

Sequence Listings

<110> CJ CheilJedang Corporation

<120> Microorganism producing O-acetyl homoserine and the method of
producing O-acetyl homoserine using the same

<130> OPA15136

<150> KR 10-2014-0076779

<151> 2014-06-23

<160> 71

<170> KopatentIn 2.0

<210> 1

<211> 427

<212> PRT

<213> Artificial Sequence

<220>

<223> GltA A145

<400> 1

Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val

1 5 10 15

Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile

20 25 30

Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr

35 40 45

Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu

50 55 60

Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp

65 70 75 80

Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro

85 90 95

Thr Gln Glu Gln Tyr Asp Glu Phe Lys Thr Thr Val Thr Arg His Thr

100 105 110

Met Ile His Glu Gln Ile Thr Arg Leu Phe His Ala Phe Arg Arg Asp

115 120 125

Ser His Pro Met Ala Val Met Cys Gly Ile Thr Gly Ala Leu Ala Ala

130 135 140

Phe Ala His Asp Ser Leu Asp Val Asn Asn Pro Arg His Arg Glu Ile

145 150 155 160

Ala Ala Phe Arg Leu Leu Ser Lys Met Pro Thr Met Ala Ala Met Cys

165 170 175

Tyr Lys Tyr Ser Ile Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu

180 185 190

Ser Tyr Ala Gly Asn Phe Leu Asn Met Met Phe Ser Thr Pro Cys Glu

195 200 205

Pro Tyr Glu Val Asn Pro Ile Leu Glu Arg Ala Met Asp Arg Ile Leu

210 215 220

Ile Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg

225 230 235 240

Thr Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly

245 250 255

Ile Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Ala

260 265 270

Leu Lys Met Leu Glu Glu Ile Ser Ser Val Lys His Ile Pro Glu Phe

275 280 285

Val Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe

290 295 300

Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg

305 310 315 320

Glu Thr Cys His Glu Val Leu Lys Glu Leu Gly Thr Lys Asp Asp Leu

325 330 335

Leu Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr

340 345 350

Phe Ile Glu Lys Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile

355 360 365

Ile Leu Lys Ala Met Gly Ile Pro Ser Ser Met Phe Thr Val Ile Phe

370 375 380

Ala Met Ala Arg Thr Val Gly Trp Ile Ala His Trp Ser Glu Met His

385 390 395 400

Ser Asp Gly Met Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr

405 410 415

Glu Lys Arg Asp Phe Lys Ser Asp Ile Lys Arg

420 425

<210> 2

<211> 427

<212> PRT

<213> Artificial Sequence

<220>

<223> GltA A167

<400> 2

Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val

1 5 10 15

Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile

20 25 30

Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr

35 40 45

Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu

50 55 60

Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp

65 70 75 80

Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro

85 90 95

Thr Gln Glu Gln Tyr Asp Glu Phe Lys Thr Thr Val Thr Arg His Thr

100 105 110

Met Ile His Glu Gln Ile Thr Arg Leu Phe His Ala Phe Arg Arg Asp

115 120 125

Ser His Pro Met Ala Val Met Cys Gly Ile Thr Gly Ala Leu Ala Ala

130 135 140

Phe Tyr His Asp Ser Leu Asp Val Asn Asn Pro Arg His Arg Glu Ile

145 150 155 160

Ala Ala Phe Arg Leu Leu Ser Ala Met Pro Thr Met Ala Ala Met Cys

165 170 175

Tyr Lys Tyr Ser Ile Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu

180 185 190

Ser Tyr Ala Gly Asn Phe Leu Asn Met Met Phe Ser Thr Pro Cys Glu

195 200 205

Pro Tyr Glu Val Asn Pro Ile Leu Glu Arg Ala Met Asp Arg Ile Leu

210 215 220

Ile Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg

225 230 235 240

Thr Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly

245 250 255

Ile Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Ala

260 265 270

Leu Lys Met Leu Glu Glu Ile Ser Ser Val Lys His Ile Pro Glu Phe

275 280 285

Val Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe

290 295 300

Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg

305 310 315 320

Glu Thr Cys His Glu Val Leu Lys Glu Leu Gly Thr Lys Asp Asp Leu

325 330 335

Leu Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr

340 345 350

Phe Ile Glu Lys Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile

355 360 365

Ile Leu Lys Ala Met Gly Ile Pro Ser Ser Met Phe Thr Val Ile Phe

370 375 380

Ala Met Ala Arg Thr Val Gly Trp Ile Ala His Trp Ser Glu Met His

385 390 395 400

Ser Asp Gly Met Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr

405 410 415

Glu Lys Arg Asp Phe Lys Ser Asp Ile Lys Arg

420 425

<210> 3

<211> 427

<212> PRT

<213> Artificial Sequence

<220>

<223> GltA A204

<400> 3

Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val

1 5 10 15

Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile

20 25 30

Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr

35 40 45

Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu

50 55 60

Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp

65 70 75 80

Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro

85 90 95

Thr Gln Glu Gln Tyr Asp Glu Phe Lys Thr Thr Val Thr Arg His Thr

100 105 110

Met Ile His Glu Gln Ile Thr Arg Leu Phe His Ala Phe Arg Arg Asp

115 120 125

Ser His Pro Met Ala Val Met Cys Gly Ile Thr Gly Ala Leu Ala Ala

130 135 140

Phe Tyr His Asp Ser Leu Asp Val Asn Asn Pro Arg His Arg Glu Ile

145 150 155 160

Ala Ala Phe Arg Leu Leu Ser Lys Met Pro Thr Met Ala Ala Met Cys

165 170 175

Tyr Lys Tyr Ser Ile Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu

180	185	190	
Ser Tyr Ala Gly Asn Phe Leu Asn Met Met Phe Ser Ala Pro Cys Glu			
195	200	205	
Pro Tyr Glu Val Asn Pro Ile Leu Glu Arg Ala Met Asp Arg Ile Leu			
210	215	220	
Ile Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg			
225	230	235	240
Thr Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly			
245	250	255	
Ile Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Ala			
260	265	270	
Leu Lys Met Leu Glu Glu Ile Ser Ser Val Lys His Ile Pro Glu Phe			
275	280	285	
Val Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe			
290	295	300	
Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg			
305	310	315	320
Glu Thr Cys His Glu Val Leu Lys Glu Leu Gly Thr Lys Asp Asp Leu			

325 330 335
Leu Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr

340 345 350
Phe Ile Glu Lys Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile

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

370 375 380
Ala Met Ala Arg Thr Val Gly Trp Ile Ala His Trp Ser Glu Met His

385 390 395 400
Ser Asp Gly Met Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr

405 410 415
Glu Lys Arg Asp Phe Lys Ser Asp Ile Lys Arg

420 425

<210> 4

<211> 427

<212> PRT

<213> Escherichia coli

<220>

<221> PEPTIDE

<222> (1)..(427)

<223> GltA

<400> 4

Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val

1 5 10 15

Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile

20 25 30

Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr

35 40 45

Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu

50 55 60

Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp

65 70 75 80

Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro

85 90 95

Thr Gln Glu Gln Tyr Asp Glu Phe Lys Thr Thr Val Thr Arg His Thr

100 105 110

Met Ile His Glu Gln Ile Thr Arg Leu Phe His Ala Phe Arg Arg Asp

115 120 125

Ser His Pro Met Ala Val Met Cys Gly Ile Thr Gly Ala Leu Ala Ala

130 135 140

Phe Tyr His Asp Ser Leu Asp Val Asn Asn Pro Arg His Arg Glu Ile

145 150 155 160

Ala Ala Phe Arg Leu Leu Ser Lys Met Pro Thr Met Ala Ala Met Cys

165 170 175

Tyr Lys Tyr Ser Ile Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu

180 185 190

Ser Tyr Ala Gly Asn Phe Leu Asn Met Met Phe Ser Thr Pro Cys Glu

195 200 205

Pro Tyr Glu Val Asn Pro Ile Leu Glu Arg Ala Met Asp Arg Ile Leu

210 215 220

Ile Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg

225 230 235 240

Thr Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly

245 250 255

Ile Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Ala

260 265 270

Leu Lys Met Leu Glu Glu Ile Ser Ser Val Lys His Ile Pro Glu Phe

275 280 285

Val Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe

290 295 300

Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg

305 310 315 320

Glu Thr Cys His Glu Val Leu Lys Glu Leu Gly Thr Lys Asp Asp Leu

325 330 335

Leu Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr

340 345 350

Phe Ile Glu Lys Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile

355 360 365

Ile Leu Lys Ala Met Gly Ile Pro Ser Ser Met Phe Thr Val Ile Phe

370 375 380

Ala Met Ala Arg Thr Val Gly Trp Ile Ala His Trp Ser Glu Met His

385 390 395 400

Ser Asp Gly Met Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr

405

410

415

Glu Lys Arg Asp Phe Lys Ser Asp Ile Lys Arg

420

425

<210> 5

<211> 1284

<212> DNA

<213> Artificial Sequence

<220>

<223> GltA A145

<400> 5

atggctgata caaaagcaaa actcacctc aacggggata cagctgttga actggatgtg 60

ctgaaaggca cgctgggtca agatgttatt gatatccgta ctctcggttc aaaaggtgtg 120

ttcacctttg acccaggctt cactcaacc gcatcctgcg aatctaaaat tacttttatt 180

gatggtgatg aaggtatatt gctgcaccgc ggtttcccga tcgatcagct ggcgaccgat 240

tctaactacc tggaagtttg ttacatcctg ctgaatgggtg aaaaaccgac tcaggaacag 300

tatgacgaat ttaaaactac ggtgaccgt cataccatga tccacgagca gattaccgt	360
ctgttccatg ctttccgtcg cgactcgcat ccaatggcag tcatgtgtgg tattaccggc	420
gcgctggcgg cgttcgcga cgactcgctg gatgttaaca atcctcgtca ccgtgaaatt	480
gccgcgttcc gcctgctgtc gaaaatgccg accatggccg cgatgtgtta caagtattcc	540
attggtcagc catttgttta cccgcgaac gatctctcct acgccgtaa cttctgaat	600
atgatgttct ccacgccgtg cgaaccgtat gaagttaatc cgattctgga acgtgctatg	660
gaccgtattc tgatctgca cgctgacat gaacagaacg cctctacctc caccgtgcgt	720
accgctggct cttcgggtgc gaaccgttt gcctgtatcg cagcaggat tgcttactg	780
tggggacctg cgcacggcgg tgctaacgaa gcggcgctga aaatgctgga agaaatcagc	840
tccgttaaac acattccgga atttgttcgt cgtgcgaaag acaaaaatga ttctttccgc	900
ctgatgggct tcggtcaccg cgtgtacaaa aattacgacc cgcgccac cgtaatgcgt	960
gaaacctgcc atgaagtgt gaaagagctg ggcacgaagg atgacctgt ggaagtggct	1020
atggagctgg aaaacatcg cgtgaacgac ccgtacttta tcgagaagaa actgtaccg	1080
aacgtcgatt tctactctgg tatcatcctg aaagcgatgg gtattccgtc ttcatgttc	1140

accgtcattt tcgcaatggc acgtaccgtt ggctggatcg cccactggag cgaaatgcac 1200

agtgacggta tgaagattgc ccgtccgct cagctgtata caggatatga aaaacgcgac 1260

tttaaaagcg atatcaagcg ttaa 1284

<210> 6

<211> 1284

<212> DNA

<213> Artificial Sequence

<220>

<223> GltA A167

<400> 6

atggctgata caaaagcaaa actcaccctc aacggggata cagctgttga actggatgtg 60

ctgaaaggca cgctgggtca agatgttatt gatatccgta ctctcggttc aaaaggtgtg 120

ttcaccttgg acccaggctt cacttcaacc gcatcctgcg aatctaaaat tacttttatt 180

gatggtgatg aaggtatatt gctgcaccgc ggtttccga tcgatcagct ggcgaccgat 240

tctaactacc tggaagtttg ttacatcctg ctgaatggtg aaaaaccgac tcaggaacag 300

tatgacgaat ttaaaactac ggtgaccgt cataccatga tccacgagca gattaccgt	360
ctgttccatg cttccgtcg cgactcgcat ccaatggcag tcatgtgtgg tattaccggc	420
gcgctggcgg cgttctatca cgactcgctg gatgttaaca atcctcgta ccgtgaaatt	480
gccgcgttcc gcctgctgtc ggcatgccg accatggccg cgatgtgtta caagtattcc	540
attggtcagc catttgttta cccgcgaac gatctctct acgccgtaa cttctgaat	600
atgatgttct ccacgccgtg cgaaccgtat gaagttaatc cgattctgga acgtgctatg	660
gaccgtattc tgatctgca cgctgaccat gaacagaacg cctctacctc caccgtgcgt	720
accgtggct cttcgggtgc gaaccgttt gcctgtatcg cagcaggat tgcttcactg	780
tggggacctg cgcacggcgg tgtaacgaa gcggcgctga aaatgctgga agaaatcagc	840
tccgttaaac acattccgga attgttcgt cgtgcgaaag acaaaaatga ttctttccgc	900
ctgatgggct tcggtcaccg cgtgtacaaa aattacgacc cgcgcgccac cgtaatgcgt	960
gaaacctgcc atgaagtgt gaaagagctg ggcacgaagg atgacctgt ggaagtggt	1020
atggagctgg aaaacatcg cgtgaacgac ccgtacttta tcgagaagaa actgtaccg	1080

aacgtcgatt tctactctgg tatcatcctg aaagcgatgg gtattccgtc ttccatgttc 1140

accgtcattt tcgcaatggc acgtaccgtt ggctggatcg ccactggag cgaaatgcac 1200

agtgcaggta tgaagattgc ccgtccgct cagctgtata caggatatga aaaacgac 1260

tttaaaagcg atatcaagcg ttaa 1284

<210> 7

<211> 1284

<212> DNA

<213> Artificial Sequence

<220>

<223> GltA A204

<400> 7

atggctgata caaaagcaaa actcacctc aacggggata cagctgttga actggatgtg 60

ctgaaaggca cgctgggtca agatgttatt gatatccgta ctctcggtc aaaaggtgtg 120

ttcaccttg acccaggctt cactcaacc gcatcctgcg aatctaaaat tacttttatt 180

gatggtgatg aaggtatatt gctgcaccgc ggtttccga tcgatcagct ggcgaccgat 240

tctaactacc tggaagtttg ttacatcctg ctgaatggg aaaaaccgac tcaggaacag	300
tatgacgaat ttaaaactac ggtgacccgt cataccatga tccacgagca gattacccgt	360
ctgttccatg ctttccgtcg cgactcgcat ccaatggcag tcatgtgtgg tattaccggc	420
gcgctggcgg cgttctatca cgactcgctg gatgttaaca atcctcgta cctgaaatt	480
gccgcgttcc gcctgctgc gaaaatgcc accatggccg cgatgtgtta caagtattcc	540
attggtcagc catttgttta cccgcgcaac gatctctct acgccggtta cttcctgaat	600
atgatgttct ccgcgccgtg cgaaccgtat gaagttaatc cgattctgga acgtgctatg	660
gaccgtattc tgatctgca cgctgacat gaacagaacg cctctacctc caccgtgcgt	720
accgctggct cttcgggtgc gaaccgttt gcctgtatcg cagcaggat tgcttcactg	780
tggggacctg cgcacggcgg tgctaacgaa gcggcgctga aaatgctgga agaaatcagc	840
tccgttaaac acattccgga attgttcgt cgtgcgaaag acaaaaatga ttctttccgc	900
ctgatgggct tcggtcaccg cgtgtacaaa aattacgacc cgcgccac cgtaatgcgt	960
gaaacctgcc atgaagtgt gaaagagctg ggcacgaagg atgacctgt ggaagtggct	1020
atggagctgg aaaacatcg gctgaacgac ccgtacttta tcgagaagaa actgtaccg	1080

aacgtcgatt tctactctgg tatcatcctg aaagcgatgg gtattccgtc ttccatgttc 1140

accgtcattt tcgcaatggc acgtaccgtt ggctggatcg cccactggag cgaaatgcac 1200

agtgacggta tgaagattgc ccgtccgct cagctgtata caggatatga aaaacgacgac 1260

tttaaaagcg atatcaagcg ttaa 1284

<210> 8

<211> 1284

<212> DNA

<213> Escherichia coli

<220>

<221> gene

<222> (1)..(1284)

<223> GltA

<400> 8

atggctgata caaaagcaaa actcaccctc aacggggata cagctgttga actggatgtg 60

ctgaaaggca cgctgggtca agatgttatt gatatccgta ctctcggttc aaaaggtgtg 120

ttcacctttg acccaggctt cacttcaacc gcatcctgcg aatctaaaat tacttttatt 180

gatggtgatg aaggtathtt gctgcaccgc ggtttcccga tcgatcagct ggcgaccgat	240
tctaactacc tggaagtttg ttacatcctg ctgaatgggtg aaaaaccgac tcaggaacag	300
tatgacgaat ttaaaactac ggtgaccgt cataccatga tccacgagca gattaccgt	360
ctgttccatg ctttccgtcg cgactcgcat ccaatggcag tcatgtgtgg tattaccggc	420
gcgctggcgg cgttctatca cgactcgctg gatgttaaca atcctcgta ccgtgaaatt	480
gccggttcc gcctgctgtc gaaaatgccg accatggccg cgatgtgtta caagtattcc	540
attggtcagc catttgttta cccgcgaac gatctctct acgccggtta cttcctgaat	600
atgatgttct ccacgccgtg cgaaccgtat gaagttaatc cgattctgga acgtgctatg	660
gaccgtattc tgatctgca cgctgaccat gaacagaacg cctctacctc caccgtgcgt	720
accgtggct cttcgggtgc gaaccgttt gcctgtatcg cagcaggtat tgcttcactg	780
tggggacctg cgcacggcgg tgctaacgaa gcggcgctga aaatgctgga agaaatcagc	840
tccgttaaac acattccgga atttgttcgt cgtgcgaaag acaaaaatga ttctttccgc	900
ctgatgggct tcggtcaccg cgtgtacaaa aattacgacc cgcgcgccac cgtaatgcgt	960

gaaacctgcc atgaagtgct gaaagagctg ggcacgaagg atgacctgct ggaagtggct 1020

atggagctgg aaaacatcgc gctgaacgac ccgtacttta tcgagaagaa actgtaccg 1080

aacgtcgatt tctactctgg tatcatcctg aaagcgatgg gtattccgtc ttccatgttc 1140

accgtcattt tcgcaatggc acgtaccgtt ggctggatcg cccactggag cgaaatgcac 1200

agtgacggta tgaagattgc ccgtccgct cagctgtata caggatatga aaaacgacgac 1260

tttaaaagcg atatcaagcg ttaa 1284

<210> 9

<211> 386

<212> PRT

<213> Escherichia coli

<220>

<221> PEPTIDE

<222> (1)..(386)

<223> metB

<400> 9

Met Thr Arg Lys Gln Ala Thr Ile Ala Val Arg Ser Gly Leu Asn Asp

1 5 10 15

Asp Glu Gln Tyr Gly Cys Val Val Pro Pro Ile His Leu Ser Ser Thr

20 25 30

Tyr Asn Phe Thr Gly Phe Asn Glu Pro Arg Ala His Asp Tyr Ser Arg

35 40 45

Arg Gly Asn Pro Thr Arg Asp Val Val Gln Arg Ala Leu Ala Glu Leu

50 55 60

Glu Gly Gly Ala Gly Ala Val Leu Thr Asn Thr Gly Met Ser Ala Ile

65 70 75 80

His Leu Val Thr Thr Val Phe Leu Lys Pro Gly Asp Leu Leu Val Ala

85 90 95

Pro His Asp Cys Tyr Gly Gly Ser Tyr Arg Leu Phe Asp Ser Leu Ala

100 105 110

Lys Arg Gly Cys Tyr Arg Val Leu Phe Val Asp Gln Gly Asp Glu Gln

115 120 125

Ala Leu Arg Ala Ala Leu Ala Glu Lys Pro Lys Leu Val Leu Val Glu

130 135 140

Ser Pro Ser Asn Pro Leu Leu Arg Val Val Asp Ile Ala Lys Ile Cys

145 150 155 160

His Leu Ala Arg Glu Val Gly Ala Val Ser Val Val Asp Asn Thr Phe

165 170 175

Leu Ser Pro Ala Leu Gln Asn Pro Leu Ala Leu Gly Ala Asp Leu Val

180 185 190

Leu His Ser Cys Thr Lys Tyr Leu Asn Gly His Ser Asp Val Val Ala

195 200 205

Gly Val Val Ile Ala Lys Asp Pro Asp Val Val Thr Glu Leu Ala Trp

210 215 220

Trp Ala Asn Asn Ile Gly Val Thr Gly Gly Ala Phe Asp Ser Tyr Leu

225 230 235 240

Leu Leu Arg Gly Leu Arg Thr Leu Val Pro Arg Met Glu Leu Ala Gln

245 250 255

Arg Asn Ala Gln Ala Ile Val Lys Tyr Leu Gln Thr Gln Pro Leu Val

260 265 270

Lys Lys Leu Tyr His Pro Ser Leu Pro Glu Asn Gln Gly His Glu Ile

275 280 285

Ala Ala Arg Gln Gln Lys Gly Phe Gly Ala Met Leu Ser Phe Glu Leu

290 295 300

Asp Gly Asp Glu Gln Thr Leu Arg Arg Phe Leu Gly Gly Leu Ser Leu

305 310 315 320

Phe Thr Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Ile Ser His

325 330 335

Ala Ala Thr Met Thr His Ala Gly Met Ala Pro Glu Ala Arg Ala Ala

340 345 350

Ala Gly Ile Ser Glu Thr Leu Leu Arg Ile Ser Thr Gly Ile Glu Asp

355 360 365

Gly Glu Asp Leu Ile Ala Asp Leu Glu Asn Gly Phe Arg Ala Ala Asn

370 375 380

Lys Gly

385

<210> 10

<211> 1161

<212> DNA

<213> Escherichia coli

<220>

<221> gene

<222> (1)..(1161)

<223> metB

<400> 10

atgacgcgta aacaggccac catcgcagtg cgtagcgggt taaatgacga cgaacagtat 60

ggttgcgttg tcccaccgat ccatctttcc agcacctata actttaccgg attaatgaa 120

ccgcgcgcgc atgattactc gcgtcgcggc aaccaacgc gcgatgtggt tcagcgtgcg 180

ctggcagaac tggaagggtg tgctgggtgca gtacttacta ataccggcat gtccgcgatt 240

cacctggtaa cgaccgtctt ttgaaacct ggcatctgc tggttgcgc gcacgactgc 300

tacggcggta gctatcgctt gttcgacagt ctggcgaaac gcggttgcta tcgcgtgttg 360

ttgttgatc aaggcgtga acaggcatta cgggcagcgc tggcagaaaa acccaaactg 420

gtactggtag aaagccaag taatccattg ttacgcgtcg tggatattgc gaaaatctgc 480

catctggcaa gggaagtcgg ggcggtgagc gtggtggata acaccttctt aagcccgcga 540

ttacaaaatc cgctggcatt aggtgccgat ctggtgttgc attcatgcac gaaatatctg 600

aacggtcact cagacgtagt ggccggcgtg gtgattgcta aagaccgga cgttgtcact 660

gaactggcct ggtgggcaaa caatattggc gtgacgggcg gcgcgttga cagctatctg	720
ctgctacgtg ggttgccaac gctggtgccg cgtatggagc tggcgagcg caacgcgag	780
gcgattgtga aatactgca aaccagccg ttggtgaaaa aactgtatca cccgtcgtt	840
ccggaaaatc aggggcatga aattgccgcg gccagcaaa aaggcttgg cgcaatgtg	900
agtttgaac tggatggcga tgagcagacg ctgcgtcgtt tcctgggcgg gctgtcgtt	960
tttacgctgg cggaatcatt agggggagtg gaaagtttaa tctctcacgc cgcaaccatg	1020
acacatgcag gcatggcacc agaagcgcgt gctgccgccg ggatctccga gacgctgctg	1080
cgatatcca ccggtattga agatggcgaa gatttaattg ccgacctgga aaatggcttc	1140
cgggctgcaa acaaggggta a	1161

<210> 11

<211> 310

<212> PRT

<213> Escherichia coli

<220>

<221> PEPTIDE

<222> (1)..(310)

<223> thrB

<400> 11

Met Val Lys Val Tyr Ala Pro Ala Ser Ser Ala Asn Met Ser Val Gly

1 5 10 15

Phe Asp Val Leu Gly Ala Ala Val Thr Pro Val Asp Gly Ala Leu Leu

20 25 30

Gly Asp Val Val Thr Val Glu Ala Ala Glu Thr Phe Ser Leu Asn Asn

35 40 45

Leu Gly Arg Phe Ala Asp Lys Leu Pro Ser Glu Pro Arg Glu Asn Ile

50 55 60

Val Tyr Gln Cys Trp Glu Arg Phe Cys Gln Glu Leu Gly Lys Gln Ile

65 70 75 80

Pro Val Ala Met Thr Leu Glu Lys Asn Met Pro Ile Gly Ser Gly Leu

85 90 95

Gly Ser Ser Ala Cys Ser Val Val Ala Ala Leu Met Ala Met Asn Glu

100 105 110

His Cys Gly Lys Pro Leu Asn Asp Thr Arg Leu Leu Ala Leu Met Gly

115 120 125

Glu Leu Glu Gly Arg Ile Ser Gly Ser Ile His Tyr Asp Asn Val Ala

130 135 140

Pro Cys Phe Leu Gly Gly Met Gln Leu Met Ile Glu Glu Asn Asp Ile

145 150 155 160

Ile Ser Gln Gln Val Pro Gly Phe Asp Glu Trp Leu Trp Val Leu Ala

165 170 175

Tyr Pro Gly Ile Lys Val Ser Thr Ala Glu Ala Arg Ala Ile Leu Pro

180 185 190

Ala Gln Tyr Arg Arg Gln Asp Cys Ile Ala His Gly Arg His Leu Ala

195 200 205

Gly Phe Ile His Ala Cys Tyr Ser Arg Gln Pro Glu Leu Ala Ala Lys

210 215 220

Leu Met Lys Asp Val Ile Ala Glu Pro Tyr Arg Glu Arg Leu Leu Pro

225 230 235 240

Gly Phe Arg Gln Ala Arg Gln Ala Val Ala Glu Ile Gly Ala Val Ala

245 250 255

Ser Gly Ile Ser Gly Ser Gly Pro Thr Leu Phe Ala Leu Cys Asp Lys

260 265 270

Pro Glu Thr Ala Gln Arg Val Ala Asp Trp Leu Gly Lys Asn Tyr Leu

275 280 285

Gln Asn Gln Glu Gly Phe Val His Ile Cys Arg Leu Asp Thr Ala Gly

290 295 300

Ala Arg Val Leu Glu Asn

305 310

<210> 12

<211> 933

<212> DNA

<213> Escherichia coli

<220>

<221> gene

<222> (1)..(933)

<223> thrB

<400> 12

atgggttaaag tttatgcccc ggcttcagtg gccaatatga gcgtcgggtt tgatgtgctc 60

ggggcggcgg tgacacctgt tgatggtgca ttgctcggag atgtagtcac gggtgaggcg 120

gcagagacat tcagtctcaa caacctcgga cgctttgccg ataagctgcc gtcagaacca	180
cgggaaaata tcgtttatca gtgctgggag cgttttgcc aggaactggg taagcaaatt	240
ccagtggcga tgacctgga aaagaatatg ccgatcggtt cgggcttagg ctccagtgcc	300
tgttcgggtg tcgcggcgct gatggcgatg aatgaacct gcggcaagcc gcttaatgac	360
actcgtttgc tggctttgat gggcgagctg gaaggccgta tctccggcag cattcattac	420
gacaacgtgg caccgtgttt tctcgggtgt atgcagttga tgatcgaaga aaacgacatc	480
atcagccagc aagtccagg gtttgatgag tggctgtggg tgctggcgta tccggggatt	540
aaagtctcga cggcagaagc cagggctatt ttaccggcg agtatcgccg ccaggattgc	600
attgcgcagc ggcgacatct ggcaggcttc attcacgctt gctattcccg tcagcctgag	660
cttgccgcga agctgatgaa agatgttatc gctgaaccct accgtgaacg gttactgcca	720
ggcttcggc aggcgcggca ggcggtcgcg gaaatcggcg cggtagcgag cggtatctcc	780
ggctccggcc cgacctgtt cgctctgtgt gacaagccgg aaaccgcca gcgcgttgcc	840
gactgggttg gtaagaacta cctgcaaaat caggaagggt ttgttcatat ttgccggctg	900
gatacggcgg gcgcacgagt actggaaaac taa	933

<210> 13

<211> 379

<212> PRT

<213> *Leptospira meyeri*

<220>

<221> PEPTIDE

<222> (1)..(379)

<223> homoserine O-acetyltransferase

<400> 13

Met Pro Thr Ser Glu Gln Asn Glu Phe Ser His Gly Ser Val Gly Val

1 5 10 15

Val Tyr Thr Gln Ser Ile Arg Phe Glu Ser Leu Thr Leu Glu Gly Gly

20 25 30

Glu Thr Ile Thr Pro Leu Glu Ile Ala Tyr Glu Thr Tyr Gly Thr Leu

35 40 45

Asn Glu Lys Lys Asp Asn Ala Ile Leu Val Cys His Ala Leu Ser Gly

50 55 60

Asp Ala His Ala Ala Gly Phe His Glu Gly Asp Lys Arg Pro Gly Trp

65 70 75 80

Trp Asp Tyr Tyr Ile Gly Pro Gly Lys Ser Phe Asp Thr Asn Arg Tyr

85 90 95

Phe Ile Ile Ser Ser Asn Val Ile Gly Gly Cys Lys Gly Ser Ser Gly

100 105 110

Pro Leu Thr Ile Asn Gly Lys Asn Gly Lys Pro Phe Gln Ser Thr Phe

115 120 125

Pro Phe Val Ser Ile Gly Asp Met Val Asn Ala Gln Glu Lys Leu Ile

130 135 140

Ser His Phe Gly Ile His Lys Leu Phe Ala Val Ala Gly Gly Ser Met

145 150 155 160

Gly Gly Met Gln Ala Leu Gln Trp Ser Val Ala Tyr Pro Asp Arg Leu

165 170 175

Lys Asn Cys Ile Val Met Ala Ser Ser Ser Glu His Ser Ala Gln Gln

180 185 190

Ile Ala Phe Asn Glu Val Gly Arg Gln Ala Ile Leu Ser Asp Pro Asn

195 200 205

Trp Asn Gln Gly Leu Tyr Thr Gln Glu Asn Arg Pro Ser Lys Gly Leu

210	215	220	
Ala Leu Ala Arg Met Met Gly His Ile Thr Tyr Leu Ser Asp Glu Met			
225	230	235	240
Met Arg Glu Lys Phe Gly Arg Lys Pro Pro Lys Gly Asn Ile Gln Ser			
245	250	255	
Thr Asp Phe Ala Val Gly Ser Tyr Leu Ile Tyr Gln Gly Glu Ser Phe			
260	265	270	
Val Asp Arg Phe Asp Ala Asn Ser Tyr Ile Tyr Val Thr Lys Ala Leu			
275	280	285	
Asp His Phe Ser Leu Gly Thr Gly Lys Glu Leu Thr Lys Val Leu Ala			
290	295	300	
Lys Val Arg Cys Arg Phe Leu Val Val Ala Tyr Thr Ser Asp Trp Leu			
305	310	315	320
Tyr Pro Pro Tyr Gln Ser Glu Glu Ile Val Lys Ser Leu Glu Val Asn			
325	330	335	
Ala Val Pro Val Ser Phe Val Glu Leu Asn Asn Pro Ala Gly Arg His			
340	345	350	
Asp Ser Phe Leu Leu Pro Ser Glu Gln Gln Asp Ser Ile Leu Arg Asp			

355 360 365

Phe Leu Ser Ser Thr Asp Glu Gly Val Phe Leu

370 375

<210> 14

<211> 379

<212> PRT

<213> Corynebacterium glutamicum

<220>

<221> PEPTIDE

<222> (1)..(379)

<223> homoserine O-acetyltransferase

<400> 14

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly

1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala

20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn

35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp

50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile

65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr

85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe

100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu

115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Val Leu Leu Gly Gly

130 135 140

Ser Met Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu

145 150 155 160

Thr Val Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala

165 170 175

Trp Gln Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp

180 185 190

His His Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala

195 200 205

Thr Gly Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly

210 215 220

Glu Leu Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu

225 230 235 240

Asn Pro Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu

245 250 255

Ser Tyr Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala

260 265 270

Gly Ser Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly

275 280 285

Arg Asp Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro

290 295 300

Val Leu Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln

305 310 315 320

Gln Glu His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys

325 330 335

Ile Val Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln

340 345 350

Met Asp Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu

355 360 365

Asp Asn Pro Ser Thr Tyr Ile Glu Phe Tyr Ile

370 375

<210> 15

<211> 334

<212> PRT

<213> Deinococcus radiodurans

<220>

<221> PEPTIDE

<222> (1)..(334)

<223> homoserine O-acetyltransferase

<400> 15

Met Thr Ala Val Leu Ala Gly His Ala Ser Ala Leu Leu Leu Thr Glu

1 5 10 15

Glu Pro Asp Cys Ser Gly Pro Gln Thr Val Val Leu Phe Arg Arg Glu

20 25 30

Pro Leu Leu Leu Asp Cys Gly Arg Ala Leu Ser Asp Val Arg Val Ala

35 40 45

Phe His Thr Tyr Gly Thr Pro Arg Ala Asp Ala Thr Leu Val Leu His

50 55 60

Ala Leu Thr Gly Asp Ser Ala Val His Glu Trp Trp Pro Asp Phe Leu

65 70 75 80

Gly Ala Gly Arg Pro Leu Asp Pro Ala Asp Asp Tyr Val Val Cys Ala

85 90 95

Asn Val Leu Gly Gly Cys Ala Gly Thr Thr Ser Ala Ala Glu Leu Ala

100 105 110

Ala Thr Cys Ser Gly Pro Val Pro Leu Ser Leu Arg Asp Met Ala Arg

115 120 125

Val Gly Arg Ala Leu Leu Asp Ser Leu Gly Val Arg Arg Val Arg Val

130 135 140

Ile Gly Ala Ser Met Gly Gly Met Leu Ala Tyr Ala Trp Leu Leu Glu

145 150 155 160

Cys Pro Asp Leu Val Glu Lys Ala Val Ile Ile Gly Ala Pro Ala Arg

165 170 175

His Ser Pro Trp Ala Ile Gly Leu Asn Thr Ala Ala Arg Ser Ala Ile

180 185 190

Ala Leu Ala Pro Gly Gly Glu Gly Leu Lys Val Ala Arg Gln Ile Ala

195 200 205

Met Leu Ser Tyr Arg Ser Pro Glu Ser Leu Ser Arg Thr Gln Ala Gly

210 215 220

Gln Arg Val Pro Gly Val Pro Ala Val Thr Ser Tyr Leu His Tyr Gln

225 230 235 240

Gly Glu Lys Leu Ala Ala Arg Phe Asp Glu Gln Thr Tyr Cys Ala Leu

245 250 255

Thr Trp Ala Met Asp Ala Phe Gln Pro Ser Ser Ala Asp Leu Lys Ala

260 265 270

Val Arg Ala Pro Val Leu Val Val Gly Ile Ser Ser Asp Leu Leu Tyr

275 280 285

Pro Ala Ala Glu Val Arg Ala Cys Ala Ala Glu Leu Pro His Ala Asp

290 295 300

Tyr Trp Glu Leu Gly Ser Ile His Gly His Asp Ala Phe Leu Met Asp

305 310 315 320

Pro Gln Asp Leu Pro Glu Arg Val Gly Ala Phe Leu Arg Ser

325

330

<210> 16

<211> 309

<212> PRT

<213> Escherichia coli

<220>

<221> PEPTIDE

<222> (1)..(309)

<223> homoserine O-succinyl transferase

<400> 16

Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg

1

5

10

15

Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu

20

25

30

Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile

35

40

45

Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln

50 55 60

Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr

65 70 75 80

Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln

85 90 95

Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu

100 105 110

Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu

115 120 125

Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala

130 135 140

Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg

145 150 155 160

Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His

165 170 175

Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser

180 185 190

Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu

195 200 205

Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser

210 215 220

Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala

225 230 235 240

Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp

245 250 255

Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr

260 265 270

Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp

275 280 285

Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met

290 295 300

Asn Pro Thr Leu Asp

305

<210> 17

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant polypeptide having homoserine O-acetyl transferase
activity, metA EL

<400> 17

Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg

1 5 10 15

Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu

20 25 30

Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile

35 40 45

Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln

50 55 60

Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr

65 70 75 80

Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln

85 90 95

Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Glu Leu

100	105	110	
Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu			
115	120	125	
Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala			
130	135	140	
Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg			
145	150	155	160
Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His			
165	170	175	
Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser			
180	185	190	
Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu			
195	200	205	
Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser			
210	215	220	
Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala			
225	230	235	240
Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp			

245 250 255

Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr

260 265 270

Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp

275 280 285

Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met

290 295 300

Asn Pro Thr Leu Asp

305

<210> 18

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant polypeptide having homoserine O-acetyl transferase
activity, metA ET

<400> 18

Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg

1 5 10 15

Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu

20 25 30

Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile

35 40 45

Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln

50 55 60

Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr

65 70 75 80

Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln

85 90 95

Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Glu Thr

100 105 110

Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu

115 120 125

Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala

130 135 140

Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg

145 150 155 160

Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His

165 170 175

Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser

180 185 190

Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu

195 200 205

Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser

210 215 220

Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala

225 230 235 240

Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp

245 250 255

Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr

260 265 270

Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp

275 280 285

Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met

290 295 300

Asn Pro Thr Leu Asp

305

<210> 19

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant polypeptide having homoserine O-acetyl transferase
activity, metA EH

<400> 19

Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg

1 5 10 15

Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu

20 25 30

Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile

35 40 45

Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln

50 55 60

Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr

65 70 75 80

Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln

85 90 95

Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Glu His

100 105 110

Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu

115 120 125

Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala

130 135 140

Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg

145 150 155 160

Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His

165 170 175

Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser

180 185 190

Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu

195 200 205

Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser

210 215 220

Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala

225 230 235 240

Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp

245 250 255

Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr

260 265 270

Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp

275 280 285

Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met

290 295 300

Asn Pro Thr Leu Asp

305

<210> 20

<211> 883

<212> PRT

<213> Escherichia coli

<220>

<221> PEPTIDE

<222> (1)..(883)

<223> phosphoenolpyruvate carboxylase

<400> 20

Met Asn Glu Gln Tyr Ser Ala Leu Arg Ser Asn Val Ser Met Leu Gly

1 5 10 15

Lys Val Leu Gly Glu Thr Ile Lys Asp Ala Leu Gly Glu His Ile Leu

20 25 30

Glu Arg Val Glu Thr Ile Arg Lys Leu Ser Lys Ser Ser Arg Ala Gly

35 40 45

Asn Asp Ala Asn Arg Gln Glu Leu Leu Thr Thr Leu Gln Asn Leu Ser

50 55 60

Asn Asp Glu Leu Leu Pro Val Ala Arg Ala Phe Ser Gln Phe Leu Asn

65 70 75 80

Leu Ala Asn Thr Ala Glu Gln Tyr His Ser Ile Ser Pro Lys Gly Glu

85 90 95

Ala Ala Ser Asn Pro Glu Val Ile Ala Arg Thr Leu Arg Lys Leu Lys

100 105 110

Asn Gln Pro Glu Leu Ser Glu Asp Thr Ile Lys Lys Ala Val Glu Ser

115 120 125

Leu Ser Leu Glu Leu Val Leu Thr Ala His Pro Thr Glu Ile Thr Arg

130 135 140

Arg Thr Leu Ile His Lys Met Val Glu Val Asn Ala Cys Leu Lys Gln

145 150 155 160

Leu Asp Asn Lys Asp Ile Ala Asp Tyr Glu His Asn Gln Leu Met Arg

165 170 175

Arg Leu Arg Gln Leu Ile Ala Gln Ser Trp His Thr Asp Glu Ile Arg

180 185 190

Lys Leu Arg Pro Ser Pro Val Asp Glu Ala Lys Trp Gly Phe Ala Val

195 200 205

Val Glu Asn Ser Leu Trp Gln Gly Val Pro Asn Tyr Leu Arg Glu Leu

210 215 220

Asn Glu Gln Leu Glu Glu Asn Leu Gly Tyr Lys Leu Pro Val Glu Phe

225 230 235 240

Val Pro Val Arg Phe Thr Ser Trp Met Gly Gly Asp Arg Asp Gly Asn

245 250 255

Pro Asn Val Thr Ala Asp Ile Thr Arg His Val Leu Leu Leu Ser Arg

260 265 270

Trp Lys Ala Thr Asp Leu Phe Leu Lys Asp Ile Gln Val Leu Val Ser

275 280 285

Glu Leu Ser Met Val Glu Ala Thr Pro Glu Leu Leu Ala Leu Val Gly

290 295 300

Glu Glu Gly Ala Ala Glu Pro Tyr Arg Tyr Leu Met Lys Asn Leu Arg

305 310 315 320

Ser Arg Leu Met Ala Thr Gln Ala Trp Leu Glu Ala Arg Leu Lys Gly

325 330 335

Glu Glu Leu Pro Lys Pro Glu Gly Leu Leu Thr Gln Asn Glu Glu Leu

340 345 350

Trp Glu Pro Leu Tyr Ala Cys Tyr Gln Ser Leu Gln Ala Cys Gly Met

355 360 365

Gly Ile Ile Ala Asn Gly Asp Leu Leu Asp Thr Leu Arg Arg Val Lys

370 375 380

Cys Phe Gly Val Pro Leu Val Arg Ile Asp Ile Arg Gln Glu Ser Thr

385 390 395 400

Arg His Thr Glu Ala Leu Gly Glu Leu Thr Arg Tyr Leu Gly Ile Gly

405 410 415

Asp Tyr Glu Ser Trp Ser Glu Ala Asp Lys Gln Ala Phe Leu Ile Arg

420 425 430

Glu Leu Asn Ser Lys Arg Pro Leu Leu Pro Arg Asn Trp Gln Pro Ser

435 440 445

Ala Glu Thr Arg Glu Val Leu Asp Thr Cys Gln Val Ile Ala Glu Ala

450 455 460

Pro Gln Gly Ser Ile Ala Ala Tyr Val Ile Ser Met Ala Lys Thr Pro

465 470 475 480

Ser Asp Val Leu Ala Val His Leu Leu Leu Lys Glu Ala Gly Ile Gly

485 490 495

Phe Ala Met Pro Val Ala Pro Leu Phe Glu Thr Leu Asp Asp Leu Asn

500 505 510

Asn Ala Asn Asp Val Met Thr Gln Leu Leu Asn Ile Asp Trp Tyr Arg

515 520 525

Gly Leu Ile Gln Gly Lys Gln Met Val Met Ile Gly Tyr Ser Asp Ser

530 535 540

Ala Lys Asp Ala Gly Val Met Ala Ala Ser Trp Ala Gln Tyr Gln Ala

545 550 555 560

Gln Asp Ala Leu Ile Lys Thr Cys Glu Lys Ala Gly Ile Glu Leu Thr

565 570 575

Leu Phe His Gly Arg Gly Gly Ser Ile Gly Arg Gly Gly Ala Pro Ala

580 585 590

His Ala Ala Leu Leu Ser Gln Pro Pro Gly Ser Leu Lys Gly Gly Leu

595 600 605

Arg Val Thr Glu Gln Gly Glu Met Ile Arg Phe Lys Tyr Gly Leu Pro

610 615 620

Glu Ile Thr Val Ser Ser Leu Ser Leu Tyr Thr Gly Ala Ile Leu Glu

625 630 635 640

Ala Asn Leu Leu Pro Pro Pro Glu Pro Lys Glu Ser Trp Arg Arg Ile

645 650 655

Met Asp Glu Leu Ser Val Ile Ser Cys Asp Val Tyr Arg Gly Tyr Val

660 665 670

Arg Glu Asn Lys Asp Phe Val Pro Tyr Phe Arg Ser Ala Thr Pro Glu

675 680 685

Gln Glu Leu Gly Lys Leu Pro Leu Gly Ser Arg Pro Ala Lys Arg Arg

690 695 700

Pro Thr Gly Gly Val Glu Ser Leu Arg Ala Ile Pro Trp Ile Phe Ala

705 710 715 720

Trp Thr Gln Asn Arg Leu Met Leu Pro Ala Trp Leu Gly Ala Gly Thr

725 730 735

Ala Leu Gln Lys Val Val Glu Asp Gly Lys Gln Ser Glu Leu Glu Ala

740 745 750

Met Cys Arg Asp Trp Pro Phe Phe Ser Thr Arg Leu Gly Met Leu Glu

755 760 765

Met Val Phe Ala Lys Ala Asp Leu Trp Leu Ala Glu Tyr Tyr Asp Gln

770 775 780

Arg Leu Val Asp Lys Ala Leu Trp Pro Leu Gly Lys Glu Leu Arg Asn

785 790 795 800

Leu Gln Glu Glu Asp Ile Lys Val Val Leu Ala Ile Ala Asn Asp Ser

805 810 815

His Leu Met Ala Asp Leu Pro Trp Ile Ala Glu Ser Ile Gln Leu Arg

820 825 830

Asn Ile Tyr Thr Asp Pro Leu Asn Val Leu Gln Ala Glu Leu Leu His

835 840 845

Arg Ser Arg Gln Ala Glu Lys Glu Gly Gln Glu Pro Asp Pro Arg Val

850 855 860

Glu Gln Ala Leu Met Val Thr Ile Ala Gly Ile Ala Ala Gly Met Arg

865 870 875 880

Asn Thr Gly

<210> 21

<211> 396

<212> PRT

<213> Escherichia coli

<220>

<221> PEPTIDE

<222> (1)..(396)

<223> aspartate aminotransferase

<400> 21

Met Phe Glu Asn Ile Thr Ala Ala Pro Ala Asp Pro Ile Leu Gly Leu

1 5 10 15

Ala Asp Leu Phe Arg Ala Asp Glu Arg Pro Gly Lys Ile Asn Leu Gly

20 25 30

Ile Gly Val Tyr Lys Asp Glu Thr Gly Lys Thr Pro Val Leu Thr Ser

35 40 45

Val Lys Lys Ala Glu Gln Tyr Leu Leu Glu Asn Glu Thr Thr Lys Asn

50 55 60

Tyr Leu Gly Ile Asp Gly Ile Pro Glu Phe Gly Arg Cys Thr Gln Glu

65 70 75 80

Leu Leu Phe Gly Lys Gly Ser Ala Leu Ile Asn Asp Lys Arg Ala Arg

85 90 95

Thr Ala Gln Thr Pro Gly Gly Thr Gly Ala Leu Arg Val Ala Ala Asp

100 105 110

Phe Leu Ala Lys Asn Thr Ser Val Lys Arg Val Trp Val Ser Asn Pro

115 120 125

Ser Trp Pro Asn His Lys Ser Val Phe Asn Ser Ala Gly Leu Glu Val

130 135 140

Arg Glu Tyr Ala Tyr Tyr Asp Ala Glu Asn His Thr Leu Asp Phe Asp

145 150 155 160

Ala Leu Ile Asn Ser Leu Asn Glu Ala Gln Ala Gly Asp Val Val Leu

165 170 175

Phe His Gly Cys Cys His Asn Pro Thr Gly Ile Asp Pro Thr Leu Glu

180 185 190

Gln Trp Gln Thr Leu Ala Gln Leu Ser Val Glu Lys Gly Trp Leu Pro

195 200 205

Leu Phe Asp Phe Ala Tyr Gln Gly Phe Ala Arg Gly Leu Glu Glu Asp

210 215 220

Ala Glu Gly Leu Arg Ala Phe Ala Ala Met His Lys Glu Leu Ile Val

225 230 235 240

Ala Ser Ser Tyr Ser Lys Asn Phe Gly Leu Tyr Asn Glu Arg Val Gly

245 250 255

Ala Cys Thr Leu Val Ala Ala Asp Ser Glu Thr Val Asp Arg Ala Phe

260 265 270

Ser Gln Met Lys Ala Ala Ile Arg Ala Asn Tyr Ser Asn Pro Pro Ala

275 280 285

His Gly Ala Ser Val Val Ala Thr Ile Leu Ser Asn Asp Ala Leu Arg

290 295 300

Ala Ile Trp Glu Gln Glu Leu Thr Asp Met Arg Gln Arg Ile Gln Arg

305 310 315 320

Met Arg Gln Leu Phe Val Asn Thr Leu Gln Glu Lys Gly Ala Asn Arg

325 330 335

Asp Phe Ser Phe Ile Ile Lys Gln Asn Gly Met Phe Ser Phe Ser Gly

340 345 350

Leu Thr Lys Glu Gln Val Leu Arg Leu Arg Glu Glu Phe Gly Val Tyr

355 360 365

Ala Val Ala Ser Gly Arg Val Asn Val Ala Gly Met Thr Pro Asp Asn

370 375 380

Met Ala Pro Leu Cys Glu Ala Ile Val Ala Val Leu

385 390 395

<210> 22

<211> 367

<212> PRT

<213> Escherichia coli

<220>

<221> PEPTIDE

<222> (1)..(367)

<223> aspartate-semialdehyde dehydrogenase

<400> 22

Met Lys Asn Val Gly Phe Ile Gly Trp Arg Gly Met Val Gly Ser Val

1 5 10 15

Leu Met Gln Arg Met Val Glu Glu Arg Asp Phe Asp Ala Ile Arg Pro

20 25 30

Val Phe Phe Ser Thr Ser Gln Leu Gly Gln Ala Ala Pro Ser Phe Gly

35 40 45

Gly Thr Thr Gly Thr Leu Gln Asp Ala Phe Asp Leu Glu Ala Leu Lys

50 55 60

Ala Leu Asp Ile Ile Val Thr Cys Gln Gly Gly Asp Tyr Thr Asn Glu

65 70 75 80

Ile Tyr Pro Lys Leu Arg Glu Ser Gly Trp Gln Gly Tyr Trp Ile Asp

85 90 95

Ala Ala Ser Ser Leu Arg Met Lys Asp Asp Ala Ile Ile Ile Leu Asp

100	105	110	
Pro Val Asn Gln Asp Val Ile Thr Asp Gly Leu Asn Asn Gly Ile Arg			
115	120	125	
Thr Phe Val Gly Gly Asn Cys Thr Val Ser Leu Met Leu Met Ser Leu			
130	135	140	
Gly Gly Leu Phe Ala Asn Asp Leu Val Asp Trp Val Ser Val Ala Thr			
145	150	155	160
Tyr Gln Ala Ala Ser Gly Gly Gly Ala Arg His Met Arg Glu Leu Leu			
165	170	175	
Thr Gln Met Gly His Leu Tyr Gly His Val Ala Asp Glu Leu Ala Thr			
180	185	190	
Pro Ser Ser Ala Ile Leu Asp Ile Glu Arg Lys Val Thr Thr Leu Thr			
195	200	205	
Arg Ser Gly Glu Leu Pro Val Asp Asn Phe Gly Val Pro Leu Ala Gly			
210	215	220	
Ser Leu Ile Pro Trp Ile Asp Lys Gln Leu Asp Asn Gly Gln Ser Arg			
225	230	235	240
Glu Glu Trp Lys Gly Gln Ala Glu Thr Asn Lys Ile Leu Asn Thr Ser			

245 250 255

Ser Val Ile Pro Val Asp Gly Leu Cys Val Arg Val Gly Ala Leu Arg

260 265 270

Cys His Ser Gln Ala Phe Thr Ile Lys Leu Lys Lys Asp Val Ser Ile

275 280 285

Pro Thr Val Glu Glu Leu Leu Ala Ala His Asn Pro Trp Ala Lys Val

290 295 300

Val Pro Asn Asp Arg Glu Ile Thr Met Arg Glu Leu Thr Pro Ala Ala

305 310 315 320

Val Thr Gly Thr Leu Thr Thr Pro Val Gly Arg Leu Arg Lys Leu Asn

325 330 335

Met Gly Pro Glu Phe Leu Ser Ala Phe Thr Val Gly Asp Gln Leu Leu

340 345 350

Trp Gly Ala Ala Glu Pro Leu Arg Arg Met Leu Arg Gln Leu Ala

355 360 365

<210> 23

<211> 933

<212> DNA

<213> Escherichia coli

<220>

<221> gene

<222> (1)..(933)

<223> homoserine O-succinyl transferase

<400> 23

atggttaaag ttatgcccc ggcttcagtg gccaatatga gcgtcgggtt tgatgtgctc 60

ggggcggcgg tgacacctgt tgatggtgca ttgctcggag atgtagtcac ggttgaggcg 120

gcagagacat tcagtctcaa caacctcgga cgctttgccg ataagctgcc gtcagaacca 180

cgggaaaata tcgtttatca gtgctgggag cgtttttgcc aggaactggg taagcaaatt 240

ccagtggcga tgacctgga aaagaatatg ccgatcggtt cgggcttagg ctccagtgcc 300

tgttcgggtg tcgcggcgct gatggcgatg aatgaacact gcggcaagcc gcttaatgac 360

actcgtttgc tggctttgat gggcgagctg gaaggccgta tctccggcag cattcattac 420

gacaacgtgg caccgtgttt ttcggtggt atgcagttga tgatcgaaga aaacgacatc 480

atcagccagc aagtgccagg gtttgatgag tggctgtggg tgctggcgta tccggggatt 540

aaagtctcga cggcagaagc cagggctatt ttaccggcgc agtatcgccg ccaggattgc 600

attgcgcacg ggcgacatct ggcaggcttc attcacgcct gctattcccg tcagcctgag 660

cttgccgca agctgatgaa agatgttatc gctgaaccct accgtgaacg gttactgcca 720

ggcttcggc aggcgcggca ggcggtcgcg gaaatcggcg cggtagcgag cggtatctcc 780

ggctccggcc cgaccttgtt cgctctgtgt gacaagccgg aaaccgccca gcgcgttgcc 840

gactggttgg gtaagaacta cctgcaaaat caggaaggtt ttgtcatat ttgccggctg 900

gatacggcgg gcgcacgagt actggaaaac taa 933

<210> 24

<211> 930

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant polypeptide having homoserine O-acetyl transferase
activity, metA EL

<400> 24

atgccgattc gtgtgccgga cgagctaccc gccgtcaatt tcttgcgtga agaaaacgtc 60

tttgtgatga caacttctcg tgcgtctggt caggaaattc gtccacttaa ggttctgac 120

cttaacctga tgccgaagaa gattgaaact gaaaatcagt ttctgagcct gcttcaaac 180

tcacctttgc aggtcgatat tcagctgttg cgcacgatt cccgtgaatc gcgcaacacg 240

cccgagagc atctgaacaa cttctactgt aacttgaag atattcagga tcagaacttt 300

gacggttga ttgtaactgg tgcgccgtg gaactggtgg agtttaatga tgtcgcttac 360

tggccgcaga tcaaacaggt gctggagtgg tcgaaagatc acgtcacctc gacgctgttt 420

gtctgctggg cggtagagc cgcgtcaat atcctctac gcattcctaa gcaaactcg 480

accgaaaaac tctctggcgt ttacgagcat catattctcc atcctcatgc gcttctgacg 540

cgtggctttg atgattcatt cctggcaccg cattcgcgt atgctgactt tccggcagcg 600

ttgattcgtg attacaccga tctggaatt ctggcagaga cggaagaagg ggatgcatat 660

ctgtttgcca gtaaagataa gcgcattgcc tttgtgacgg gccatcccga atatgatgcg 720

caaacgctgg cgcaggaatt tttccgcat gtggaagccg gactagaccc ggatgtaccg 780

tataactatt tccgcacaa tgatccgcaa aatacaccgc gagcgagctg gcgtagtcac 840

ggtaatttac tgttaccaa ctggctcaac tattacgtct accagatcac gccatacgat 900

ctacggcaca tgaatccaac gctggattaa 930

<210> 25

<211> 930

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant polypeptide having homoserine O-acetyl transferase
activity, metA ET

<400> 25

atgccgattc gtgtgccgga cgagctaccc gccgtcaatt tcttgcgtga agaaaacgtc 60

tttgtgatga caacttctcg tgcgtctggt caggaaattc gtccacttaa ggttctgatc 120

cttaacctga tgccgaagaa gattgaaact gaaaatcagt ttctg'gcct gctttcaaac 180

tcacctttgc aggtcgatat tcagctgttg cgcacgatt cccgtgaatc gcgcaacacg 240

ccgcagagc atctgaacaa cttctactgt aactttgaag atattcagga tcagaacttt 300

gacggtttga ttgtaactgg tgcgccgctg gaaaccgtgg agtttaatga tgcgcttac	360
tggccgcaga tcaaacaggt gctggagtgg tcgaaagatc acgtcacctc gacgctgttt	420
gtctgctggg cggtagagcg cgcgctcaat atcctctacg gcattcctaa gcaaactcgc	480
accgaaaaac tctctggcgt ttacgagcat catattctcc atcctcatgc gcttctgacg	540
cgtggctttg atgattcatt cctggcaccg cattcgcgct atgctgactt tccggcagcg	600
ttgattcgtg attacaccga tctggaaatt ctggcagaga cggaagaagg ggatgcatat	660
ctgtttgccg gtaaagataa gcgcattgcc tttgtgacgg gccatcccga atatgatgcg	720
caaacgctgg cgcaggaatt tttccgcgat gtggaagccg gactagaccc ggatgtaccg	780
tataactatt tccgcacaa tgatccgcaa aatacaccgc gagcgagctg gcgtagtcac	840
ggtaatttac tgtttacaa ctggctcaac tattacgtct accagatcac gccatacgat	900
ctacggcaca tgaatccaac gctggattaa	930

<210> 26

<211> 930

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant polypeptide having homoserine O-acetyl transferase
activity, metA EH

<400> 26

atgccgattc gtgtgccgga cgagctaccc gccgtcaatt tcttgcgtga agaaaacgtc 60

tttgtgatga caacttctcg tgcgtctggt caggaaattc gtccacttaa ggttctgac 120

cttaacctga tgccgaagaa gattgaaact gaaaatcagt ttctgcgctt gcttcaaac 180

tcacctttgc aggtcgatat tcagctgttg cgcacgatt cccgtgaatc gcgcaacacg 240

ccgcagagc atctgaacaa cttctactgt aactttgaag atattcagga tcagaacttt 300

gacggtttga ttgtaactgg tgcgccgctg gaacatgtgg agtttaatga tgcgcttac 360

tggccgcaga tcaaacaggt gctggagtgg tcgaaagatc acgtcacctc gacgctgttt 420

gtctgtctgg cggtacaggc cgcgctcaat atcctctacg gcattcctaa gcaaactcgc 480

accgaaaaac tctctggcgt ttacgagcat catattctcc atcctcatgc gcttctgacg 540

cgtggctttg atgattcatt cctggcaccg cattcgcgct atgctgactt tccggcagcg 600

ttgattcgtg attacaccga tctggaaatt ctggcagaga cggaagaagg ggatgcatat 660

ctgtttgccg gtaaagataa gcgcattgcc tttgtgacgg gccatcccga atatgatgcg 720

caaacgctgg cgcaggaatt tttccgcgat gtggaagccg gactagaccc ggatgtaccg 780

tataactatt tcccgcacaa tgatccgcaa aatacaccgc gagcgagctg gcgtagtcac 840

ggtaatttac tgtttacaa ctggctcaac tattacgtct accagatcac gccatacgat 900

ctacggcaca tgaatccaac gctggattaa 930

<210> 27

<211> 2652

<212> DNA

<213> Escherichia coli

<220>

<221> gene

<222> (1)..(2652)

<223> phosphoenolpyruvate carboxylase

<400> 27

atgaacgaac aatattccgc attgcgtagt aatgtcagta tgctcggcaa agtgctggga 60

gaaacatca aggatgcgtt gggagaacac attcttgaac gcgtagaaac tatccgtaag	120
ttgtcgaaat cttcacgcgc tggcaatgat gctaaccgcc aggagttgct caccacctta	180
caaaatttgt cgaacgacga gctgctgccc gttgcgcgtg cgtttagtca gttcctgaac	240
ctggccaaca ccgccgagca ataccacagc atttcgccga aaggcgaagc tgccagcaac	300
ccggaagtga tcgcccgcac cctgcgtaaa ctgaaaaacc agccggaact gagcgaagac	360
accatcaaaa aagcagtgga atcgctgtcg ctggaactgg tcctcacggc tcaccaacc	420
gaaattaccc gtcgtacct gatccacaaa atggtggaag tgaacgcctg tttaaacag	480
ctcgataaca aagatatcgc tgactacgaa cacaaccagc tgatgcgtcg cctgcgccag	540
ttgatcgccc agtcatggca taccgatgaa atccgtaagc tgcgtccaag cccggtagat	600
gaagccaaat ggggctttgc cgtagtggaa aacagcctgt ggcaaggcgt accaaattac	660
ctgcgcgaac tgaacgaaca actggaagag aacctcggt acaaactgcc cgtcgaattt	720
gttcgggtcc gttttacttc gtggatgggc ggcgaccgcg acggcaacct gaacgtcact	780
gccgatatca cccgccacgt cctgtactc agccgctgga aagccaccga tttgttcctg	840

aaagatattc aggtgctggt ttctgaactg tcgatggtg aagcgacccc tgaactgctg	900
gcgctggttg gcgaagaagg tgccgcagaa ccgtatcgct atctgatgaa aaacctgcgt	960
tctcgctga tggcgacaca ggcatggctg gaagcgcgcc tgaaaggcga agaactgcca	1020
aaaccagaag gcctgtgac aaaaaacgaa gaactgtggg aaccgctcta cgcttgctac	1080
cagtcacttc aggcgtgtgg catgggtatt atcgccaacg gcgatctgct cgacaccctg	1140
cgccgcgtga aatgtttcgg cgtaccgctg gtccgtattg atatccgtca ggagagcacg	1200
cgctataccg aagcgctggg cgagctgacc cgctacctcg gtatcggcga ctacgaaagc	1260
tggtcagagg ccgacaaaca ggcgctcctg atccgcgaac tgaactcaa acgtccgctt	1320
ctgccgcga actggcaacc aagcgccgaa acgcgcgaag tgctcgatac ctgccaggtg	1380
attgccgaag caccgcaagg ctccattgcc gcctacgtga tctcgatggc gaaaacgccg	1440
tccgacgtac tggctgtcca cctgtgctg aaagaagcgg gtatcgggtt tgcgatgccg	1500
gttgctccgc tgtttgaaac cctcgatgat ctgaacaacg ccaacgatgt catgaccag	1560
ctgctcaata ttgactggta tcgtggcctg attcagggca aacagatggt gatgattggc	1620
tattccgact cagcaaaaga tgcgggagtg atggcagctt cctgggcgca atatcaggca	1680

caggatgcat taatcaaac ctgcgaaaaa gcgggtattg agctgacgtt gttccacggt	1740
cgcggcgggt ccattggtcg cggcggcgca cctgctcatg cggcgtgct gtcacaaccg	1800
ccaggaagcc tgaaaggcgg cctgcgcgta accgaacagg gcgagatgat ccgctttaa	1860
tatggtctgc cagaaatcac cgtcagcagc ctgtcgctt ataccggggc gattctggaa	1920
gccaacctgc tgccaccgcc ggagccgaaa gagagctggc gtcgcattat ggatgaactg	1980
tcagtcatct cctgcgatgt ctaccgcggc tacgtacgtg aaaacaaaga tttgtgcct	2040
tacttccgct ccgctacgcc ggaacaagaa ctgggcaaac tgccgttggg ttcacgtccg	2100
gcgaaacgtc gcccaaccgg cggcgtcgag tcactacgcg ccattccgtg gatcttcgcc	2160
tggacgcaa accgtctgat gctccccgcc tggctgggtg caggtacggc gctgcaaaaa	2220
gtggtcgaag acggcaaaca gagcgagctg gaggctatgt gccgcgattg gccattcttc	2280
tcgacgctc tcggcatgct ggagatggtc ttcgcaaag cagacctgtg gctggcggaa	2340
tactatgacc aacgcctggt agacaaagca ctgtggccgt taggtaaaga gttacgcaac	2400
ctgcaagaag aagacatcaa agtggtgctg gcgattgcca acgattcca tctgatggcc	2460

gatctgccgt ggattgcaga gtctattcag ctacggaata ttacaccga cccgctgaac 2520

gtattgcagg ccgagttgct gcaccgtcc cgccaggcag aaaaagaagg ccaggaaccg 2580

gacctcgcg tcgaacaagc gttaatggc actattgccg ggattgcggc aggtatgcgt 2640

aataccggct aa 2652

<210> 28

<211> 1191

<212> DNA

<213> Escherichia coli

<220>

<221> gene

<222> (1)..(1191)

<223> aspartate aminotransferase

<400> 28

atgtttgaga acattaccgc cgctcctgcc gaccgattc tgggcctggc cgatctgttt 60

cgtgccgatg aacgtcccgg caaaattaac ctccgggattg gtgtctataa agatgagacg 120

ggcaaaaccc cggctactgac cagcgtgaaa aaggctgaac agtatctgct cgaaaatgaa 180

accaccaaaa attacctcgg cattgacggc atccctgaat ttggtcgtg cactcaggaa	240
ctgctgtttg gtaaaggtag cgccctgac aatgacaaac gtgctgcac ggcacagact	300
ccggggggca ctggcgact acgcgtggct gccgatttcc tggcaaaaaa taccagcgtt	360
aagcgtgtgt gggtagagcaa cccaagctgg ccgaaccata agagcgtctt taactctgca	420
ggtctggaag ttcgtgaata cgcttattat gatgcggaaa atcacactct tgacttcgat	480
gcactgatta acagcctgaa tgaagctcag gctggcgacg tagtgctgtt ccatggctgc	540
tgccataacc caaccgtat cgaccctacg ctggaacaat ggcaaacact ggcacaactc	600
tccgttgaga aaggctggtt accgctgtt gacttcgctt accagggttt tgcccgtggt	660
ctggaagaag atgctgaagg actgcgcgct ttcgcgcta tgcataaaga gctgattgtt	720
gccagttcct actctaaaaa cttggcctg tacaacgagc gtgttggcgc ttgtactctg	780
gttgctgccg acagtgaac cgttgatcgc gcattcagcc aaatgaaagc ggcgattcgc	840
gctaactact ctaaccacc agcacacggc gcttctgtt ttgccacat cctgagcaac	900
gatgcgttac gtgcgatttg ggaacaagag ctgactgata tgcgccagcg tattcagcgt	960
atgcgtcagt tgttcgtcaa tacgtgcag gaaaaaggcg caaacgcga cttcagcttt	1020

atcatcaaac agaacggcat gttctccttc agtggcctga caaaagaaca agtgctgcgt 1080

ctgcgcgaag agtttggcgt atatgcggtt gcttctggtc gcgtaaatgt ggccgggatg 1140

acaccagata acatggctcc gctgtgcgaa gcgattgtgg cagtgcgtga a 1191

<210> 29

<211> 1104

<212> DNA

<213> Escherichia coli

<220>

<221> gene

<222> (1)..(1104)

<223> aspartate-semialdehyde dehydrogenase

<400> 29

atgaaaaatg ttggttttat cggctggcgc ggtatggtcg gctccgttct catgcaacgc 60

atggttgaag agcgcgactt cgacgccatt cgcctgtct tcttttctac ttctcagctt 120

ggccaggctg cgccgtcttt tggcggaacc actggcacac ttcaggatgc ctttgatctg 180

gaggcgctaa aggccctcga tatcatttg acctgtcagg gcggcgatta taccaacgaa 240

atctatccaa agcttcgtga aagcggatgg caaggttact ggattgacgc agcatcgtct	300
ctgcgcatga aagatgacgc catcatcatt cttgaccccg tcaatcagga cgtcattacc	360
gacggattaa ataatggcat caggactttt gttggcgga actgtaccgt aagcctgatg	420
ttgatgtcgt tgggtggttt attcgccaat gatcttgttg attgggtgtc cgttgcaacc	480
taccaggccg cttccggcgg tggcgcgga catatgcgtg agttattaac ccagatgggc	540
catctgtatg gccatgtggc agatgaactc gcgaccccg cctctgctat tctcgatac	600
gaacgcaaag tcacaacctt aaccgtagc ggtgagctgc cggtgataa ctttggcgtg	660
ccgctggcgg gtagcctgat tccgtggatc gacaaacagc tcgataacgg tcagagccgc	720
gaagagtga aagggcaggc ggaaccaac aagatcctca acacatcttc cgtaattccg	780
gtagatggtt tatgtgtcgc tgcggggca ttgcgtgcc acagccaggc attcactatt	840
aaattgaaaa aagatgtgtc tattccgacc gtggaagaac tgctggctgc gcacaatccg	900
tgggcgaaag tcgttccgaa cgatcgggaa atcactatgc gtgagctaac cccagctgcc	960
gttaccggca cgctgaccac gccggtaggc cgcctgcgta agctgaatat gggaccagag	1020

ttcctgtcag cctttaccgt gggcgaccag ctgctgtggg gggccgcgga gccgctgcgt 1080

cggatgcttc gtcaactggc gtaa 1104

<210> 30

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 30

ttactctggt gcctgacatt tcaccgacaa agcccaggga acttcacac gtgtaggctg 60

gagctgcttc 70

<210> 31

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 31

ttacccttg ttgcagccc ggaagccatt ttccaggtcg gcaattaaat catatgaata 60

tcctccttag 70

<210> 32

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 32

aaagaatatg ccgatcggtt cgggcttagg ctccagtgcc tggtcggtgg gtgtaggctg 60

gagctgcttc 70

<210> 33

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 33

agacaaccga catcgctttc aacattggcg accggagccg ggaaggcaaa catatgaata 60

tcctccttag 70

<210> 34

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 34

aattgatatc atgccgattc gtgtgccgg 29

<210> 35

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 35

aattaagctt ttaatccagc gttggattca tgtg 34

<210> 36

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 36

ttgtaactgg tgcgccgctg gaactggtgg ggtttaatga tgtc 44

<210> 37

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 37

gacatcatta aacccaccca gttccagcgg cgcaccagtt acaa 44

<210> 38

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 38

tgtaactggt gcgccgctgg aacatgtggg gtttaatgat gtcg 44

<210> 39

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 39

cgacatcatt aaacccaca tgtccagcg gcgcaccagt taca 44

<210> 40

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 40

tttcgaaac gtacctcagc aggtgtaggc tggagctgct tc 42

<210> 41

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 41

gaataaaatt tattcacctg ctgcatatga atatcctcct tag 43

<210> 42

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 42

aattgatatc atgccgattc gtgtgccgg 29

<210> 43

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 43

aattaagcct gctgaggtac gtttcgg

27

<210> 44

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 44

cagcaggtga ataaatttta ttc

23

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 45

cgcgaatgga agctgtttcc

20

<210> 46

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 46

gccggaattc tgcggatgc gatactgcg c

31

<210> 47

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 47

gaaggagctc agaaaaccct cgcgcaaaag

30

<210> 48

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 48

gccggagctc tgcggatgc gatacttgcg c

31

<210> 49

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 49

gaagggtacc agaaaaccct cgcgcaaaag

30

<210> 50

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 50

tccgagctca taagcgtagc gcatcaggca

30

<210> 51

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 51

tccgagctcg tccacctatg ttgactacat

30

<210> 52

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 52

ccggaattcc caggagagca ataagca

27

<210> 53

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 53

ctagtctaga tgctctattt aactcccg

28

<210> 54

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 54

ctagtctaga ccaggagagc aataagca 28

<210> 55

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 55

ccggaattct gctctattta actcccg 27

<210> 56

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 56

aggcgctaag gagaccttaa atggctgata caaaagcaaa actcacctc tgtaggctgg 60

agctgcttcg 70

<210> 57

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 57

gggttaaaat attacaact tagcaatcaa ccattaacgc ttgatatcgc atgggaatta 60

gccatggtcc

70

<210> 58

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 58

cctttctata actgcgctc at

22

<210> 59

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 59

aggggtatag ctaccaga a

21

<210> 60

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 60

gaaggcaaat ttaagttccg 20

<210> 61

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 61

cgaagcagct ccagcctaca ggtatagata gacgtcattt 40

<210> 62

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 62

cggcgcgctg gcggcggttcg cgcacgactc gctggatgtt aa

42

<210> 63

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 63

ttaacatcca gcgagtcgtg cgcgaacgcc gccagcgcgc cg

42

<210> 64

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 64

cgcgttccgc ctgctgtcgg cgatgccgac catggccgcg at 42

<210> 65

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 65

atcgcggccca tggtcggcat cgccgacagc aggcggaacg cg 42

<210> 66

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 66

tcctgaatat gatgttctcc gcgccgtgcg aaccgtatga 40

<210> 67

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 67

tcatacggtt cgcacggcgc ggagaacatc atattcagga 40

<210> 68

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 68

aaatgacgtc tatctatacc ttaggctgg agctgcttcg 40

<210> 69

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 69

gcaaaactaa attattgga tcatgaattt gttgtatgat gaataaaata taggggatgg 60

gaattagcca tgggcc 76

<210> 70

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 70

ccatggagga ggaattaacc atgcagtggg ggtgggtggg gtgcgataac agctgtatcc 60

ccgttga 67

<210> 71

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 71

aagcttagga ggaattaacc atgcagtggg ggtgggtggg gtgcatgca aatttaagtt 60

ccggcag 67