
The complete nucleotide sequence of bovine liver cytochrome b₅ mRNA

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Using a cDNA probe corresponding to rabbit liver cytochrome b₅ mRNA (1) we have screened a bovine λgt11 cDNA library (Clontech, Palo Alto, CA) using low stringency conditions (2) and have isolated clones for bovine liver cytochrome b₅ mRNA. The 715 base pair (bp) sequence contains an open reading frame of 402bp giving the complete amino acid sequence of bovine liver cytochrome b₅. This has enabled us to make the following corrections to the published amino acid sequence (3). The NH₂ terminal sequence is met-ala-glu-glu-ser not met-(glx,glx,ala)-ser, amino acids 16,18 and 62 are glu, gln and asn, not gln, glu and asp. The availability of this cDNA will enable studies to begin on determining the molecular relationships between the bovine liver and erythrocyte cytochrome b₅ mRNA's.

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1  CGGCGAGCCTAAGGCCCTAAAGGCAGCAGGAGAGCTGAGTTAAGAA ATG GCC GAG
                                     M A E
56 GAG TCC AGC AAA GCC GTT AAG TAC TAC ACC CTG GAA GAG ATC CAG
   E S S K A V K Y Y T L E E I Q
101 AAG CAC AAC AAC AGC AAG AGC ACC TGG CTG ATC CTG CAC TAC AAA
   K H N N S K S T W L I L H Y K
146 GTG TAC GAT TTG ACC AAA TTT TTG GAG GAG CAT CCT GGT GGG GAG
   V Y D L T K F L E E H P G G E
191 GAA GTC TTA AGG GAA CAA GCT GGA GGT GAT GCC ACT GAA AAC TTT
   E V L R E Q A G G D A T E N F
236 GAG GAT GTT GGA CAC TCT ACA GAT GCT CGA GAA TTG TCC AAA ACG
   E D V G H S T D A R E L S K T
281 TTC ATC ATT GGG GAG CTG CAC CCG GAT GAC AGA TCA AAG ATA ACC
   F I I G E L H P D D R S K I T
326 AAG CCT TCG GAA AGT ATT ACT ACC ATT GAT TCA AAT CCC AGC
   K P S E S I I T T I D S N P S
371 TGG TGG ACC AAC TGG CTG ATC CCA GCT ATC TCA GCG CTG TTT GTA
   W W T N W L I P A I S A L F V
416 GCC CTG ATA TAT CAC CTC TAC ACT TCG GAG AAC TAA ACACATTCTCA
   A L I Y H L Y T S E N xxx
463 GAAGCCAATGGAAGAAAAGACTGCTTTGGTCCAGGGAGAAAGAAGCCACCCTTTAAC
522 TTCAACGGACAAACCCCTTACCTGAAAATAATCTGAATACACCTATTTTCCTTCCCTCC
581 TACATTAGACACAAAACAAACCATAACTGTTCCATTCTTTGGACTATTGAACCTCTAAA
640 GTGTGCCTTCTATTCCCAACTTTGTTTTGCTGTTCCATCCTACATCATTTGCTTAT
699 GGTGGTATGTTTTAAAA

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