

Nucleotide sequence of murine triosephosphate isomerase cDNA

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Triosephosphate isomerase [(TPI), E.C.5.3.1.1] catalyzes the interconversion of glyceraldehyde 3-phosphate and dihydroxyacetone phosphate, and has an essential role in glycolysis, gluconeogenesis, fatty acid synthesis, and the pentose shunt (1). In mammals, the enzyme consists of two polypeptide chains that are 248 amino acids and identical except for possible post-translational modifications (2). We report here the cDNA sequence and deduced amino acid sequence for murine TPI. The cDNA was isolated from a pcDpolyBN⁻ expression library that was prepared using poly(A)⁺ RNA from murine P19 cells (3). The cDNA was identified by hybridization to the human counterpart (4, 5). Murine and human TPI cDNA sequences are 87.7% similar within the translated regions and encode proteins that are 94.4% similar. Murine and human 5' and 3' untranslated regions differ in both size and sequence (e.g., the murine 3' untranslated region is 554 bp whereas the human 3' untranslated region is 448 bp), and because of this it is difficult to determine if we have isolated the entire 5' end.

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1  TTTTGTACTG ACCTTCAGAG ACTTGAGCCT GGTACA ATG GCG CCT ACC AGG AAG TTC TTC GTT GGG GGC
   N W K M N G R K K C L G E L I C T L N A A 31
70  AAC TGG AAG ATG AAC GGG AGG AAG AAG TGC CTG GGA GAA CTC ATC TGC ACC CTG AAC GCA GCC
   N V P A G T E V V C A P P T A Y I D F A R 52
133 AAC GTG CCG GCA GGC ACC GAG GTG GTT TGT GCA CCG CCC ACC GCT TAC ATC GAC TTT GCC AGA
   Q K L D P K I A V A A Q N C Y K V T N G P 73
195 CAG AAG CTG GAT CCC AAA ATT GCT GTG GCC GCA CAG AAC TGC TAC AAA GTG ACC AAT GGG CCT
   F T G E I S P G M I K D L G A T W V V L G 94
259 TTC ACT GGG GAA ATC AGC CCT GGC ATG ATC AAA GAC TTA GGA GCC ACC TGG GTC GTG CTG GGG
   H S E R R H V F G E S D E L I G Q K V S H 115
322 CAC TCA GAA AGA AGA CAT GTC TTT GGA GAA TCA GAT GAG CTG ATT GGC CAG AAA GTG AGC CAC
   A L A E G L G V I A C I G E K L D E R E A 136
385 GCC CTA GCA GAG GGA CTC GGG GTG ATC GCC TGC ATC GGG GAG AAG CTA GAC GAA AGG GAA GCC
   G I T E K V V F E Q T K V I A D N V K D W 157
448 GGC ATC ACC GAG AAG GTC GTG TTC GAG CAA ACC AAG GTC ATC GCA GAT AAT GTG AAA GAC TGG
   S K V V L A Y E P V W A I G T G K T A T P 178
511 AGC AAG GTG GTC CTG GCC TAT GAA CCT GTG TGG GCC ATT GGG ACT GGC AAG ACG GCA ACC CCT
   Q Q A Q E V H E K L R G W L K S N V N D G 199
574 CAG CAG GCA CAG GAA GTA CAC GAG AAG CTC CGG GGA TGG CTG AAA TCC AAT GTC AAT GAT GGG
   V A Q S T R I I Y G G S V T G A T C K E L 220
637 GTG GCT CAG AGC ACC CGG ATC ATT TAT GGA GGT TCT GTG ACT GGA GCA ACC TGC AAA GAG CTG
   A T P A D V D G F L V G G A S L K P E F V 241
700 GGA ACG CCA GCT GAC GTG GAC GGC TTC CTT GTG GGT GGC GCA TCT CTC AAG CCT GAA TTT GTG
   D I I N A K Q *** 248
763 GAC ATC ATC AAT GCC AAA CAA TGAGCACTGG CCCATCCCTC TACCTGGCTG CATAGCATGG ACTAGGTTCC
834 CAGAAGTTTA GTAACGTCTC CCACGGGTCA CATGTTCTG ATGACATCAT CTGCCCATC TTGTGGCCTA ATCCAGGCTG
914 TACCCTCCTG AGCGGTTTCC ACCGCCCTAT TATGGTTGGG ACCAGGCCAA TCCCTTTACC ACTTACAGTG GGTAGAATCA
994 ACTGTACCCA AGTGGCTCC TAGTGAGGGG AGGGAGTAGA ACTGACTGTC CCTTTGGGCC CTGACAAGTG AAATCACCTT
1074 CCATTGGTTT GGGCTGAAA CTCATGGTTG GAGCACAGGA AGTGGGCTTC GTGTCACTTT GGCCTGTAC TTAGATGGCC
1154 TTGGCTCTAG CTTCACTCCC AAGTCTACT GGATGTCTGA TGCAGAAATT CAGAGCTTTT GGGTCTGAAT TCGGTATACA
1234 TGAGACCCTA AGAGGCCTGG GATAGTCCCC TCCGCCACGG TGCCAAAGCC CCTGTATTGT GTTTGTGAAC CATCCTACAT
1314 GTAAGGGA TAAACACCTG GGCCTGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

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