

Human nonsarcomeric 20,000 Da myosin regulatory light chain cDNA

James W. Grant*, Rui Q. Zhong, Pat M. McEwen and Susan L. Church

Department of Pediatrics, Washington University School of Medicine, St Louis, MO 63110, USA

Submitted August 20, 1990

EMBL accession no. X54304

We have isolated from a human placental cDNA library a novel full length cDNA representing human RLC. This clone shares 86% homology with the rat RLC-A amino acid coding region nucleotide sequence and 70% homology with the rat 3'-untranslated region including identical polyadenylation sequences (underlined below) (1, 2). The derived amino acid sequence contains only 2 substitutions (letters in parentheses below are from the rat RLC-A sequence) and one deletion (represented by the asterisks-*). There is no significant homology with the 3'-untranslated region of the human umbilical vein RLC cDNA reported by Kumar (3). This sequence supports the

presence of a RLC multigene family in humans and provides the necessary information to isolate the corresponding genes.

REFERENCES

1. Grant, J., Taubman, M.B., Church, S.L., Johnson, R.L. and Nadal-Ginard, B. (1990) *J. Cell. Biol.* in press.
2. Taubman, M.B., Grant, J.W. and Nadal-Ginard, B. (1987) *J. Cell. Biol.* **104**, 1501-1513.
3. Kumar, C.C., Mohan, S.R., Zavodny, P.J., Narula, S.K. and Leibowitz, P.J. (1989) *Biochemistry* **28**, 4027-4035.

```

                    5'-gcccagcgcgtggttttagcggctc 28
tctgggtagcagggtggtgatagcggccgagggtcgggaaggtgctcggattctcgtagctgtccgg 99
gacttaaccaccacc ATG TCG AGC AAA AGA ACA AAG ACC AAG AAC *** AAG AAG CGC 153
                    M S S K R T K T K T K K R
                    (A) (T)

CCT CAG CGT GCA ACA TCC AAT GTG TTT GCT ATG TTT GAC CAG TCA CAG ATT CAG 207
P Q R A T S N V F A M F D Q S Q I Q

GAG TTC AAA GAG GCC TTC AAC ATG ATT GAT CAG AAC AGA GAT GGT TTC ATC GAC 261
E F K E A P N M I D Q N R D G F I D

AAG GAA GAT TTG CAT GAT ATG CTT GCT TCA TTG GGG AAG AAT CCA ACT GAT GAG 315
K E D L H D M L A S L G K N P T D E

TAT CTA GAT GCC ATG ATG AAT GAG GCT CCA GGC CCC ATC AAT TTC ACC ATG TTC 369
Y L D A M M N E A P G P I N F T M F
                    (R)

CTC ACC ATG TTT GGT GAG AAG TTA AAT GGC ACA GAT CCT GAA GAT GTC ATC AGA 423
L T M F G E K L N G T D P E D V I R

AAT GCC TTT GCT TGC TTT GAT GAA GAA GCA ACT GGC ACC ATA CAG GAA GAT TAC 477
N A F A C F D E E A T G T I Q E D Y

TTG AGA GAG CTG CTG ACA ACC ATG GGG GAT CGG TTT ACA GAT GAG GAA GTG GAT 531
L R E L L T T M G D R F T D E E V D

GAG CTG TAC AGA GAA GCA CCT ATT GAT AAA AAG GGG AAT TTC AAT TAC ATC GAG 585
E L Y R E A P I D K K G N F N Y I E

TTC ACA CGC ATC CTG AAA CAT GGA GCC AAA GAC AAA GAT GAC tgaataactcaaa 642
F T R I L K H G A K D K D D *

tccagccaacgtccttgtgcactttgggtattctgagattttctcttgccattcccttagccttagca 713
gctttgcaatttcctgttatttattctcagccattttggccatagtatctttataatcagactggaaac 784
gggactttctattaatcattttcagaataaaaaataggataatttaacctaccagcccttctcccaca 855
taactgtgggtctatacagagtcaatatatttttcagagaaagttagttcggctcgattttttctgaa 926
ataattaaactttattgc-3' 944

```

* To whom correspondence should be addressed