Figure 1: DNA and protein sequence of A. calcoaceticus s-GDH (without signalpeptide)

```
    1 GATGTTCCTCTAACTCCATCTCAATTTGCTAAAGCGAAATCAGAGAACTT 50
      ||||||||||||||||||||||||||||||||||||||||||||||||||
    1 AspValProLeuThrProSerGlnPheAlaLysAlaLysSerGluAsnPh 17

   51 TGACAAGAAAGTTATTCTATCTAATCTAAATAAGCCGCACGCGTTGTTAT 100
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   18 eAspLysLysValIleLeuSerAsnLeuAsnLysProHisAlaLeuLeuT 34

  101 GGGGACCAGATAATCAAATTTGGTTAACTGAGCGAGCAACAGGTAAGATT 150
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   35 rpGlyProAspAsnGlnIleTrpLeuThrGluArgAlaThrGlyLysIle 50

  151 CTAAGAGTTAATCCAGAGTCGGGTAGTGTAAAAACAGTTTTTCAGGTACC 200
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   51 LeuArgValAsnProGluSerGlySerValLysThrValPheGlnValPr 67

  201 AGAGATTGTCAATGATGCTGATGGGCAGAATGGTTTATTAGGTTTTGCCT 250
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   68 oGluIleValAsnAspAlaAspGlyGlnAsnGlyLeuLeuGlyPheAlaP 84

  251 TCCATCCTGATTTTAAAAATAATCCTTATATCTATATTTCAGGTACATTT 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   85 heHisProAspPheLysAsnAsnProTyrIleTyrIleSerGlyThrPhe 100

  301 AAAAATCCGAAATCTACAGATAAAGAATTACCGAACCAAACGATTATTCG 350
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  101 LysAsnProLysSerThrAspLysGluLeuProAsnGlnThrIleIleAr 117

  351 TCGTTATACCTATAATAAATCAACAGATACGCTCGAGAAGCCAGTCGATT 400
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  118 gArgTyrThrTyrAsnLysSerThrAspThrLeuGluLysProValAspL 134

  401 TATTAGCAGGATTACCTTCATCAAAAGACCATCAGTCAGGTCGTCTTGTC 450
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  135 euLeuAlaGlyLeuProSerSerLysAspHisGlnSerGlyArgLeuVal 150

  451 ATTGGGCCAGATCAAAAGATTTATTATACGATTGGTGACCAAGGGCGTAA 500
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  151 IleGlyProAspGlnLysIleTyrTyrThrIleGlyAspGlnGlyArgAs 167

  501 CCAGCTTGCTTATTTGTTCTTGCCAAATCAAGCACAACATACGCCAACTC 550
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  168 nGlnLeuAlaTyrLeuPheLeuProAsnGlnAlaGlnHisThrProThrG 184

  551 AACAAGAACTGAATGGTAAAGACTATCACACCTATATGGGTAAAGTACTA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  185 lnGlnGluLeuAsnGlyLysAspTyrHisThrTyrMetGlyLysValLeu 200

  601 CGCTTAAATCTTGATGGAAGTATTCCAAAGGATAATCCAAGTTTTAACGG 650
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  201 ArgLeuAsnLeuAspGlySerIleProLysAspAsnProSerPheAsnGl 217

  651 GGTGGTTAGCCATATTTATACACTTGGACATCGTAATCCGCAGGGCTTAG 700
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  218 yValValSerHisIleTyrThrLeuGlyHisArgAsnProGlnGlyLeuA 234

  701 CATTCACTCCAAATGGTAAATTATTGCAGTCTGAACAAGGCCCAAACTCT 750
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  235 laPheThrProAsnGlyLysLeuLeuGlnSerGluGlnGlyProAsnSer 250
```

Figure 1: Continued (second and last page)

```
751 GACGATGAAATTAACCTCATTGTCAAAGGTGGCAATTATGGTTGGCCGAA 800
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
251 AspAspGluIleAsnLeuIleValLysGlyGlyAsnTyrGlyTrpProAs 267

801 TGTAGCAGGTTATAAAGATGATAGTGGCTATGCTTATGCAAATTATTCAG 850
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
268 nValAlaGlyTyrLysAspAspSerGlyTyrAlaTyrAlaAsnTyrSerA 284

851 CAGCAGCCAATAAGTCAATTAAGGATTTAGCTCAAAATGGAGTAAAAGTA 900
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
285 laAlaAlaAsnLysSerIleLysAspLeuAlaGlnAsnGlyValLysVal 300

901 GCCGCAGGGGTCCCTGTGACGAAAGAATCTGAATGGACTGGTAAAAACTT 950
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
301 AlaAlaGlyValProValThrLysGluSerGluTrpThrGlyLysAsnPh 317

951 TGTCCCACCATTAAAAACTTTATATACCGTTCAAGATACCTACAACTATA 1000
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
318 eValProProLeuLysThrLeuTyrThrValGlnAspThrTyrAsnTyrA 334

1001 ACGATCCAACTTGTGGAGAGATGACCTACATTTGCTGGCCAACAGTTGCA 1050
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
335 snAspProThrCysGlyGluMetThrTyrIleCysTrpProThrValAla 350

1051 CCGTCATCTGCCTATGTCTATAAGGGCGGTAAAAAAGCAATTACTGGTTG 1100
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
351 ProSerSerAlaTyrValTyrLysGlyGlyLysLysAlaIleThrGlyTr 367

1101 GGAAAATACATTATTGGTTCCATCTTTAAAACGTGGTGTCATTTTCCGTA 1150
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
368 pGluAsnThrLeuLeuValProSerLeuLysArgGlyValIlePheArgI 384

1151 TTAAGTTAGATCCAACTTATAGCACTACTTATGATGACGCTGTACCGATG 1200
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
385 leLysLeuAspProThrTyrSerThrThrTyrAspAspAlaValProMet 400

1201 TTTAAGAGCAACAACCGTTATCGTGATGTGATTGCAAGTCCAGATGGGAA 1250
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
401 PheLysSerAsnAsnArgTyrArgAspValIleAlaSerProAspGlyAs 417

1251 TGTCTTATATGTATTAACTGATACTGCCGGAAATGTCCAAAAAGATGATG 1300
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
418 nValLeuTyrValLeuThrAspThrAlaGlyAsnValGlnLysAspAspG 434

1301 GCTCAGTAACAAATACATTAGAAAACCCAGGATCTCTCATTAAGTTCACC 1350
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
435 lySerValThrAsnThrLeuGluAsnProGlySerLeuIleLysPheThr 450

1351 TATAAGGCTAAG 1362
     ||||||||||||
451 TyrLysAlaLys 454
```

Figure 2: Amino acid sequences of A. calcoaceticus (top) and A. baumannii (bottom)

```
          1 DVPLTPSQFAKAKSENFDKKVILSNLNKPHALLWGPDNQIWLTERATGKI 50
            |:||||.||||||.||||||||||||||||||||||||||||||||||||
          1 DIPLTPAQFAKAKTENFDKKVILSNLNKPHALLWGPDNQIWLTERATGKI 50

         51 LRVNPESGSVKTVFQVPEIVNDADGQNGLLGFAFHPDFKNNPYIYISGTF 100
            ||||| ||| ||||||||||.||||||||||||||||||.||||||||||
         51 LRVNPVSGSAKTVFQVPEIVSDADGQNGLLGFAFHPDFKHNPYIYISGTF 100

        101 KNPKSTDKELPNQTIIRRYTYNKSTDTLEKPVDLLAGLPSSKDHQSGRLV 150
            ||||||||||||||||||||||.||| |||:||:|||||||||||||||
        101 KNPKSTDKELPNQTIIRRYTYNKTTDTFEKPIDLIAGLPSSKDHQSGRLV 150

        151 IGPDQKIYYTIGDQGRNQLAYLFLPNQAQHTPTQQELNGKDYHTYMGKVL 200
            |||||||||||||||||||||||| |||||||||||| ||||||||||
        151 IGPDQKIYYTIGDQGRNQLAYLFLSNQAQHTPTQQELNSKDYHTYMGKVL 200

        201 RLNLDGSIPKDNPSFNGVVSHIYTLGHRNPQGLAFTPNGKLLQSEQGPNS 250
            |||||||||||||||||||||||||||||||||||| ||||||||||||||
        201 RLNLDGSIPKDNPSFNGVVSHIYTLGHRNPQGLAFAPNGKLLQSEQGPNS 250

        251 DDEINLIVKGGNYGWPNVAGYKDDSGYAYANYSAAANKS.IKDLAQNGVK 299
            ||||||:.|||||||||||||||||||||||||||||| ||| ||||||||:|
        251 DDEINLVLKGGNYGWPNVAGYKDDSGYAYANYSAATNKSQIKDLAQNGIK 300

        300 VAAGVPVTKESEWTGKNFVPPLKTLYTVQDTYNYNDPTCGEMTYICWPTV 349
            || |||||||||||||||||||||||||||||||||||||||||| |||||||
        301 VATGVPVTKESEWTGKNFVPPLKTLYTVQDTYNYNDPTCGEMAYICWPTV 350

        350 APSSAYVYKGGKKAITGWENTLLVPSLKRGVIFRIKLDPTYSTTYDDAVP 399
            |||||||| |||||| ||||||||||||||||||||||||||||| |||:|
        351 APSSAYVYTGGKKAIPGWENTLLVPSLKRGVIFRIKLDPTYSTTLDDAIP 400

        400 MFKSNNRYRDVIASPDGNVLYVLTDTAGNVQKDDGSVTNTLENPGSLIKF 449
            ||||||||||||||:|| ||||||||||||||||||.||||||||||||
        401 MFKSNNRYRDVIASPEGNTLYVLTDTAGNVQKDDGSVTHTLENPGSLIKF 450

        450 TYKAK 454
            ||  |
        451 TYNGK 455
```

Figure 3: Schematic diagram of the plasmide with gene for s-GDH (pACSGDH)

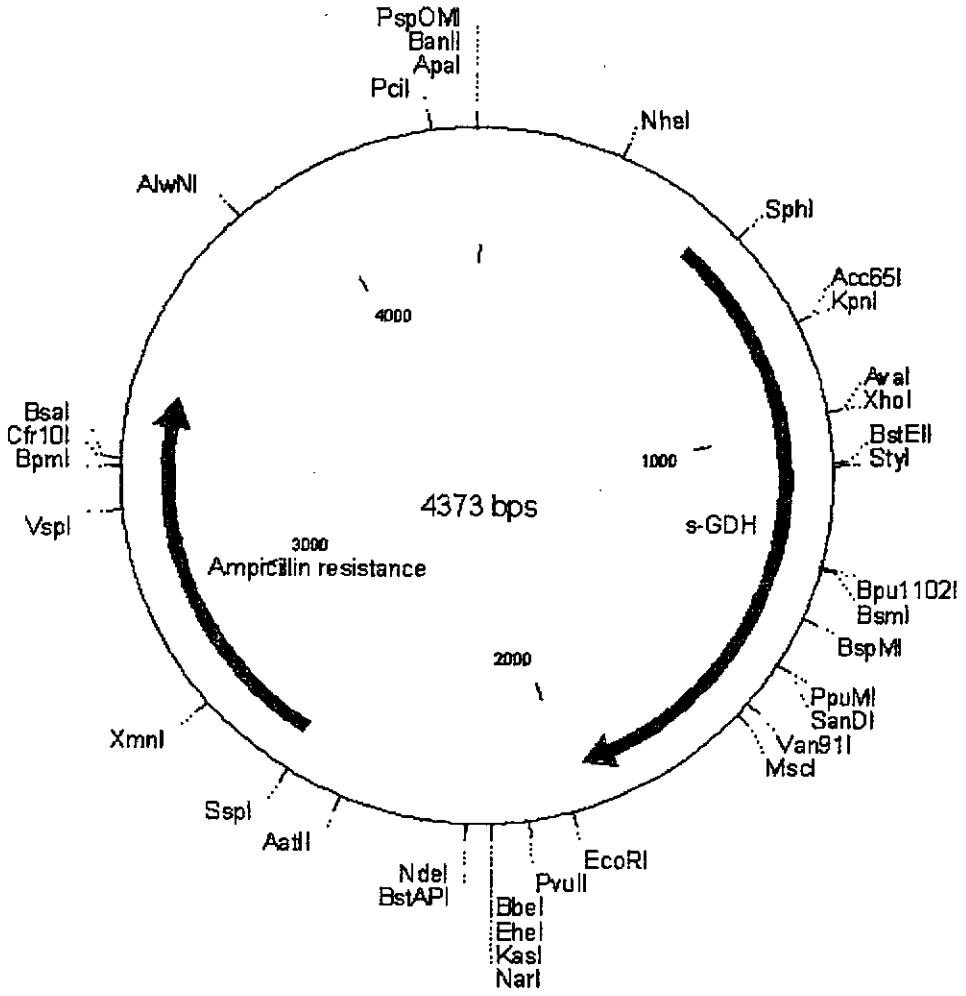


Figure 4: Nucleotide (DNA) sequence of the pACSGDH vector

```
     1  CACTAACTGA TTACGCACCG CATGTAACCG TTTTCAATCT GTGAGTAAAT
    51  TCACAGTTTA TTAACATTGT GATAGCTATG ATGACAACGT TTGTCGCACT
   101  GTAACTAACG TGTAACAGTT AGTTGTCAGT TTTGCTGGGG TATTTCGCTT
   151  ATAAAAACCG TTATCACAAT ATCCCGCGAC TACCGGACAA AAATAAAGAG
   201  TTGAATAAGA GCTTATCCCA TTAGGGCTAT TTTACTTGCC ATTTTGGACC
   251  TGGGCAGTGC TCGCCAAAAC GCGTTAGCGT TTTGAACGCG CTAGCGGCGG
   301  CCCGAAGGGC GAGCGTAGCG AGTCAAACCT CACGTACTAC GTGTACGCTC
   351  CGGTTTTTGC GCGCTGTCCG TGTCCAAACT GCTGCGCCAA TAACGCCTGG
   401  TGGGATAGGC TCTAAATACG CTTCGGCGTT CAGTAACACG CGTTAACGTG
   451  CTGAACAGCC GGGCATTTTT TTACGCTATA CCCTACATAA TAAAACCGGA
   501  GCTACCATGA ATAAGAAGGT ACTGACCCTT TCTGCCGTGA TGGCAAGTCT
   551  GTTATTCGGC GCGCACGCGC ATGCCGCCGA TGTTCCTCTA ACTCCATCTC
   601  AATTTGCTAA AGCGAAATCA GAGAACTTTG ACAAGAAAGT TATTCTATCT
   651  AATCTAAATA AGCCGCACGC GTTGTTATGG GGACCAGATA ATCAAATTTG
   701  GTTAACTGAG CGAGCAACAG GTAAGATTCT AAGAGTTAAT CCAGAGTCGG
   751  GTAGTGTAAA AACAGTTTTT CAGGTACCAG AGATTGTCAA TGATGCTGAT
   801  GGGCAGAATG GTTTATTAGG TTTTGCCTTC CATCCTGATT TTAAAAATAA
   851  TCCTTATATC TATATTTCAG GTACATTTAA AAATCCGAAA TCTACAGATA
   901  AAGAATTACC GAACCAAACG ATTATTCGTC GTTATACCTA TAATAAATCA
   951  ACAGATACGC TCGAGAAGCC AGTCGATTTA TTAGCAGGAT TACCTTCATC
  1001  AAAAGACCAT CAGTCAGGTC GTCTTGTCAT TGGGCCAGAT CAAAAGATTT
  1051  ATTATACGAT TGGTGACCAA GGGCGTAACC AGCTTGCTTA TTTGTTCTTG
  1101  CCAAATCAAG CACAACATAC GCCAACTCAA CAAGAACTGA ATGGTAAAGA
  1151  CTATCACACC TATATGGGTA AAGTACTACG CTTAAATCTT GATGGAAGTA
  1201  TTCCAAAGGA TAATCCAAGT TTTAACGGGG TGGTTAGCCA TATTTATACA
  1251  CTTGGACATC GTAATCCGCA GGGCTTAGCA TTCACTCCAA ATGGTAAATT
  1301  ATTGCAGTCT GAACAAGGCC CAAACTCTGA CGATGAAATT AACCTCATTG
  1351  TCAAAGGTGG CAATTATGGT TGGCCGAATG TAGCAGGTTA TAAAGATGAT
  1401  AGTGGCTATG CTTATGCAAA TTATTCAGCA GCAGCCAATA AGTCAATTAA
  1451  GGATTTAGCT CAAAATGGAG TAAAAGTAGC CGCAGGGGTC CCTGTGACGA
  1501  AAGAATCTGA ATGGACTGGT AAAAACTTTG TCCCACCATT AAAAACTTTA
```

Figure 4: Continued (second out of three pages)

```
1551  TATACCGTTC AAGATACCTA CAACTATAAC GATCCAACTT GTGGAGAGAT
1601  GACCTACATT TGCTGGCCAA CAGTTGCACC GTCATCTGCC TATGTCTATA
1651  AGGGCGGTAA AAAAGCAATT ACTGGTTGGG AAAATACATT ATTGGTTCCA
1701  TCTTTAAAAC GTGGTGTCAT TTTCCGTATT AAGTTAGATC CAACTTATAG
1751  CACTACTTAT GATGACGCTG TACCGATGTT TAAGAGCAAC AACCGTTATC
1801  GTGATGTGAT TGCAAGTCCA GATGGGAATG TCTTATATGT ATTAACTGAT
1851  ACTGCCGGAA ATGTCCAAAA AGATGATGGC TCAGTAACAA ATACATTAGA
1901  AAACCCAGGA TCTCTCATTA AGTTCACCTA TAAGGCTAAG TAATACAGTC
1951  GCATTAAAAA ACCGATCTAT AAAGATCGGT TTTTTTAGTT TTAGAAAAGA
2001  ATTCACTGGC CGTCGTTTTA CAACGTCGTG ACTGGGAAAA CCCTGGCGTT
2051  ACCCAACTTA ATCGCCTTGC AGCACATCCC CCTTTCGCCA GCTGGCGTAA
2101  TAGCGAAGAG GCCCGCACCG ATCGCCCTTC CCAACAGTTG CGCAGCCTGA
2151  ATGGCGAATG GCGCCTGATG CGGTATTTTC TCCTTACGCA TCTGTGCGGT
2201  ATTTCACACC GCATATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCGC
2251  ATAGTTAAGC CAGCCCCGAC ACCCGCCAAC ACCCGCTGAC GCGCCCTGAC
2301  GGGCTTGTCT GCTCCCGGCA TCCGCTTACA GACAAGCTGT GACCGTCTCC
2351  GGGAGCTGCA TGTGTCAGAG GTTTTCACCG TCATCACCGA AACGCGCGAG
2401  ACGAAAGGGC CTCGTGATAC GCCTATTTTT ATAGGTTAAT GTCATGATAA
2451  TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA
2501  ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT
2551  GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA
2601  TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TGCGGCATTT
2651  TGCCTTCCTG TTTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC
2701  TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA
2751  GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG
2801  AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC
2851  CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG
2901  TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA
2951  AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA
3001  CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC
3051  ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG
```

Figure 4: Continued (third and last page)

```
3101  AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC CTGTAGCAAT
3151  GGCAACAACG TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT
3201  CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA
3251  CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG
3301  AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG
3351  GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT
3401  ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA
3451  GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT
3501  TAAAACTTCA TTTTTAATTT AAAAGGATCT AGGTGAAGAT CCTTTTTGAT
3551  AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC
3601  AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTTTCTGC
3651  GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT
3701  TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT
3751  CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG
3801  GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA
3851  ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG
3901  GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA
3951  CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA
4001  CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG
4051  GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC
4101  GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCCTGTC
4151  GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GCTCGTCAGG
4201  GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT TTACGGTTCC
4251  TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT
4301  GATTCTGTGG ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG
4351  CCGCAGCCGA ACGACGGGGC CCG
```