

A cDNA sequence encoding cytoskeletal gamma-actin from rat

Chester W.Brown*, Kirk M.McHugh and James L.Lessard
Children's Hospital Medical Center, Division of Basic Science Research, Elland and Bethesda Avenues, Cincinnati, OH 45229, USA

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We have isolated and sequenced three clones from rat stomach or kidney cDNA libraries. These clones encode the cytoskeletal isoform of γ-actin as determined by comparison with published protein sequence (1), as well as with cDNA sequences from the human (2) and mouse (3). The sequence of the longest kidney clone, pRCγA-2, is shown below. It displays poly 'G' and 'C' homopolymeric tails, 12 nucleotides (nt) of 5′ untranslated sequence, the entire cytoskeletal γ-actin coding sequence, and 716 nt of 3′ untranslated region (3′UTR) which contains a consensus polyadenylation signal and poly-A tail. Two other clones, pRCγA-15 were isolated from a rat stomach signal and poly-A tail. Two other clones, pRCγA-4 and pRCγA-4 and pRCγA-15 were isolated from a rat stomach library. These clones are identical in nucleic acid sequence to pRCγA-2 in aligned regions, but are truncated on both the 3′ and 5′ ends. In addition, clone pRCγA-4 contains an internal deletion of 145 nt in the 3′UTR. The deleted sequence has been underlined below.

The 3′ untranslated region of the rat cytoskeletal γ-actin mRNA has been well-conserved throughout evolution as demonstrated by a 94.6% and 81.5% similarity with mouse and human 3′UTR's, respectively (3, 2). There are a number of structural features in this region of the molecule which should be mentioned. First, there are two inverted repeat sequences which are predicted to be very stable, according to the rules of Tinoco *et al.* (4). These regions are boxed below. Also, a consensus 'TATA' transcription initiation signal is evident beginning at nt 1488. Interestingly, transcription of the human salivary α-amylase gene has been shown to initiate approximately 20 nt downstream of a comparable site in a cytoskeletal γ-actin pseudogene (5, 6). This finding demonstrates that the 3′UTR of cytoskeletal γ-actin in an altered form can serve as a functional promoter.

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-21 GGGGGGGGGCTGCCGATCGCAATGGAAGAAGAAATCGCCGCCCTCGTCATTGACAATGGCTCCGGCATGTGCAAAGCTGGCTTTGCTGGGGACGACGCCCCCAGGGCC
                    MetGluGluGluIleAlaAlaLeuValIleAspAsnGlySerGlyMetCysLysAlaGlyPheAlaGlyAspAspAlaProArgAla
  88 GTGTTTCCTTCCATCGTCGGGCGCCCCCGACACCAGGGTGTCATGGTGGGCATGGGCCAGAAAGACTCGTACGTGGGTGATGAGGCCCAGAGCAAGAGGGGTATTCTG
     ValPheProSerIleValGlyArgProArgHisGlnGlyValMetValGlyMetGlyGlnLysAspSerTyrValGlyAspGluAlaGlnSerLysArgGlyIleLeu
 196 ACCCTGAAGTACCCTATTGAGCACGGCATTGTCACCAACTGGGACGACATGGAGAAGATCTGGCACCACACCTTCTACAACGAGCTGCGTGTGGCCCCTGAGGAGCAC
     ThrLeuLysTyrProIleGluHisGlyIleValThrAsnTrpAspAspMetGluLysIleTrpHisHisThrPheTyrAsnGluLeuArgValAlaProGluGluHis
 304 CCGGTGCTTCTGACCGAGGCCCCCCTGAACCCCAAAGCTAACAGAGAGAAGATGACGCAGATAATGTTTGAAACCTTCAATACCCCAGCCATGTACGTGGCCATTCAG
     ProValLeuLeuThrGluAlaProLeuAsnProLysAlaAsnArgGluLysMetThrGlnIleMetPheGluThrPheAsnThrProAlaMetTyrValAlaIleGln
 412 GCGGTGCTCTCCTTGTATGCATCTGGGCGTACCACTGGCATTGTCATGGACTCTGGTGACGGGGTCACACACACAGTGCCCATCTATGAGGGCTACGCCCTTCCCCAC
     AlaValLeuSerLeuTyrAlaSerGlyArgThrThrGlyIleValMetAspSerGlyAspGlyValThrHisThrValProIleTyrGluGlyTyrAlaLeuProHis
 520 GCCATCTTGCGTCTGGACCTGGCTGGCCGGGACCTGACAGACTACCTCATGAAGATCCTGACTGAAAGGGGCTACAGCTTTACCACCACTGCTGAGAGGGAAATTGTT
     AlaIleLeuArgLeuAspLeuAlaGlyArgAspLeuThrAspTyrLeuMetLysIleLeuThrGluArgGlyTyrSerPheThrThrThrAlaGluArgGluIleVal
 628 CGTGACATAAAGGAGAAGCTGTGCTATGTTGCCCTGGATTTTGAGCAAGAAATGGCTACTGCTGCATCATCTTCCTCTTTGGAGAAGAGTTATGAGCTGCCTGATGGG
     ArgAspIleLysGluLysLeuCysTyrValAlaLeuAspPheGluGlnGluMetAlaThrAlaAlaSerSerSerLeuGluLysSerTyrGluLeuProAspGly
 736 CAGGTGATCACCATTGGCAATGAGCGCTTCCGGTGTCCAGAGGCTCTCTTCCAGCCTTCCTTCCTGGGCATGGAGTCCTGTGGCATCCACGAGACCACCTTCAACTCC
     GlnValIleThrIleGlyAsnGluArgPheArgCysProGluAlaLeuPheGlnProSerPheLeuGlyMetGluSerCysGlyIleHisGluThrThrPheAsnSer
 844 ATCATGAAGTGTGATGTGGACATCCGCAAAGACCTGTATGCCAACACAGTGCTGTCTGGTGGTACCACCATGTATCCAGGCATTGCTGACAGGATGCAGAAGGAGATC
     IleMetLysCysAspValAspIleArgLysAspLeuTyrAlaAsnThrValLeuSerGlyGlyThrThrMetTyrProGlyIleAlaAspArgMetGlnLysGluIle
 952 ACAGCCCTGGCTCCCAGCACAATGAAGATTAAGATCATTGCTCCTCCTGAACGCAAGTACTCAGTCTGGATTGGCGGCTCCATCCTGGCCTCACTGTCCACCTTCCAG
     ThrAlaLeuAlaProSerThrMetLysIleLysIleIleAlaProProGluArgLysTyrSerValTrpIleGlyGlySerIleLeuAlaSerLeuSerThrPheGln
1060 CAGATGTGGATCAGCAAGCAGGAGTATGACGAGTCAGGCCCCTCCATTGTCCACCGCAAATGCTTCTAGATGGACTGAGCAGGTGCCAGGCATCTGCTGCATGAGCTG
     GlnMetTrpIleSerLysGlnGluTyrAspGluSerGlyProSerIleValHisArgLysCysPheEnd
1168 ATTCTGAAGTATCGATTTGCCCTGGCAAATGTACACACGTCATGCTAGCCTCATGAAACTGGAATAAGCCTTTGAAAAGAAATTTGTCCTTGAAGCTTGTATCTGATA
1276 TCAGCACTGGATCGTAGAACTTGTTGCTGATTTTTGACCTTGTATTCAAGTTAACTGTTCCCTTGGTATATGTTTAATACCCTGTGCATATCTTGATTTAGTCCTTAG
1384 TTCATGTGGCTCGGTCACTTGGTGGCTGGGGAGATCTGTGGAAAAGTCAGTCAGTCCCCAGCCTAGTGGATCTCTGTGAGCACCATGTAGTGATCTGTGCAGGGTATT
1492 AACCAACAGCAGACTTCCAGGATTTCCCGAGGCTGGCAAGGGTTCCTGAACTAGTTACCACTTCTTTTCTTGCCAGTCTAACAGGGTGGGAAAGTCCGAGCCTTAGGA
1600 CCCAGTTTCTGTTCTGGTTTTTTCCCTCCTGACCTCCATGGGTTGTTACTTGCCTTGAGTTGGGAACGTTTGCATCGACACCTGTAAATGTATTCATCCTTTTAATTT
1708 ATGTAAGGTTTTTGTACTCAATTCTTTAAGAAATGACAAATTTTGGTTTTCTACTGTTCAGTGAGAACATTAGGCCCCAGCAACACGTCATTGTGTAAAGAGAAATAA
1816 AAGTGCTGCAGTAAAAAAAAAAAAAAACCCCCCCCCCCCCCC 1857
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* To whom correspondence should be addressed