

A cDNA clone encoding human cAMP-dependent protein kinase catalytic subunit C $\alpha$ 

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We have determined the nucleotide sequence from both complementary strands of a human cDNA coding for cAMP-dependent protein kinase catalytic subunit type  $\alpha$  (cAPK-C $\alpha$ ). This cDNA was one of many protein kinase cDNAs isolated from a HeLa cell library by screening with oligonucleotide probes designed to recognize target sequences encoding highly conserved segments within the catalytic domains (1). The deduced human cAPK-C $\alpha$  amino acid sequence of 350 residues (excluding the initiator methionine) differs from the bovine (2) and murine (3) sequences at 3 and 7 positions, respectively. In the figure, we have indicated these variant positions in boxes, with substituted residues indicated at upper right (bovine) and upper left (murine). At the nucleotide level, the sequence coding for human cAPK-C $\alpha$  is 91% identical to the murine (3) protein-coding sequence. (Supported by N.I.H. grant GM-38793).

1 CAGTNGCTCCGGGCGCCGGCCGCGAGCCAGCACCCGCGCGCGCAGCTCCGGGACCGGCCCGCGCCGCGCC

1 (M) G N A A A A K K G S E Q E S V K E F L A K A  
75 GCCGCGATGGGCAACGCGCCGCGCCGCAAGAAGGGCAGCGAGCAGGAGCGGTGAAAGAATTCTTAGCCAAAGCC

23 K E D F L K K W E <sup>T N</sup> [S] P <sup>S</sup> [A] Q N T A <sup>O</sup> [H] L D Q F <sup>D</sup> [E] R I K  
150 AAAGAAGATTTTCTTAAAAAATGGGAAAGTCCCGCTCAGAACACAGCCACTTGGATCAGTTGAACGAATCAAG

48 T L G T G S F G R V M L V K H <sup>M</sup> [K] E <sup>S</sup> [T] G N H Y A M K  
225 ACCTCGGCAGGGGCTCCTTCGGGGGGTGATGCTGGTGAACACAAGGAGACCGGGGAACCACATGCCATGAAG

73 I L D K Q K V V K L K Q I E H T L N E K R I L Q A  
300 ATCCTCGACAAACAGAAGTGGTGAACAGATCGAACACACCCCTGAATGAAAAGCGCATCTGCAAGCT

98 V N F P F L V K L E F S F K D N S N L Y M V M E Y  
375 GTCAACTTTCGGTTCCTCGTCAAACCTCGAGTTCTCCTTCAAGGACAACCTCAAACCTTATACATGGTTCATGGAGTAC

123 V <sup>A</sup> [P] G G E M F S H L R R I G R F S E P H A R F Y A  
450 GTGCCCGGGGGGAGATGTTCTCACACCTACGGCGGATCGGAAGGTTTCAGTGAGCCCCATGCCCGTTTCTACGCG

148 A Q I V L T F E Y L H S L D L I Y R D L K P E N L  
525 GCCCAGATCGTCTGACCTTTGAGTATCTGCACTCGCTGGATCTCATCTACAGGGACCTGAAGCCGGGAAATCTG

173 L I D Q Q G Y I Q V T D F G F A K R V K G R T W T  
600 CTCATTGACCAGCAGGGCTACATTCAGGTGACAGACTTCGGTTTCGCCAAGCGCGTGAAGGGCCGCACTTGGACC

198 L C G T P E Y L A P E I I L S K G Y N K A V D W W  
675 TTGTCCGGCACCCCTGAGTACCTGGCCCTGAGATTATCCTGAGCAAAGGCTACAACAAGCCGTTGGACTGGTGG

223 A L G V L I Y E M A A G Y P P F F A D Q P I Q I Y  
750 GCCCTGGGGTTCTTATCTATGAAATGGCCGCTGGCTACCGCCCTTCTTCGCAGACCAGCCCATCCAGATCTAT

248 E K I V S G K V R F P S H F S S D L K D L L R N L  
825 GAGAAGATCGTCTCTGGGAAGGTGCGCTTCCCTTCCCACTTCAGCTCTGACTTGAAGGACCTGCTGCGGAACCTC

273 L Q V D L T K R F G N L K <sup>D</sup>[N] G V N D I K N H K W F  
900 CTGCAGGTAGATCTACCAAGCGCTTTGGGAACCTCAAGAATGGGGTCAACGATATCAAGAACCACAAGTGTTT

298 A T T D W I A I Y Q R K V E A P F I P K F K G P G  
975 GCCACAACACTGACTGGATTGCCATCTACCAGAGGAAGGTGGAAGCTCCCTTCATACCAAAGTTTAAAGCCCTGGG

323 D T S N F D D Y E E E E I R V S I N E K C G K E F  
1050 GATACGAGTAACTTTGACGACTATGAGGAAGAAGAAATCCGGGTCTCCATCAATGAGAAGTGTGGCAAGGAGTTT

348 <sup>T</sup>[S] E F \*

1125 TCTGAGTTTTAGGGGCATGCCTGTGCCCCCATGGGTTTTCTTTTTCTTTTTCTTTTTTTGGTGGGGGGGGT  
1200 GGAGGGTTGGATTGAACAGCCAGAGGGCCCCAGAGTTCCTTGCATCTAATTTACACCCCAACCCACCCCTCCAGGG  
1275 TTAGGGGAGCAGGAAGCCAGATAATCAGAGGGACAGAAACACCAGTGCCTCCCCCTCATCCCTTCACCCCTCC  
1350 TGCCCTCTCCCACTTTCCCTTCTCTTTCCCCACAGCCCCCAGCCCTCAGCCCTCCAGCCCACTTCTGC  
1425 CTGTTTTAAACGAGTTTCTCAACTCCAGTCAGACCAGGCTTGTCTGGTGTATCCAGGGACAGGGTATGAAAAGAG  
1500 GGGCTCACGCTTAACTCCAGCCCCACCCACACCCCATCCCAACCAACAGGCCCACTTGCTAAGGGCAAA  
1575 TGAACGAAGCGCCAACCTTCCTTTCCGGAGTAATCCTGCCTGGGAAGGAGAGATTTTAGTGACATGTTTCTAGTGGG  
1650 TTGCTTGCTAGAAATTTTTTAAAAAACAAATTTAAAAATCTTATTTAAGTCCACCAGTGCCTCCCTCCCTCC  
1725 TTCCTTACTCCACCCCTCCCATGTCCCCCATTCCTCAAAATCCATTTTAAAGAGAAGCAGACTGACTTTGGAA  
1800 AGGGAGGCGCTGGGGTTTGAACCTCCCGCTGCTAATCTCCCTGGGCCCTCCCGGGGAATCCTCTCTGCCAA  
1875 TCCTGCGAGGGTCTAGGCCCTTTAGGAAGCCTCCGCTCTCTTTTCCCAACAGACCTGTCTTCCACCTTGGGC  
1950 TTTGAAAGCCAGACAAAGCAGCTGCCCTCTCCCTGCCAAAGAGGAGTCATCCCCAAAAGACAGAGGGGGAGC  
2025 CCAAAGCCAAAGTCTTTCCCTCCAGCAGCGTTTCCCCCAACTCCTTAATTTTATCTCCGCTAGATTTTAAAGT  
2100 CAGCCTTCCCTCAGCTGAGTGGGGAGGGCATCCCTGCAAAAGGGAACAGAAAGAGGCCAAGTCCCCCAAGCCAC  
2175 GGCCCGGGTTCAAGGCTAGAGCTGCTGGGGAGGGGCTGCCTGTTTTACTCACCCACCAGCTTCCGCTCCCCCA  
2250 TCCTGGGCGCCCTCCTCCAGCTTAGCTGTACAGTGTCCATCACCTCTCCCCACTTTCTCATTGTGCTTTTTT  
2325 CTCTCGTAATAGAAAAGTGGGGAGCCGCTGGGGAGCCACCCCATTCATCCCGTATTTCCCCCTCTCATAACTTC  
2400 TCCCATCCAGGAGGAGTTCTCAGGCTGGGGTGGGGCCCCGGTGGGTGCGGGGGCGATTCAACCTGTGTGCT  
2475 GCGAAGGACGAGACTTCCTCTTGAACAGTGTGCTGTTGTAACATATTTGAAAACATTACCAATAAAGTTTGT

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