

eolf-othd-000002.txt  
SEQUENCE LISTING

<110> BASF Aktiengesellschaft  
<120> BASF Aktiengesellschaft  
<130> B 8571 / DB  
<150> EP 07 102 257.9  
<151> 19.02.2007  
<160> 35  
<170> PatentIn version 3.3  
<210> 1  
<211> 1545  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> nucleic acid sequence  
<222> (1)..(1545)  
<223> glucose-6-phosphate-dehydrogenase

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gctcgaaaga agctgctccc cgccatttat gatctagcaa accgcggatt gctgccccca    180
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ccaatttctt tcgtgccagc gcagctgcag gcagaaaaga tcaagggtgct ctctgcgaca    900
aagccgtgct acccattgga taaaacctcc gctcgtggtc agtacgctgc cggttggcag    960
ggctctgagt tagtcaaggg acttcgcgaa gaagatggct tcaaccctga gtccaccact   1020
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gacgcaccac accagccttt cgacggcgac atgactgtat cccttgcca aaacgccatc   1200
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tctgccatgg aagtccgtga cgtcaacatg gacttctcct actcagaatc cttcactgaa 1320  
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<210> 2  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<220>  
 <221> amino acid sequence  
 <222> (1)..(514)  
 <223> glucose-6-phosphate-dehydrogenase

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Met Ser Thr Asn Thr Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp  
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 35 40 45

Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu  
 50 55 60

Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr  
 65 70 75 80

Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn  
 85 90 95

Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe  
 100 105 110

Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile  
 115 120 125

Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile  
 130 135 140

Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly  
 145 150 155 160

Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys  
 165 170 175

Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val

180

185

190

Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu  
 195 200 205

Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln  
 210 215 220

Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile  
 225 230 235 240

Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp  
 245 250 255

Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu  
 260 265 270

Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln  
 275 280 285

Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr  
 290 295 300

Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln  
 305 310 315 320

Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro  
 325 330 335

Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser  
 340 345 350

Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu  
 355 360 365

Gly Arg Arg Val Thr Glu Ile Ala Val Val Phe Lys Asp Ala Pro His  
 370 375 380

Gln Pro Phe Asp Gly Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile  
 385 390 395 400

Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser  
 405 410 415

Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe  
 420 425 430

Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg  
 435 440 445

Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn  
 450 455 460

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Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala  
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Arg Pro

<210> 3  
<211> 708  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> nucleic acid sequence  
<222> (1)..(708)  
<223> 6-phosphogluconolactonase

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<211> 235  
<212> PRT  
<213> Corynebacterium glutamicum

<220>  
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<222> (1)..(235)  
<223> 6-phosphogluconolactonase

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Leu Glu Lys Leu Ser Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile
      50      55      60
His Val Phe Phe Gly Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu
      65      70      75      80
Ser Asn Glu Gly Gln Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile
      85      90      95
Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala
      100      105      110
Glu Ala Ala Arg Ala Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn
      115      120      125
Gly Phe Asp Leu His Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn
      130      135      140
Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val
      145      150      155      160
Ile Ala Val Phe Asp Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu
      165      170      175
Thr Leu Pro Ala Val His Ser Ala Lys Arg Val Trp Leu Leu Val Ser
      180      185      190
Gly Ala Glu Lys Ala Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro
      195      200      205
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Leu Phe Leu Ala Asp Asp Ala Ala Gly Asn Leu
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<210> 5
<211> 1455
<212> DNA
<213> Corynebacterium glutamicum

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<220>
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<222> (1)..(1455)
<223> 6-phospho-gluconate-dehydrogenase

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accgtcgaag agttcgtagc atccctggaa aagccacgcc gcgccatcat catggttcag 240
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atcatcatcg acggcggcaa cgccctctac accgacacca ttcgtcgcga gaaggaaatc 360
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<210> 6
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

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<220>
<221> amino acid sequence
<222> (1)..(483)
<223> phospho-gluconate-dehydrogenase

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<220>
<221> amino acid sequence
<222> (1)..(484)
<223> phospho-gluconate-dehydrogenase

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

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Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala  
275 280 285

Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala  
290 295 300

Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly  
305 310 315 320

Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala  
325 330 335

Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly  
340 345 350

Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile  
355 360 365

Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val  
370 375 380

Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro  
385 390 395 400

Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val  
405 410 415

Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser  
420 425 430

Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala  
435 440 445

Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg  
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Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser  
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Glu Val Glu Ala

<210> 7  
<211> 660  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> nucleic acid sequence  
<222> (1)..(660)  
<223> ribulose-5-phosphate epimerase

<400> 7



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gccaaagacca tcaagcaggc tgccgacgct ggcgtggatg ccttcgttgc aggttccgct    600
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<210> 8
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

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<220>
<221> amino acid sequence
<222> (1)..(219)
<223> ribulose-5-phosphate epimerase

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<400> 8

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Met Ala Gln Arg Thr Pro Leu Ile Ala Pro Ser Ile Leu Ala Ala Asp
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Phe Ser Arg Leu Gly Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp
          20           25           30

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Ile His Val Asp Ile Met Asp Gly His Phe Val Pro Asn Leu Ser Phe
        35           40           45

```

```

Gly Ala Asp Ile Thr Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu
        50           55           60

```

```

Asp Val His Leu Met Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr
65           70           75           80

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Ile Asp Ala Gly Ala Asp Cys Ile Val Phe His Val Glu Ala Thr Glu
          85           90           95

```

```

Gly His Val Glu Leu Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala
        100          105          110

```

```

Gly Phe Ser Leu Arg Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp
        115          120          125

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```

Leu Glu His Phe Asp Glu Val Ile Val Met Ser Val Glu Pro Gly Phe

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130

135

140

Gly Gly Gln Ser Phe Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu  
 145 150 155 160

Arg Lys Val Ile Asp Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp  
 165 170 175

Gly Gly Ile Ser Ala Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val  
 180 185 190

Asp Ala Phe Val Ala Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn  
 195 200 205

Lys Ala Ile Gln Glu Leu Arg Ala Leu Ala Gln  
 210 215

<210> 9  
 <211> 474  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> nucleic acid sequence  
 <222> (1)..(474)  
 <223> ribose-5-phosphate isomerase

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 <211> 157  
 <212> PRT  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(157)  
 <223> ribose-5-phosphate isomerase

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20 25 30

Gly Ala His Thr Tyr Asp Ala Glu Asp Asp Tyr Pro Ala Phe Cys Ile  
35 40 45

Glu Ala Ala Ser Arg Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val  
50 55 60

Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys  
65 70 75 80

Gly Ala Arg Cys Ala Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala  
85 90 95

Arg Glu His Asn Asn Ala Asn Leu Ile Gly Ile Gly Gly Arg Met His  
100 105 110

Ser Glu Glu Glu Ala Leu Ala Ile Val Asp Ala Phe Leu Glu Gln Glu  
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Trp Ser Asn Ala Glu Arg His Gln Arg Arg Ile Asp Ile Leu Ala Asp  
130 135 140

Tyr Glu Arg Thr Gly Ile Ala Pro Val Val Pro Asn Glu  
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<210> 11  
<211> 2103  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (1)..(2103)  
<223> transketolase

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tccaagggaa cccagatgt gatcctcatg ggctccggct ccgagggtca gcttgcagtt 1800
aacgtgcga aggtcttgga agctgagggc gttgcagctc gcgttgtttc cgttccttgc 1860
atggattggt tccaggagca ggacgcagag tacatcgagt ccgttctgcc tgcagctgtg 1920
accgctcgtg tgtctgttga agctggcatc gcaatgcctt ggtaccgctt cttgggcacc 1980
cagggccgtg ctgtctccct tgagcacttc ggtgcttctg cggattacca gaccctgttt 2040
gagaagttcg gcatcaccac cgatgcagtc gtggcagcgg ccaaggactc cattaacggt 2100
taa 2103

```

```

<210> 12
<211> 700
<212> PRT
<213> Corynebacterium glutamicum

```

```

<220>
<221> amino acid sequence
<222> (1)..(700)
<223> transketolase

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<400> 12

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Met Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg
1           5           10          15

```

eolf-othd-000002.txt

Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr  
20 25 30

Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His  
35 40 45

Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln  
50 55 60

Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp  
65 70 75 80

Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln  
85 90 95

Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu  
100 105 110

Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr  
115 120 125

Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser  
130 135 140

Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp  
145 150 155 160

Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val  
165 170 175

Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser  
180 185 190

Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp  
195 200 205

Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu  
210 215 220

Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val  
225 230 235 240

Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala  
245 250 255

Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile  
260 265 270

Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala  
275 280 285

Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe

290

295

300

Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr  
 305 310 315 320

Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val  
 325 330 335

Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe  
 340 345 350

Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu  
 355 360 365

Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser  
 370 375 380

Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly  
 385 390 395 400

Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser  
 405 410 415

Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu  
 420 425 430

Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly  
 435 440 445

Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly  
 450 455 460

Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu  
 465 470 475 480

Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser  
 485 490 495

Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu  
 500 505 510

Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp  
 515 520 525

Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu  
 530 535 540

Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu  
 545 550 555 560

Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val  
 565 570 575

eo1f-othd-000002.txt

Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser  
580 585 590

Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala  
595 600 605

Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe  
610 615 620

Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val  
625 630 635 640

Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg  
645 650 655

Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala  
660 665 670

Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp  
675 680 685

Ala Val Val Ala Ala Ala Lys Asp Ser Ile Asn Gly  
690 695 700

<210> 13  
<211> 1083  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> nucleic acid sequence  
<222> (1)..(1083)  
<223> Transaldolase

<400> 13  
atgtctcaca ttgatgatct tgcacagctc ggcacttcca cttggctcga cgacctctcc 60  
cgcgagcgca ttacttccgg caatctcagc cagggttattg aggaaaagtc tgtagtcggt 120  
gtcaccacca acccagctat tttcgcagca gcaatgtcca agggcgattc ctacgacgct 180  
cagatcgagc agctcaaggc cgctggcgca tctgttgacc aggctgttta cgccatgagc 240  
atcgacgacg ttcgcaatgc ttgtgatctg ttcaccggca tcttcgagtc ctccaacggc 300  
tacgacggcc gcgtgtccat cgaggttgac ccacgtatct ctgctgaccg cgacgcaacc 360  
ctggctcagg ccaaggagct gtgggcaaag gttgatcgtc caaacgtcat gatcaagatc 420  
cctgcaaccc caggttcttt gccagcaatc accgacgctt tggttgaggg catcagcggt 480  
aacgtcacct tgatcttctc cgttgctcgc taccgcgagg tcatcgctgc gttcatcgag 540  
ggcatcaagc aggctgctgc aaacggccac gacgtctcca agatccactc tgtggcttcc 600  
ttcttcgtct cccgcgtcga cgttgagatc gacaagcgcc tcgaggcaat cggatccgat 660  
gaggctttgg ctctgcgcgg caaggcaggc gttgccaacg ctacgcgcgc ttacgctgtg 720

eolf-othd-000002.txt

```
tacaaggagc ttttcgacgc cgccgagctg cctgaagggtg ccaacactca gcgcccactg 780
tgggcatcca ccggcgtgaa gaaccctgcg tacgctgcaa ctctttacgt ttccgagctg 840
gctggtccaa acaccgtcaa caccatgcca gaaggcacca tcgacgcggt tctggagcag 900
ggcaacctgc acggtgacac cctgtccaac tccgcggcag aagctgacgc tgtgttctcc 960
cagcttgagg ctctgggcgt tgacttggca gatgtcttcc aggtcctgga gaccgagggt 1020
gtggacaagt tcgttgcttc ttggagcgaa ctgcttgagt ccatggaagc tcgcctgaag 1080
tag 1083
```

```
<210> 14
<211> 360
<212> PRT
<213> Corynebacterium glutamicum
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```
<220>
<221> amino acid sequence
<222> (1)..(360)
<223> Transaldolase
```

```
<400> 14
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```
Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu
1 5 10 15
```

```
Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val
20 25 30
```

```
Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe
35 40 45
```

```
Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
50 55 60
```

```
Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
65 70 75 80
```

```
Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
85 90 95
```

```
Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
100 105 110
```

```
Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
115 120 125
```

```
Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
130 135 140
```

```
Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
145 150 155 160
```



eolf-othd-000002.txt

Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala  
165 170 175

Ala Phe Ile Glu Gly Ile Lys Gln Ala Ala Asn Gly His Asp Val  
180 185 190

Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val  
195 200 205

Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala  
210 215 220

Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val  
225 230 235 240

Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr  
245 250 255

Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala  
260 265 270

Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr  
275 280 285

Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His  
290 295 300

Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser  
305 310 315 320

Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu  
325 330 335

Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu  
340 345 350

Glu Ser Met Glu Ala Arg Leu Lys  
355 360

<210> 15  
<211> 960  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> nucleic acid sequence  
<222> (1)..(960)  
<223> C. glutamicum OCPA

<400> 15  
atgatctttg aacttccgga taccaccacc cagcaaattt ccaagaccct aactcgactg 60  
cgtgaatcgg gcaccaggt caccaccggc cgagtgtctca ccctcatcgt ggctactgac 120  
tccgaaagcg atgtcgtgc agttaccgag tccaccaatg aagcctcgcg cgagcaccca 180

eolf-othd-000002.txt

```
tctcgcgtga tcattttggt ggttggcgat aaaactgcag aaaacaaagt tgacgcagaa 240
gtccgtatcg gtggcgacgc tgggtgcttc gagatgatca tcatgcatct caacggacct 300
gtcgtgaca agctccagta tgtcgtcaca ccactgttgc ttcctgacac ccccatcggt 360
gcttgggtggc caggtgaatc accaaagaat ccttcccagg acccaattgg acgcatcgca 420
caacgacgca tcatgatgc tttgtacgac cgtgatgacg cactagaaga tcgtgttgag 480
aactatcacc caggtgatac cgacatgacg tgggcgcgcc ttaccagtg gcggggactt 540
gttgccctct cattggatca cccaccacac agcgaaatca cttccgtgag gctgaccggt 600
gcaagcggca gtacctcggg ggatttggct gcaggctggg tggcgcggag gctgaaagt 660
cctgtgatcc gcgaggtgac agatgctccc accgtgccaa ccgatgagtt tgggtactca 720
ctgctggcta tccagcgcct ggagatcggt cgcaccaccg gctcgatcat catcaccatc 780
tatgacgctc ataccttcca ggtagagatg ccggaatccg gcaatgcccc atcgctgggt 840
gctattgggtc gtcgaagtga gtccgactgc ttgtctgagg agcttcgcca catggatcca 900
gatttgggct accagcacgc actatccggc ttgtccagcg tcaagctgga aaccgtctaa 960
```

```
<210> 16
<211> 319
<212> PRT
<213> Corynebacterium glutamicum
```

```
<220>
<221> amino acid sequence
<222> (1)..(319)
<223> C. glutamicum OCPA
```

```
<400> 16
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```
Met Ile Phe Glu Leu Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr
1 5 10 15
```

```
Leu Thr Arg Leu Arg Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val
20 25 30
```

```
Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val
35 40 45
```

```
Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile
50 55 60
```

```
Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu
65 70 75 80
```

```
Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
85 90 95
```

```
Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu
100 105 110
```

eolf-othd-000002.txt

Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro  
115 120 125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile  
130 135 140

Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu  
145 150 155 160

Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln  
165 170 175

Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu  
180 185 190

Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp  
195 200 205

Leu Ala Ala Gly Trp Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg  
210 215 220

Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro  
225 230 235 240

Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile  
245 250 255

Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu  
260 265 270

Ser Gly Asn Ala Pro Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser  
275 280 285

Asp Cys Leu Ser Glu Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr  
290 295 300

Gln His Ala Leu Ser Gly Leu Ser Ser Val Lys Leu Glu Thr Val  
305 310 315

<210> 17  
<211> 445  
<212> PRT  
<213> artificial

<220>  
<223> homoserine dehydrogenase

<400> 17

Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly  
1 5 10 15

Ser Ala Val Gly Ile Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu  
20 25 30

eolf-othd-000002.txt

Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile  
35 40 45

Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys  
50 55 60

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
65 70 75 80

Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly  
85 90 95

Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys  
100 105 110

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu  
115 120 125

Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala  
130 135 140

Ala Val Ala Gly Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu  
145 150 155 160

Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr  
165 170 175

Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp  
180 185 190

Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr  
195 200 205

Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala  
210 215 220

Ser Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu  
225 230 235 240

Gly Ile Ser Asn Ile Ser Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala  
245 250 255

Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys  
260 265 270

Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro  
275 280 285

Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe  
290 295 300

eolf-othd-000002.txt

Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala  
305 310 315 320

Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala  
325 330 335

Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr  
340 345 350

Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His  
355 360 365

Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala  
370 375 380

Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu  
385 390 395 400

Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu  
405 410 415

Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val  
420 425 430

Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp  
435 440 445

<210> 18  
<211> 421  
<212> PRT  
<213> artificial

<220>  
<223> aspartate kinase

<400> 18

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala  
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
85 90 95

eolf-othd-000002.txt

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg  
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
340 345 350

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

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg  
 370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
 385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
 405 410 415

Ala Gly Thr Gly Arg  
 420

<210> 19  
 <211> 309  
 <212> PRT  
 <213> artificial

<220>  
 <223> homoserine kinase

<400> 19

Met Ala Ile Glu Leu Asn Val Gly Arg Lys Val Thr Val Thr Val Pro  
 1 5 10 15

Gly Ser Ser Ala Asn Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala  
 20 25 30

Leu Ser Val Tyr Asp Thr Val Glu Val Glu Ile Ile Pro Ser Gly Leu  
 35 40 45

Glu Val Glu Val Phe Gly Glu Gly Gln Gly Glu Val Pro Leu Asp Gly  
 50 55 60

Ser His Leu Val Val Lys Ala Ile Arg Ala Gly Leu Lys Ala Ala Asp  
 65 70 75 80

Ala Glu Val Pro Gly Leu Arg Val Val Cys His Asn Asn Ile Pro Gln  
 85 90 95

Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Ala Val Ala Gly Val Ala  
 100 105 110

Ala Ala Asn Gly Leu Ala Asp Phe Pro Leu Thr Gln Glu Gln Ile Val  
 115 120 125

Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser  
 130 135 140

Val Leu Gly Gly Ala Val Val Ser Trp Thr Asn Leu Ser Ile Asp Gly  
 145 150 155 160

Lys Ser Gln Pro Gln Tyr Ala Ala Val Pro Leu Glu Val Gln Asp Asn  
 165 170 175

eolf-othd-000002.txt

Ile Arg Ala Thr Ala Leu Val Pro Asn Phe His Ala Ser Thr Glu Ala  
180 185 190

Val Arg Arg Val Leu Pro Thr Glu Val Thr His Ile Asp Ala Arg Phe  
195 200 205

Asn Val Ser Arg Val Ala Val Met Ile Val Ala Leu Gln Gln Arg Pro  
210 215 220

Asp Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg  
225 230 235 240

Ala Glu Val Leu Pro Ile Thr Ser Glu Trp Val Asn Arg Leu Arg Asn  
245 250 255

Arg Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Ala Met Val  
260 265 270

Leu Ser Thr Glu Pro Ile Pro Asp Lys Val Leu Glu Asp Ala Arg Glu  
275 280 285

Ser Gly Ile Lys Val Leu Glu Leu Glu Val Ala Gly Pro Val Lys Val  
290 295 300

Glu Val Asn Gln Pro  
305

<210> 20  
<211> 192  
<212> DNA  
<213> artificial

<220>  
<223> promotor P3119 = PSOD

<400> 20  
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ttcgttgcaa tatcaacaaa aaggcctatc attgggaggt gtcgcaccaa gtacttttgc 120  
gaagcgccat ctgacggatt ttcaaaagat gtatatgctc ggtgcggaaa cctacgaaag 180  
gatttttttac cc 192

<210> 21  
<211> 184  
<212> DNA  
<213> artificial

<220>  
<223> promotor P497 = PgroES

<400> 21  
ggtcgagcgg cttaaagttt ggctgccatg tgaattttta gcaccctcaa cagttgagtg 60  
ctggcactct cgggggtaga gtgcaaata ggttgtttga cacacagttg ttcacccgcg 120  
acgacggctg tgctggaaac ccacaaccgg cacacacaaa atttttctca tggagggatt 180



catc 184

<210> 22  
 <211> 192  
 <212> DNA  
 <213> artificial

<220>  
 <223> promotor P1284 = PEFTU

<400> 22  
 gagctgcca ttattccggg cttgtgaccc gctacccgat aaatagggtcg gctgaaaaat 60  
 ttcgttgcaa tatcaacaaa aaggcctatc attgggaggt gtcgcaccaa gtacttttgc 120  
 gaagcgccat ctgacggatt ttcaaaagat gtatatgtc ggtgcggaaa cctacgaaag 180  
 gattttttac cc 192

<210> 23  
 <211> 114  
 <212> DNA  
 <213> artificial

<220>  
 <223> promotor

<400> 23  
 gtcgactcat acgttaaadc tatcaccgca agggataaat atctaaccac gtgcgtgttg 60  
 actattttac ctctggcggt gataatgggt gcatgtacta aggaggatta atta 114

<210> 24  
 <211> 7070  
 <212> DNA  
 <213> artificial

<220>  
 <223> Plasmid pH273

<400> 24  
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 cctcagcatc tgccccaagc ttttaacccc gcaagggtcc cggctcagca gtcggaattg 120  
 cccttttagg attcggaaca gtcggcactg aggtgatgcg tctgatgacc gactacgggtg 180  
 atgaacttgc gcaccgcatt ggtggccac tggaggttcg tggcattgct gtttctgata 240  
 tctcaaagcc acgtgaaggc gttgcacctg agctgctcac tgaggacgct tttgactca 300  
 tcgagcgcga ggatgttgac atcgtcgttg aggttatcgg cggcattgag taccacgtg 360  
 aggtagtctt cgcagctctg aaggccggca agtctgttgt taccgccaat aaggctcttg 420  
 ttgcagctca ctctgctgag cttgctgatg cagcggaaag cgcaaacgtt gacctgtact 480  
 tcgaggctgc tgttgaggc gcaattccag tgggtggccc actgcgtcgc tccctggctg 540  
 gcgatcagat ccagtctgtg atgggcatcg ttaacggcac caccaacttc atcttgacg 600  
 ccatggattc caccggcgct gactatgcag attctttggc tgaggcaact cgtttgggtt 660  
 acgccgaagc tgatccaact gcagacgtcg aaggccatga cgccgcatcc aaggctgcaa 720

eo1f-othd-000002.txt

ttttggcatc	catcgctttc	cacacccgtg	ttaccgcgga	tgatgtgtac	tgcaaggta	780
tcagcaacat	cagcgctgcc	gacattgagg	cagcacagca	ggcaggccac	accatcaagt	840
tgttggccat	ctgtgagaag	ttcaccaaca	aggaaggaaa	gtcggctatt	tctgctcgcg	900
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