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Nucleotide sequence of the gene coding for quinoprotein glucose dehydrogenase from *Acinetobacter calcoaceticus*

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We recently reported the cloning and characterization of the gene coding for quinoprotein glucose dehydrogenase from *Acinetobacter calcoaceticus* LMD 79.41 (1). In this paper we present the complete nucleotide sequence of this gene as determined by the chain termination method of Sanger et al (2). From the putative start codon to the ochre codon the gene is 2400 bp in lenght, coding for a protein of 86.9 kD. The 140 amino acids long N-terminal part of the protein is highly hydrophobic, suggesting that this domain anchors the protein in the plasma membrane. Putative membrane spanning segments within the hydrophobic domain (hydrophobic regions separated by hydrophilic amino acid residues) are boxed. The translation start site and the possible ribosomal binding site are underlined.

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     GGAATATGTCGTCATGTGTCGATAAAATGGTGATAACACTGGTGCGGTATAAATCTCAACTCGATCTAAGCGTAATTACTCGAAAACGGATGTCAGGGCTAAATCATTGATTGAATTAT
120  CCTGACCTTCCGTTTTTTCTTGATGCCTGAATTTGTTTTAGATGTATTGGTGATGCCATTTTTCTATAAGGCTCTTGGCACATCTTTCCTATAAAAATGATGATTGATAAGAGGTGGTTT
     MetAsnGlnProThrSerArgSerGlyLeuThrThrPheThrValIleIleIleGlyLeuLeuAlaLeuPheLeuLeuIleGlyGlyIleTrpLeuAlaThrLeuGlyGlySerIleTyr
240  ATGAATCAACCTACTTCAAGATCAGGTTTAACGACTTTACCGTAATTATTATTGGGTTACTGGCGTTATTCCTGTTAATTGGAGGTATTTGGCTCGCTACACTAGGCGGTTCAATTTAC
     TyrIleIleAlaGlyValLeuLeuLeuIleValAlaTrpGlnLeuTyrLysArgAlaSerThrAlaLeuTrpPheTyrAlaAlaLeuMetLeuGlyThrIleIleTrpSerValTrpGlu
360  TACATTATAGCTGGAGTATTACTCCTCATTGTTGCATGGCAACTCTACAAGCGTGCTTCTACTGCTTTGTGGTTTTATGCTGCATTAATGCTAGGTACCATTATCTGGAGTGTCTGGGAA
     ValGlyThrAspPheTrpAlaLeuAlaProArgLeuAspIleLeuGlyIleLeuGlyLeuTrpLeuLeuValProAlaValThrArgGlyIleAsnAsnLeuGlySerSerLysValAla
480  GTTGGAACAGACTTTTGGGCGCTTGCACCACGTTTAGATATTTTAGGTATTCTTGGTTTATGGTTATTGGTTCCGGCTGTAACTCGTGGAATCAACAACCTTGGATCAAGTAAAGTTGCC
     LeuSerSerThrLeuAlaIleAlaIleValLeuMetValTyrSerIlePheAspAspProGlnGluIleAsnGlyGluIleLysThrProGlnProGluThrAlaGlnAlaValProGly
600  TTATCTTCAACTTTAGCAATTGCAATCGTGTTGATGGTTTATTCTATCTTCAATGATCCGCAAGAAATTAATGGTGAAATCAAAACACCTCAACCAGAAACAGCTCAAGCCGTGCCTGGT
     ValAlaGluSerAspTrpProAlaTyrGlyArgThrGlnAlaGlyValArgTyrSerProLeuLysGlnIleAsnAspGlnAsnValLysAspLeuLysValAlaTrpThrLeuArgThr
720  GTTGCTGAAAGTGATTGGCCAGCTTATGGTCGTACTCAAGCAGGCGTGCGTTATTCTCCATTGAAACAGATCAATGATCAAAACGTAAAAGACTTGAAAGTTGCTTGGACTTTACGTACT
     GlyAspLeuLysThrAspAsnAspSerGlyGluThrThrAsnGlnValThrProIleLysIleGlyAsnAsnMetPheIleCysThrAlaHisGlnGlnLeuIleAlaIleAspProAla
840  GGCGATCTTAAGACAGATAACGACTCTGGCGAAACGACTAATCAGGTTACACCGATTAAAATCGGTAATAACATGTTTATCTGTACAGCTCACCAGCAGTTAATTGCTATTGATCCTGCT
     ThrGlyLysGluLysTrpArgPheAspProLysLeuLysThrAspLysSerPheGlnHisLeuThrCysArgGlyValMetTyrTyrAspAlaAsnAsnThrThrGluPheAlaThrSer
960  ACAGGTAAAGAAAAATGGCGTTTTGATCCGAAACTTAAAACGGATAAATCGTTCCAGCATCTAACTTGTCGTGGTGTGATGTACTACGATGCAAACAATACAACTGAGTTTGCAACGAGT
     LeuGlnSerLysLysSerSerSerThrGlnCysProArgLysValPheValProValAsnAspGlyArgLeuValAlaValAsnAlaAspThrGlyLysAlaCysThrAspPheGlyGln
1080 CTTCAAAGCAAGAAATCTAGCTCTACACAATGTCCACGTAAGGTATTTGTACCAGTCAACGATGGCCGTTTAGTGGCTGTAAATGCTGACACTGGTAAAGCATGTACTGACTTTGGTCAA
     AsnGlyGlnValAsnLeuGlnGluPheMetProTyrAlaTyrProGlyGlyTyrAsnProThrSerProGlyIleValThrGlySerThrValValIleAlaGlySerValThrAspAsn
1200 AATGGTCAAGTGAACTTACAAGAGTTCATGCCATATGCTTATCCAGGCGGTTATAACCCGACATCTCCTGGTATCGTGACTGGTTCAACTGTTGTTATTGCTGGTTCTGTAACAGATAAC
     TyrSerAsnLysGluProSerGlyValIleArgGlyTyrAspValAsnThrGlyLysLeuLeuTrpValPheAspThrGlyAlaAlaAspProAsnAlaMetProGlyGluGlyThrThr
1320 TACTCAAATAAAGAGCCATCTGGTGTGATTCGTGGATACGACGTTAACACTGGTAAACTTCTTTGGGTATTTGACACTGGCGCAGCGGATCCAAATGCAATGCCGGGCGAAGGTACTACT
     PheValHisAsnSerProAsnAlaTrpAlaProLeuAlaTyrAspAlaLysLeuAspIleValTyrValProThrGlyValGlyThrProAspIleTrpGlyGlyAspArgThrGluLeu
1440 TTTGTTCACAACTCACCAAATGCGTGGGCACCTTTAGCATACGATGCCAAACTTGACATCGTTTATGTACCAACAGGTGTAGGTACACCAGACATCTGGGGTGGTGACCGTACCGAGCTG
     LysGluArgTyrAlaAsnSerMetLeuAlaIleAsnAlaSerThrGlyLysLeuValTrpAsnPheGlnThrThrHisHisAspLeuTrpAspMetAspValProSerGlnProSerLeu
1560 AAAGAGCGTTATGCAAACTCAATGTTAGCGATTAATGCTTCTACTGGTAAATTAGTGTGGAACTTCCAGACAACCCATCACGATTTATGGGATATGGATGTACCATCACAACCATCTTTA
     AlaAspIleLysAsnLysAlaGlyGlnThrValProAlaIleTyrValLeuThrLysThrGlyAsnAlaPheValLeuAspArgArgAsnGlyGlnProIleValProValThrGluLys
1680 GCTGATATCAAAAACAAAGCTGGCCAAACTGTTCCTGCAATCTATGTATTGACGAAAACAGGTAATGCCTTTGTGCTTGATCGCCGTAATGGTCAACCGATTGTTCCTGTAACTGAGAAA
     ProValProGlnThrValLysArgGlyProGlnThrLysGlyGluPheTyrSerLysThrGlnProPheSerAspLeuAsnLeuAlaProGlnAspLysLeuThrAspLysAspMetTrp
1800 CCAGTTCCACAAACAGTTAAACGTGGACCACAAACTAAAGGTGAGTTCTATTCAAAAACTCAGCCATTCTCTGACTTGAACTTGGCGCCACAAGATAAATTGACTGATAAAGACATGTGG
     GlyAlaThrMetLeuAspGlnLeuMetCysArgValSerPheLysArgLeuAsnTyrAspGlyIleTyrThrProProSerGluAsnGlyThrLeuValPheProGlyAsnLeuGlyVal
1920 GGTGCCACTATGCTTGATCAGCTCATGTGTCGTGTATCTTTCAAACGTCTAAATTACGATGGTATTTATACGCCACCATCTGAAAACGGTACTTTAGTTTTCCCTGGTAACTTAGGTGTA
     PheGluTrpGlyGlyMetSerValAsnProAspArgGlnValAlaValMetAsnProIleGlyLeuProPheValSerArgLeuIleProAlaAspProAsnArgAlaGlnThrAlaLys
2040 TTTGAATGGGGCGGTATGTCAGTTAACCCTGATCGTCAGGTTGCTGTAATGAACCCGATTGGTCTGCCATTCGTCAGTCGTTTAATTCCTGCTGATCCAAACCGTGCACAAACTGCAAAA
     GlyAlaGlyThrGluGlnGlyValGlnProMetTyrGlyValProTyrGlyValGluIleSerAlaPheLeuSerProLeuGlyLeuProCysLysGlnProAlaTrpGlyTyrValAla
2160 GGTGCGGGAACTGAGCAGGGCGTACAACCGATGTACGGCGTACCATATGGTGTTGAAATTAGCGCATTCTTATCTCCGCTTGGTTTACCTTGTAAACAACCGGCTTGGGGCTATGTAGCT
     GlyValAspLeuLysThrHisGluValValTrpLysLysArgIleGlyThrIleArgAspSerLeuProAsnLeuPheGlnLeuProAlaValLysIleGlyValProGlyLeuGlyGly
2280 GGCGTTGATTTGAAAACTCATGAAGTGGTATGGAAAAAACGTATTGGTACAATCCGTGACAGTTTACCGAACTTGTTCCAGTTGCCAGCTGTGAAAATTGGTGTGCCTGGTTTAGGTGGT
     SerIleSerThrAlaGlyAsnValMetPheValGlyAlaThrGlnAspAsnTyrLeuArgAlaPheAsnValThrAsnGlyLysLysLeuTrpGluAlaArgLeuProAlaGlyGlyGln
2400 TCAATTTCTACTGCCGGTAATGTCATGTTTGTTGGTGCAACTCAAGATAACTACTTACGTGCGTTAACGTTACTAACGGTAAGAAACTTTGGGAAGCGCGTTTACCAGCAGGTGGACAA
     AlaThrProMetThrTyrGluIleAsnGlyLysGlnTyrValValIleMetAlaGlyGlyHisGlySerPheGlyThrLysMetGlyAspTyrLeuValAlaTyrAlaLeuProAspAsn
2520 GCAACACCAATGACTTATGAAATCAATGGTAAGCAATATGTTGTAATCATGGCTGGTGGTCATGGTTCATTTGGTACGAAAATGGGCGACTATTTAGTGGCTTATGCCTTACCAGATAAC
     Lys
2640 AAATAAAAAGCTT
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2. Sanger,F., Nicklen,S. and Coulson,A.R. (1977) Proc.Natl.Acad.Sci.USA 74, 5463-5467

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