

The nucleotide sequence of chicken smooth muscle myosin light chain two

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Chicken smooth muscle regulatory, phosphorylatable myosin light chain (MLC₂) was isolated from a chicken gizzard cDNA library constructed in lambda gt10. The 1075 base pair clone (including poly A tail) was obtained by screening the library with a rat aorta smooth muscle MLC₂ cDNA obtained from Dr. Mark Taubman(1). Prior to obtaining this cDNA, two sequences had been published from amino acid analysis of chicken smooth muscle MLC₂ tryptic peptides which differed at the amino terminus(2,3). The coding region (deduced from the cDNA sequence presented here, initiation and termination codons boxed) predicts a 171 amino acid MLC₂, which is identical to that obtained by Pearson et al.(2) from analysis of the purified chicken gizzard protein over the first seventeen amino acids containing the phosphorylation site. The remainder of the predicted protein is identical to that obtained by Maita et al.(3). Although the DNA sequence for the MLC₂ coding region shares 82% homology with the rat cDNA(1), the proteins encoded by the DNAs are 94% homologous. Since most of the DNA changes are at third base positions (and the untranslated regions are divergent) there is a strong evolutionary conservation pressure to maintain the smooth muscle MLC₂ protein sequence.

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GCTGTCACT TCCCCAAC GCACTGAGGC CGGATCCCC CCCCAGGTA CCACCCAGC TGCCAACATG TCCAGCAAC GTGCCAAGC CAAGACCACC 100
AAGAAGCGCC CGCAGCGCGC CACCTCCAAT GTCTTCGCTA TGTTGCACCA GTCACAGATC CAGGAGTTCA AGGAAGCTTT CAACATGATC GACCAGAACC 200
GTGACGGGT CATTGACAAG GAGGATCTGC ATGACATGCT GCCTTCATG GGGAAAAACC CCACCGACGA GTACCTGGAG GGGATGATGA GTGAGGCACC 300
GGGGCCCATC AACTTCACCA TGTTCCCTAC CATGTTTGGG GAGAAGCTGA ATGGCACCGA CCCGGAGGAT GTAATCCGCA ATGCCCTTTC CTGCTTTGAC 400
GAGGAGCCGT CAGGGTTCAT TCACGAGGAC CATCTGCGTG AACTGCTGAC CACCATGGGA GACAGGTCA CTGACGAGGA GGTGACGAG ATGTACCGGG 500
AGGCGCCCAT CGACAAGAAG GGCAACTTCA ACTATGTGGA GTTCACCCGC ATCCTGAAGC ACGGAGCTAA GGACAAGGAC GATTAGAGCT GAGAGCCGCC 600
CCCCTGCCTT CCCGCACGTG CCACCCACGC TCCCGACAGT GCCACCCAGC CCCCTGCCCC TCGCTGCCCA GCCCCACCAT AGGCTCCCC TGCCGGGACA 700
GCCCTGCTCC GTGCTGGTGC TGCCATCGCG TGCTGCTGCT TCCTCTCCCA TTGCCCCGGG ATCCAGCCA GGCTCCCCC CACGACGACC GCTGGCTCAC 800
CCTGCTCAGC AGAGGGTCCA GACAGGGGCA GCGACCGGG GAGTGTGGC CGGGGGAGTT CCGGCTGGCT CAAAGCAGTG CAACCTTCC AGAGGACCTA 900
ACACAGAAGG AAGCTCTCCC TTTCTCCACA CTCCTTCTCT TAGGAAAGAA AGAAAAAAGC TTTTGTTC TCCTCTTTGG CTGTTTTATG GCTTTAGAGC 1000
CTGTGATCTA CGGGATTGAG AAAGCTGAAG CAGCCTATAA AGTCTGATGG GTGTGACAAA AAAAAA AAAA

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