl2644)

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 gaaattgtca ttcctgatga tcagcttgag gtgattaaga ttttgtcgcc gcgcaccatt 240
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aatgagtggc atgatggttg gctgctgcgt gccggtgatg gcattgcgga gcgtttctaataat 360
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<211> 408
<212> PRT
<213> Unknown

<220>
<223> E.coli argE

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20 25 30
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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

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	130					135					140				
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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			
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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

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Ala Glu Leu Thr Ala Gln Arg Lys
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<211> 1227
<212> DNA
<213> Unknown

<220>
<223> E.coli argE

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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
ccgcatgggtg atattcgcgt cgcctttacc ccggatgaag aagtgggcaa aggggcgaaa 540
cattttgatg ttgacgcctt cgatgcccgc tgggcttaca ctgttgatgg tgggtggcgta 600
ggcgaactgg agtttgaaaa cttcaacgcc gcgtcggta atatcaaaat tgtcggtaac 660
aatgttcatc cgggcacggc gaaaggagt atggtaaata cgctgtcgct ggccggcacgt 720
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tatcatctgg cgagcatgaa aggcaccgtt gaacgggccg atatgcacta catcatccgt 840
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<210> 5
<211> 388
<212> PRT
<213> Unknown

<220>
<223> C. glutamicum 13869 argJ

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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 Thr 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 Asp 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
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<210> 6
<211> 1167
<212> DNA
<213> Unknown

<220>
<223> C. glutamicum 13869 argJ

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gcagcggccg tgtttacacg caaccgagtt ttcgcagcgc ctgtgaaggt gagccgggag 180
aacgttgctg atggccagat cagggctgtt ttgtacaacg ctggtaatgc taatgcgtgt 240

aatggtctgc aggggtgagaa ggatgctcgt gagtctgttt ctcatctagc tcaaaatttg	300
ggcttgagg attccgatat tgggtgtgtg tccactggtc ttattggtga gttgcttccg	360
atggataagc tcaatacagg tattgatcag ctgaccgctg agggcgcttt gggtgacaat	420
ggtgcagctg ctgccaaggc gatcatgacc actgacacgg tggataagga aaccgtcgtg	480
tttgctgatg gttggactgt cggcggaatg ggcaagggcg tgggcatgat ggcgccgtct	540
cttgccacca tgctggctctg cttgaccact gatgcatccg ttactcagga aatggctcag	600
attgcgctgg ctaatgctac ggccgttacg ttgacaccc tggatattga tggatcaacc	660
tccaccaatg acaccgtggt cctgctggca tctggcgcta gcggaatcac cccaactcag	720
gatgaactca acgatgcggt gtacgcagct tgttctgata tcgcagcgaa gcttcaggct	780
gatgcagagg gggtgaccaa gcgcgttgct gtgacagtgg tgggaaccac caacaacgag	840
caggcgatca atgcggctcg cacggttgct cgtgacaatt tgttcaagtg cgcaatgttt	900
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gaaccagaga agatttctgt gttcttcaat gatcaagcag tatgccttga ttccactggc	1020
gctcctggtg ctctgtgaggt ggatctttcc ggcgctgaca ttgatgtccg aattgatttg	1080
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<210> 7
 <211> 388
 <212> PRT
 <213> Unknown

<220>
 <223> C. glutamicum 13032 argJ

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 35 40 45
 Arg Val Phe Ala Ala Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp

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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> 8
 <211> 1167
 <212> DNA
 <213> Unknown

<220>
 <223> C. glutamicum 13032 argJ

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gcagcggccg tgtttacacg taaccgagtt ttcgcagcgc ctgtgaaggt gagccgagag	180
aacgttgctg atggccagat cagggtctgtt ttgtacaacg ctggtaatgc taatgcgtgt	240
aatggtctgc aggggtgagaa ggatgctcgt gagtctgttt ctcatctagc tcaaaatttg	300
ggcttgagg attccgatat tgggtgtgtg tccactggtc ttattggtga gttgcttccg	360
atggataagc tcaatgcagg tattgatcag ctgaccgctg agggcgcttt gggtgacaat	420
ggtgcagctg ctgccaaggc gatcatgacc actgacacgg tggataagga aaccgtcgtg	480
tttgctgatg gttggactgt cggcggaatg ggcaagggcg tgggcatgat ggcgccgtct	540
cttgccacca tgctggctctg cttgaccact gatgcatccg ttactcagga aatggctcag	600
atcgcgctgg ctaatgctac ggccgttacg ttgacaccc tggatattga tggatcaacc	660
tccaccaatg acaccgtgtt cctgctggca tctggcgcta gcggaatcac cccaactcag	720
gatgaactca acgatgcggt gtacgcagct tgttctgata tcgcagcgaa gcttcaggct	780
gatgcagagg gtgtgaccaa gcgcgttgct gtgacagtgg tgggaaccac caacaacgag	840
caggcgatta atgcggctcg cactgttgct cgtgacaatt tgttcaagtg cgcaatgttt	900
ggatctgatc caaactgggg tcgctgtgtg gctgcagtcg gcatggctga tgctgatatg	960

gaaccagaga agatttctgt gttcttcaat ggtcaagcag tatgccttga ttccactggc	1020
gctcctgggtg ctctgtgaggt ggatctttcc ggcgctgaca ttgatgtccg aattgatttg	1080
ggcaccagtg gggaaggcca ggcaacagtt cgaaccactg acctgagctt ctcctacgtg	1140
gagatcaact ccgctacag ctcttaa	1167

<210> 9
 <211> 289
 <212> DNA
 <213> Unknown

<220>
 <223> lysCP1

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actaaagagt tgctcgcgaa gtagcacctg tcacttttgt ctcaaatatt aaatcgaata	120
tcaatatatg gtctgtttat tggaacgcgt cccagtggct gagacgcacg cgctaaagcc	180
ccaggaaccc tgtgcagaaa gaaaacactc ctctggctag gtagacacag tttattgtgg	240
tagagttgag cgggtaactg tcagcacgta gatcgaaagg tgcacaaag	289

<210> 10
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Tn-A-F

<400> 10	
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<210> 11
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Tn-A-R

<400> 11	
gggcccacta gtctcgagtt caccgcggga gccaaagcc	38

<210> 12
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Tn-B-F

<400> 12
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<210> 13
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Tn-B-R

<400> 13
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<210> 14
 <211> 510
 <212> DNA
 <213> Unknown

<220>
 <223> Tn-A

<400> 14
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 atccgtctac ctcgctaccg ctgcaccaac cccacatgta agcaaaagta tttccaagca 180
 gaactaagct gcgctgacca cggtaaaaag gtcaccacc gggtcaccg ctggatttta 240
 caacgccttg ctattgaccg gatgagtgtt cagcaaccg cgaaagcact tgggctaggg 300
 tgggatttaa cctgccaact agccctcgat atgtgccgtg agctgggtcta taacgatacct 360
 caccatcttg atggagtgtg tgtcattggg gtggatgagc ataagtggc acataatagg 420
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tcacggtgtc ctgcccgggtt attagatgtc 510

<210> 15
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 <212> DNA
 <213> Unknown

<220>
 <223> Tn-B

<400> 15
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 gccaggatcc gttgtataaa aaccggaaga cttgtttgac cacgcacaag tggttgagtc 180
 ctcgtcagca agaaagcttg gagcagttgt gggcgtatga caaagactac ggggcgttaa 240
 agcttgctgt gcttgctgat caggcgatta ttgattgtta tcagatgggt aataagcgtg 300
 aagcgaagaa gaaaatgcgg accattattg atcagcttcg ggtgttgaag gggccgaata 360
 aggaactcgc gcagttgggt cgtagtttgt ttaaacgact tggatgatgtg ttggcgtatt 420
 tcgatgttgg tgtctccaac ggtccggctg aagcgatcaa cggacggttg gagcatttg 479

<210> 16
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> lysCP1 promotor_F

<400> 16
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<210> 17
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<220>
 <223> lysCP1 promotor_R

<400> 17
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<210> 18
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 <212> DNA
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<220>
 <223> argJ _F

<400> 18
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