Sequence of human liver 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase

Alex J.Lange* and Simon J.Pilkis
Department of Physiology and Biophysics, SUNY at Stony Brook, Stony Brook, NY 11794, US

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6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase catalyzes the synthesis and hydrolysis of fructose-2,6-bisphosphate, a potent positive effector of 6-phospho-1-kinase and a negative effector of fructose-2,6-bisphosphatase. Levels of this metabolite control the flow of carbon through glycolysis and gluconeogenesis (1). A partial sequence of human liver 6-PF-2-K/Fru-2,6-P_2ase has been reported by Algaier and Uyeda (2). We report here the sequence of the full coding length cDNA of human liver 6-PF-2-K/Fru-2,6-P_2ase isolated from a human liver library in lambda gt11 using the rat cDNA (3) as a probe (4). The nucleotide sequence consists of 1801 nucleotides coding for a 471 amino acid protein. The deduced amino acid sequence is 95% identical to the rat liver enzyme (3).

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REFERENCES

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DNA SEQUENCE

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   1  GAATTCCGGA CAGGTAGTAA GATAGGAAGT GAGGCCAGGT ACCTTGTGGG CAGTGATGTC ATTCGGTGCG ACTCCTAAGA TGTCTCCAGA
  91  GATGGGAGAG CTCACCCAAA CCAGGTTGCA GAAGATCTGG ATTCCACACA GCAGCGGCAG CAGCAGGCTG CAACGGAGAA GGGGCTCATC
 181  CATACCCCAG TTTACCAATT CCCCCACAAT GGTGATCATG GTGGGTTTAC CAGCTCGAGG CAAGACCTAT ATCTCCACAA AGCTCACACG
 271  ATATCTCAAC TGGATAGGAA CACCAACTAA AGTGTTTAAT TTAGGCCAGT ATCGACGAGA GGCAGTGAGC TACAAGAACT ATGAATTCTT
 361  TCTTCCAGAC AACATGGAAG CCCTGCAAAT CAGGAAGCAG TGCGCCCTGG CAGCCCTGAA GGATGTTCAC AACTATCTCA GCCATGAGGA
 451  AGGTCATGTT GCGGTTTTTG ATGCCACCAA CACTACCAGA GAACGACGGT CACTGATCCT GCAGTTTGCA AAAGAACATG GTTACAAGGT
 541  GTTTTTCATT GAGTCCATTT GTAATGACCC TGGCATAATT GCAGAAAACA TCAGGCAAGT GAAACTTGGC AGCCCTGATT ATATAGACTG
 631  TGACCGGGAA AAGGTTCTGG AAGACTTTCT AAAGAGAATT GAGTGCTATG AGGTCAACTA CCAACCCTTG GATGAGGAAC TGGACAGCCA
 721  CCTGTCCTAC ATCAAGATCT TCGACGTGGG CACACGCTAC ATGGTGAACC GAGTGCAGGA TCACATCCAG AGCCGCACAG TCTACTACCT
 811  CATGAATATC CATGTCACAC CTCGCTCCAT CTACCTTTGC CGACATGGCG AGAGTGAACT CAACATCAGA GGCCGCATCG GAGGTGACTC
 901  TGGCCTCTCA GTTCGCGGCA AGCAGTATGC CTATGCCCTG GCCAACTTCA TTCAGTCCCA GGGCATCAGC TCCCTGAAGG TGTGGACCAG
 991  TCGCATGAAG AGGACCATCC AGACAGCTGA GGCCCTGGGT GTCCCCTATG AGCAGTGGAA GGCCCTGAAT GAGATTGATG CGGGTGTCTG
1081  TGAGGAGATG ACCTATGAAG AAATCCAGGA ACATTACCCT GAAGAATTTG CACTGCGAGA CCAAGATAAA TATCGCTACC GCTATCCCAA
1171  GGGAGAGTCC TATGAGGATC TGGTTCAGCG TCTGGAGCCA GTGATAATGG AGCTAGAACG ACAGGAGAAT GTACTGGTGA TCTGCCACCA
1261  GGCTGTCATG CGGTGCCTCC TGGCCTATTT CCTGGATAAA AGTTCAGATG AGCTTCCATA TCTCAAGTGC CCTCTGCACA CAGTGCTCAA
1351  ACTCACTCCT GTGGCTTATG GCTGCAAAGT GGAATCCATC TACCTGAATG TGGAGGCCGT GAACACACAC CGGGAGAAGC CTGAGAATGT
1441  GGACATCACC CGGGAACCTG AGGAAGCCCT GGATACTGTC CCAGCCCACT ACTGAGCCCT TTCCAAGAAG TCAAACTGCC TGTGTCCTCA
1531  TCGCCTTCCA CCTTTAGGAA ATGCTATCTT TGCTCTTCTC CTACTCTGCC TTGGCCTCAC TGAGGCACCC CACTTCCAGT GAAGAAGTCC
1621  TCCGCAACTC CCAAACAAGC CTCGCTTGCT GGCCGCAACC AAGGAGCTAT CTAGCTCTGG AGGAAACTTT CTTTCTTAAT TCCTATTCTC
1711  TGACGAATAA AGACTTACTG CCTACAAGAG GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AC(A)29
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PROTEIN SEQUENCE

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human    1 MSPEMGELTQTRLQKIWIPHSSGSSRLQRRRGSSIPQFTNSPTMVIMVGLPARGKTYISTKLTRYLNWIGTPTKVFNLGQYRREAVSYKN
  rat    1 MSREMGELTQTRLQKIWIPHSSSSSVLQRRRGSSIPQFTNSPTMVIMVGLPARGKTYISTKLTRYLNWIGTPTKVFNLGQYRREAVSYRN
human   76 YEFFLPDNMEALQIRKQCALAALKDVHNYLSHEEGHVAVFDATNTTRERRSLILQFAKEHGYKVFFIESICNDPGIIAENIRQVKLGSPD
  rat   76 YEFFRPDNTEAQLIRKQCALAALKDVHKYLSREEGHVAVFDATNYTRERRSLILQFAKEHGYKVFFIESICNDPEIIAENIKQVKLGSPD
human  151 YIDCDREKVLEDFLKRIECYEVNYQPLDEELDSHLSYIKIFDVGTRYMVNRVQDHIQSRTVYYLMNIHVTPRSIYLCRHGESELNIRGRI
  rat  151 YIDCDQEKVLEDFLKRIECYEINYQPLDEELDSHLSYIKIFDVGTRYMVNRVQDHVQSRTAYYLMNIHVTPRSIYLCRHGESELNLRGRI
human  226 GGDSGLSVRGKQYAYALANFIQSQGISSLKVWTSRMKRTIQTAEALGVPYEQWKALNEIDAGVCEEMTYEEIQEHYPEEFALRDQDKYRY
  rat  226 GGDSGLSARGKQYAYALANFIRSQGISSLKVWTSHMKRTIQTAEALGVPYEQWKALNEIDAGVCEEMTYEEIQEHYPEEFALRDQDKYRY
human  301 RYPKGESYEDLVQRLEPVIMELERQENVLVICHQAVMRCLLAYFLDKSSDELPYLKCPLHTVLKLTPVAYGCKVESIYLNVEAVNTHREK
  rat  301 RYPKGESYEDLVQRLEPVIMELERQENVLVICHQAVMRCLLAYFLDKSSDELPYLKCPLHTVLKLTPVAYGCRVESIYLNVEAVNTHRDK
human  451 PENVDITREPEEALDTVPAHY 471
  rat  451 PENVDITREAEEALDTVPAHY 471
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* To whom correspondence should be addressed