

Nucleotide sequence of the *aceA* gene coding for isocitrate lyase in *Escherichia coli*

Corinne Rieul, Françoise Bleicher, Bertrand Duclos, Jean-Claude Cortay and Alain J. Cozzone

Laboratory of Molecular Biology, University of Lyon, 69622 Villeurbanne, France  
 Submitted May 17, 1988

Accession no.X07543

DNA sequence analysis of the *aceA* gene coding for *E.coli* isocitrate lyase (1,2) has revealed an open reading frame of 1302 bp. This gene is located in a *BamHI-AvaI* fragment of the *ace* operon (3,4). The 5'-flanking region contains a GGAG sequence (underlined) similar to the consensus ribosome-binding site sequence. The deduced amino acid sequence indicates a protein of 47700 daltons containing 434 amino acid residues.

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-30   -20   -10           1   10   20   30   40   50   60   70   80
GTTAGGGAATACCCACACATAACTATGGAGCATCTGCACATGAAACCCGATACACACAAATTGAAGAATTACAGAAAGAGTGGAAGTCAACCCGCGTGGGAGGCGATTACGGCCATAC
          <u>GGAG</u>
          >aceA
90   100   110   120   130   140   150   160   170   180   190   200
SerAlaGluAspValValLysLeuArgGlySerValAsnProGluCysThrLeuAlaGlnLeuGlyAlaAlaLysMetTrpArgLeuLeuHisGlyGluSerLysLysGlyTyrIleAsn
AGTGGGAGATGTGGTAAATTAAGCGGTTACGTCAATCTGAAATGCAAGCTGGGGCAACTGGGGCAGGAAATGTGGCGTCTGCTGCAAGGTGAGTGGAAAMAGGCTACATCAAC
210  220  230  240  250  260  270  280  290  300  310  320
SerLeuGlyAlaLeuThrGlyGlyGlnAlaLeuGlnAlaLysAlaGlyIleGluAlaValTyrLeuSerGlyTrpGlnValAlaAlaAspAlaAsnTrpArgProAlaCysIleAspG
ACCTCGGGCAGTGTGCTGGGGTCAGGGCTGCAACAGAGGGAAGCGGATATGAGCAGTCTATCTGCGGATGGCAGGTAGCGGGGAGCTACTGGCGCCAGCATGTATCGGG
330  340  350  360  370  380  390  400  410  420  430  440
IleSerArgSerIleArgGlnThrArgCysProAlaValValGluArgIleAsnAsnThrPheArgArgAlaAspGlnIleGlnTrpSerAlaGlyIleGluProGlyAspProArgTyr
ATCAGTGTCTTATCGGCAACCTGGTGTCCAGCTGGTGGAGGGGATCAACAACACTTCGGTGTGGCCATCAGATCAAATGGTGGCGGGCATTGAGCGGGCGCATCGGGCTAT
450  460  470  480  490  500  510  520  530  540  550  560
ValAspTyrPheLeuProIleValAlaAspAlaGluAlaGlyPheGlyGlyValLeuAsnAlaPheGluLeuMetLysAlaMetIleGluAlaGlyAlaAlaValIleHisPheGluAsp
GTGGATTAATCTCTCGGATGGTGGCGATGGGAGCGGTTTGGGGTGTCTGAAATGCGCTTGAACATGATGAAGCGATGATTAAGCGGGTCCAGCGGCAGTCTACTCGAAGAT
570  580  590  600  610  620  630  640  650  660  670  680
GlnLeuAlaSerValLysLysCysGlyHisMetGlyGlyLysValLeuValProThrGlnGluAlaIleGlnLysLeuValProAlaArgLeuAlaAlaAspValThrGlyValProThr
CAGCTGGGTCAGTAGAAATAGCGGTACATGGGGCAGAAAGTTTTAGTGCCAACTCAGGAGCTATTTCAGAACTGGTGGCGGGGCTGGCAGCTGAGGTGAGCGGGTTCACAGC
690  700  710  720  730  740  750  760  770  780  790  800
LeuLeuValAlaArgThrAspAlaAspAlaAspLeuIleThrSerAspCysAspProTyrAspSerGluPheIleThrGlyGluArgThrSerAlaGlyPhePheArgThrHisAla
CTGCTGGTGGCGTACCGATGCTGATGGCGGATCTGATCACTCGGATTTGGACCGGTATGACAGGGAATTTATTACGGGGAGGTTACAGTGAAGGCTTCTCGGACTCATCGG
810  820  830  840  850  860  870  880  890  900  910  920
GlyIleGluGlnAlaIleSerArgGlyLeuAlaTyrAlaProTyrAlaAspLeuValTrpCysGluThrSerThrProAspLeuGluLeuAlaArgArgPheAlaGlnAlaIleHisAla
GCATTGAGCAAGCGATCAGCGGTGGCTGGGATATGGCCATATCTGACTGGTCTGGTGTGAACCTCCAGCCGATCTGGAACTGGGGGTGGCTTTCAGCAAGCTATCCAGCGG
930  940  950  960  970  980  990  1000 1010 1020 1030 1040
LysTyrProGlyLysLeuLeuAlaTyrAsnCysSerProSerPheAsnTrpGlnLysAsnLeuAspLysThrIleAlaSerPheGlnGluGlnLeuSerAspMetGlyTyrLysPhe
AAATATCGGGCAACTGCTGGCTTATACTGCTGGCGGTGTTCAACTGGCAGAAACCTCGAGCAAAACTATTGGCAGCTCCAGGAGCAGTGTGGGATATGGGCTACAAGTTC
1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160
GlnPheIleThrLeuAlaGlyIleHisSerMetTrpPheAsnMetPheAspLeuAlaAsnAlaTyrAlaGlnGlyGluGlyMetLysHisTyrValGluLysValGlnGlnProGluPhe
CAGTTCATCACTGGCAGGTATCAGCAGCATGTGGTTCAACATGTTTGAACCTGGCAAGGCTATGGCCAGGGGAGGGTATGAAAGCAGTACTAGTGGAAAGTCCAGCAGCGGAAATTT
1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280
AlaAlaAlaLysAspGlyTyrThrPheValSerHisGlnGlnGluValGlyThrGlyTyrPheAspLysValThrThrIleIleGlnGlyGlyThrSerSerValThrAlaLeuThrGly
GCCGCGGAAGATGGTAACTGTATCTCAACAGCAGGAAGTGGTACAGGTACTTGTGATAAGTGGAGCACTATTATTCAGGGGCGAGCTTCTCAGTCAACCGGCTGACCGGCG
1290 1300
SerThrGluSerGlnPheTer
TCCACTGAAGATGGCAGTTCTAA
          <u>aceA</u>
    
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