

Nucleotide sequence of rat liver glutamate dehydrogenase cDNA

Naoki Amuro, Kaoru Ooki, Akiko Ito, Yoshitaka Goto and Taro Okazaki

Department of Biochemistry, Nippon Medical School, 1-1-5 Sendagi, Bunkyo-ku, Tokyo 113, Japan

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Glutamate dehydrogenase (GDH), a mitochondrial matrix enzyme, catalyzes the NAD or NADP specific interconversion between alpha-ketoglutarate and L-glutamate. We have isolated cDNA clones from a rat liver lambda gt11 cDNA library by crosshybridization with a human liver GDH cDNA clone (pGDHh1) (1). The rat liver GDH cDNA contains a 5'-untranslated sequence of 33 bp, an open reading frame of 1677 bp, a 3'-untranslated sequence of 1124 bp and a 56 base poly(A) tract. The predicted amino acid sequence reveals that the rat liver GDH precursor consists of 558 amino acids, having an amino terminal presequence of 53 amino acids (indicated by arrow). This sequence shows a strong homology to the sequence published for human liver GDH (1), 98 % in the mature protein and 85 % in the presequence regions, respectively.

GTGCTCCCGCCGCTCTGCTCCCTCAGCCGCGCCGCTCC
ATGTACCCGCGCTCTGGGCGAAGTCTGCTACTCTCCCGGCGCCGGCCGCTCCCTGGGCTCTGGGCTGCGACTCAGCCGACTGCTGGGCTGGGCGAACCCCTCTGCTGTC 120
MetTyrArgArgLeuGlyGluValLeuLeuLeuSerArgAlaGlyProAlaAlaLeuGlySerAlaAlaAlaAspSerAlaAlaLeuLeuGlyTyrPheAlaArgGlyGlnProSerAlaVal 40
CCGCAACCCGCGCTCAGCCGCTCTGGGCGAAGCTTACGGGAAGGCCACCGGAGCGAGCCGCAACTCTTCAAGATCTGGGAGGCTCTCTGCGCCGGGGCCAGCAGCTC 240
ProGlnProGlyLeuThrProValAlaArgArgHisTyrSerGluGlyProThrAspArgGluAspAspProAsnPhePheLysMetValGluGlyPhePheAspArgGlyAlaSerIle 80
GTGGAGGACAGACTGCTGGGAGACCTGAGACCGCCGGGAGAGCGAGGAGCGGAACCGAGTGGCGGGCATCTGGGATCATCAAGCCCTTGCACCAACTGTGTGAGCCCTCCCTC 360
ValGluAspLysLeuValGluAspLeuLysThrArgGluAsnGluGluGlnLysArgAsnArgValArgGlyIleLeuArgIleIleLysProCysAsnHisValLeuSerLeuSerPhe 120
CCCATCCGCGCGGAGCCGCTCTGGGAGTCTATCGAAGCTTACCGGGCCAGCAGCCGCGCCCTTGGAGGGAGGTATCCGCTTCAGCAGCTCAGCTGATGTGGATGAG 480
ProIleArgArgAspAspGlySerTyrTrpGluValIleGluGlyTyrArgAlaGlnHisSerGlnHisArgThrProCysLysGlyGlyIleArgTyrSerThrAspValSerValAspGlu 180
GTGAAAGGCTGGGCTCCATAGCCTAGCAGCTCTGGGCTGTGGATGTGGAGTCTGTAAGCGAGGCTTAAAGCACTCCCAAGCACTTACAGATTAATGATTGAAAG 600
ValLysAlaLeuAlaSerLeuMetThrTyrLysCysAlaValAlaAspValProPheGlyGlyAlaLysAlaGlyValLysIleAsnProLysAsnTyrThrAspAsnGluLeuGlyLys 160
ATTACAGGAGATTTACCGTAGCTGGCAAGAGCGCTTTTATTGTGCTGGCATTGATGTGCTCCCGCCAGACTGAGCAGCGCGGAGCGGAGATTTCCCTGGATGCTGACACCTAT 720
IleThrArgArgPheThrMetGluLeuAlaLysLysGlyPheIleGlyProGlyIleLeuAspValIleProAlaProAspPheSerThrGlyGluArgGluMetSerTyrPheLeuAspThrTyr 240
GGCAGCAGCATCGGCATATGATCAATGACAGCCCTCTGCTACTGTAAACCCATCAGCAAGGAGGATCCAGCAGCCATCTCCCGTACTGCGCGGGCTGTTTTCCTGGATGGGATT 280
AlaSerThrIleGlyHisTyrAspIleAsnAlaHisAlaCysValIleGlyLysProIleSerGlnGlyGlyIleHisIleGlyArgIleSerAlaThrGlyArgGlyValIleHisLysIle 400
GAGAACCTCATCAATGAAGCTCTCAGTACGAGCATCTTAGGATGACCCCGCGGCTTGGCGATTAAGACCTTTTCTTTCAGCGATTTGCTTAATCTGGCCCTGCATCTATGATGATTTTA 960
GluAsnPheIleAsnGluAlaSerTyrMetSerIleLeuGlyMetThrProGlyLeuGlyAspLysThrPheValIleValGlnGlyPheGlyAsnValGlyLeuHisSerMetArgTyrLeu 360
CATCTTTCGCTGCTAACTGCTTCTGTTGGAGAATCTGATGGAGCTATATGGAATCCGATGGTATTTGACCCAAAGGACTGGAGATTTCAAGTTCACAACTGGATCAATTTCTGGCC 1080
HisArgPheGlyAlaLysCysValGlyValGlyGlyLysSerIleLeuAspAsnProAspGlyIleAspProLysGluLeuGluAspPheLysLeuGlnHisGlySerIleLeuGly 360
TTCCCAAGGCGAAGCTCTATGAAGGAGCAGCTCTGGGAGCTGACTGGACATTTTAACTTCCAGCCAGCGAGAGGAGTTCAGCAATTCACCCAGAGCTCAAGCCAGATC 1200
PheProLysAlaLysValTyrGluGlySerIleLeuGluAlaAspCysAspIleLeuIleProAlaAlaSerGlyLysGlnLeuThrLysSerAsnAlaProArgValLysAlaLysIle 400
ATTGCTGAAGGCGCAATGGCCCAACCACTCCAGAGCGCGGATTAAGATTTTCTAGAAAGAAACATCATGCTTATTCAGATCTCTACCTGAAATCTGAGGAGTGCAGATTTCTACCTT 1420
IleAlaGluGlyAlaSerGlyProThrThrProGluAlaAspLysIlePheLeuGluArgAsnIleMetValIleProAspLeuTyrLeuAsnAlaGlyGlyValIleValSerTyrPhe 480
GAGTGGCTAAAGATCTAAATCACTGACTATGCGGATTTGACCTCTCAAAATTAAGAAAGGAGTCTGAACTTACCACTTCCCTGATCTCCGTCACAGAGATTTAGAGAGAAAGTPTTGGAAAG 1440
GluTrpLeuLysAsnLeuAsnHisValSerTyrGlyArgLeuThrPheLysTyrGluArgAspSerAsnTyrIleLeuLeuMetSerValGluGlnLysLeuGlnAurLysIleGlyLys 480
CACCGGGGACTTCCCTCTGCTCCCGCAGCGAGGCTTCACGAGAGAAATATCCGCTGCTATGAGAAAGAGATCTGCACTTCCCTCTCCGCTTACAGAAATGGAGGATTTCTCAAGGAA 1560
HisGlyGlyThrIleProValIleProThrAlaGluPheGluAspArgIleSerGlyAlaSerGlyLysAspIleValHisSerGlyLeuAlaThrPheGluAspSerAlaArgGln 520
ATTATGGCAGCAGCAGTCAAGATTAACCTTGGATTTGGAGCTGAGAACAGCTGCTTACTGCAATCTCATTTGAGAAAGTCTTCAAGGTTTCAAAATAGCTTGGCTTGGCTTACATGACACA 1680
IleMetArgThrAlaAspLysTyrAsnLeuGlyLeuAspLeuArgThrAlaAlaTyrValAsnAlaIleGlnLysValIlePheLysValIleAsnGluAlaGlyValIleThrPheThrIad
GCTCAGACTGCTCTTTTACACCCTCTTCCCTTATTTTCTGAGAGCTTCCAGAGTTCACCTTFAACACAGAAATCTGCTTCTTCTGACTCTGATTTTAAITGAGCACTTCTTCCAGC 1800
ACTGCTGTGATGTCGCTCCCTTTAGCAAAAGATTAACTTTAGCGGATCTATCCCACTGATTTTCTTAAAGCTAGGATACAGCTCTTCTCTCCGCTTACGCTTTTCTCTTTTAACTTAA 1920
TTTCTGCTCTCCGCTGCTCCCTTCTGCTGACTTCTTCCCAACAGGCTTACTGCTGCTTCCAGGAGGAGGAGCAGTCAAGACTTCTTCCAGCAATTTCTGATTTTCTGATGATA 2040
AGAGTATGGCTGCTTGGCATTTCGAAAGTGGCTGCTGCTGCTGCTGCTTACATTCAGCAAAATTAACCTGACTCTTAAAGTCCCAAGCAAAATTAAGCAATTTCTGATGATA 2160
TTTTTATTTTTCAGATTAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
TTTTTAACTAAACAGCTTAAATTTAGCTTTTACGATTTTTCAGATTTTTCAGATTTTTCAGATTTTTCAGATTTTTCAGATTTTTCAGATTTTTCAGATTTTTCAGATTTTTCAG 2400
CTTATGCACTTCAGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
GCTGCGAGACTTCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
GCAGGCTTTTGAACAGGACTTCTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
AACTTGTGATAAAAGAGTCTTTAAAATCTACCTTTTCCAG

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