

# Nucleotide sequence of hamster glyceraldehyde-3-phosphate dehydrogenase mRNA

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Glyceraldehyde-3-phosphate dehydrogenase (GAPDH, EC 1.2.1.12) mRNA level quantitation is widely used as an invariant control for gene expression analysis. Only three vertebrate GAPDH cDNAs have been hitherto isolated: human (1), rat (2) and chick (3). In order to get a probe for RNase-mapping experiments on hamster (*Cricetulus griseus*) mRNAs, we constructed a cDNA library in pBluescript KSII (Stratagene) from CCL39 cell line (adult lung fibroblastic cells). A full-length cDNA encoding GAPDH was then isolated. DNA sequence was determined on both strands and processed using BISANCE package (CITI2, Paris). The sequence spans 1266 nucleotides, and exhibits a high degree of identity to each of the previously

known vertebrates sequences. Northern blot analysis (not shown) revealed the presence of a single mRNA species expressed from hamster GAPDH multigenic family (4).

## REFERENCES

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10      20      30      40      50      60      70      80      90      100     110     120
GGCTCTGCTCCTCCCTGTTCTAGAGACAGCCGCATCTTTCCGTGCAATGCCAGCCTCGCTCCGGAGACGCAATGGTGAAGGTCGGCGTGAACGGATTTGGCCGCTATTGGACGCTGGT
                                     M V K V G V N G F G R I G R L V
130     140     150     160     170     180     190     200     210     220     230     240
TACCAAGGCTGCCTTCACTTCTGCAAAAGTGGAAAGTTGTTGCCATCAATGACCCCTTCACTTGCACTCACTACATGGTCTACATGTTCCAGTATGACTCTACCCATGGCAAGTTCAAAGG
T R A A F T S G K V E V V A I N D P F I D L N Y M V Y M F Q Y D S T H G K F K G
250     260     270     280     290     300     310     320     330     340     350     360
CACAGTCAAGGCTGAGAATGGAAAGCTTGTCAATCAACGGGAAGGCCATCACCATCTTCCAGGAGCGAGATCCCGCCAAACATCAAATGGGGTATGCTGGCCGCGAGTATGTTGTGGAATC
T V K A E N G K L V I N G K A I T I F Q E R D P A N I K W G D A G A E Y V V E S
370     380     390     400     410     420     430     440     450     460     470     480
TACTGGCGTCTTCCACCACCATGGAGAAGGCTGGGGCCCACTTGAAGGGCGGGCCAAAGAGGGTATCATCTCCGCCCTTCTGCTGATGCCCCCATGTTTGTGGTGGTGTGAACCAAGA
T G V F T T N E K A G A H L K G G A K R V I I S A P S A D A P M F V M G V N Q D
490     500     510     520     530     540     550     560     570     580     590     600
CAAGTATGACAACTCCCTCAAGATTGTCAGCAATGGCTGTCACCAACCACTGCTTAGCCCCCTGGCCAAAGTTCATCCATGACAACTTTGGCATTGTGGAAGGACTCATGACCAAGGT
K Y D N S L K I V S N A S C T T N C L A P L A K V I H D N F G I V E G L M T T V
610     620     630     640     650     660     670     680     690     700     710     720
CCATGCCATCACTGCCACCCAGAAGACTGTGGATGGCCCTCCGGAAAGCTGTGGCGTATGGCCGTGGGGCTGCCAGAACATCATCCCTGCATCCACTGGCGCTGCCAAGGCTGTGGG
H A I T A T Q K T V D G P S G K L W R D G R G A A Q N I I P A S T G A A K A V G
730     740     750     760     770     780     790     800     810     820     830     840
CAAAGTCAATCCAGAGCTGAACGGGAAGCTGACTGGCATGGCCTTCCGTGTTCTACCCCCAAAGTGTCCGTTTGGTATCTGACATGTCGCCTGGAGAAAACCTGCCAAGTATGAGGACAT
K V I P E L N G K L T G M A F R V P T P N V S V V D L T C R L E K P A K Y E D I
850     860     870     880     890     900     910     920     930     940     950     960
CAAGAAGTGGTGAAGCAGGCACTCTGAGGGCCCACTGAAGGGCATCCTGGGTACACCCAGGACAGGTTGTCTCCTCGCACTTCAACAGTGACTCCCACTTCTCCACCTTTGATGCTGG
K K V V K Q A S E G P L K G I L G Y T E D Q V V S C D F N S D S H S S T F D A G
970     980     990     1000    1010    1020    1030    1040    1050    1060    1070    1080
GGCTGGCATTGCTCTCAATGACAACTTTGTAAGCTCATTTCTGGTATGACAATGAAATTTGGCTACAGCAACAGAGTGGTGGACCTCATGGCCCTACATGGCCCTCCAAGGAGTAAGAAGC
A G I A L N D N F V K L I S W Y D N E F G Y S N R V V D L M A Y M A S K E *
1090    1100    1110    1120    1130    1140    1150    1160    1170    1180    1190    1200
CCACCTGGACCATCCACCCCAAGCACTCGAGCAAGAGGGAGGCCCTGGCTGCTGAGCAGTCCCTGTCCAATAACCCCCACACCGATCATCTCCCTCACAGTTTCCATCCCAGACCC
1210    1220    1230    1240    1250    1260
CCAGAATAAGGAGGGGCTTAGGGAGCCCTACTCTCTTGAATACCATCAATAAAGTTCACTGCACCC
    
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