

Sequence of a mouse U2 snRNA gene expressed in transfected mouse cells

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We have described a B1 cluster containing a unique B1 dimer upstream from a mouse U2 snRNA gene (1). This U2 snRNA gene is distinct from a previously reported mouse gene as determined by sequence and genomic blot analyses. The sequence immediately downstream from the B1 cluster through the U2 snRNA gene and into its 3' flank is shown below. Regions I (-50 to -60) and II (-224 to -240) are homologous to sequences in human (2) and *Xenopus* (3) U2 snRNA genes which function to determine correct initiation and activation of transcription, respectively, in *Xenopus* oocytes. Sequences from Region III (+208 to +221) are essential for 3' end formation of human U2 snRNA (4). The Dde I fragment from -1057 to +21 displays strong promoter activity when ligated, in the normal orientation only, to a promoterless CAT gene and transfected into Ltk- and PCC3 embryonal carcinoma mouse cells. Deletion mutants of U2 snRNA-CAT constructs indicate that sequences from -114 to -381 are essential for efficient promotion of mammalian U2 snRNA transcription in a homologous system. No transcription was detected in constructs containing sequences from -114 to +167.

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-1060      TCTGAGCTT TGTAATTTT ATTCACTTCT TGTGCTTTT AGATTTTTTT CTTACATTTA CTTATGTATG AATGTCACA CACACACACA CACACACATA
-960      CGTCATGTAA ATATGTATGC CACAGTGCC TGCTGCTCT CTAGAACGAA GGTAAAGAT AACTGTGAGC CACCATCGGG TGTGGGAAT CGAACCTGGA
-860      TCTTTTCCA ATCTATAGAA CGTGTAGACC CTGCCTCAA AACAGAATAG CGATATATT TTAGATAATG TATGATATGA AATTTAATAT GATTAGGGAG
-760      TTCTTGCTG ACCCATGCCA AAGTGCCCC TTGAGAAATG ACGCCAAGCA ACAGAGATCT GGTGGGGAGT TATTTGGGGG AAGAGAGGGG AGGGAGGGCT
-660      TGGAGAAGGG GTTGAGGTAG ATGAACAGAT AGGCAGACAG AGGGGAACAG AGTCACGAGG GCAGAGAAAG CAGGGGACAG AGAAGGAGAG AATGGGGGCT
-560      GGGGCCAGAG ACCGCAAGGA ACAGCTGGGA ACAGAGAGAG CTGGAGTGGT GAAGCAGTCG TTATCACCAC ACCTGAAGAA GCACCATAAG CTGGTTGCTT
-460      GATCCTAGGG AGGAGCCTAG CGGAATCGCC TGTAACATAA TAAATTAAGC AGAAAATCGA AAGGCCCTTT TTCCTCAAGG ACCTTTTGTG GTGGGTGTGG
-360      TCTGAAAGAC TGGCAAGAAG AACCTGGTGT TATCGCAGGG AAAGTCAAT ACGTCCCTTC TGCGCCCGGG TTGCGCTCTA CAGGCGAGAA GCGGAAAAAG
-260      CAGTCCAGGT TCGAGCTTTC GGCCTGGTTC GGCGGGGCAT GCAAAATACT GCTCTGTGGA ACTCTGGGAG CAAAAACAAA AAAGTCAAC CAAAATCTCT
-160      CGGCCCTCTT GAATCTTACA GGCTTTTCTG GCGTAAAGG TGGTGTACTC AATGAAGAGG AGAGTCTGTG TTGGCTGCAT GTTTGAGTCG GTTGGTTGGT
-60      GACTGTGAAT TAAAGGTGTG GTCGCTGTTG AGTGTATGGG GCGTGTGGCC GTAGTTCGGT ATCGCTTCTC GGCCTTTTGG CTAAGATCAA GTGTAGTATC
Region I                                     U2 snRNA gene                                     +140
CGGCCCTCTT GAATCTTACA GGCTTTTCTG GCGTAAAGG TGGTGTACTC AATGAAGAGG AGAGTCTGTG TTGGCTGCAT GTTTGAGTCG GTTGGTTGGT
+1
GACTGTGAAT TAAAGGTGTG GTCGCTGTTG AGTGTATGGG GCGTGTGGCC GTAGTTCGGT ATCGCTTCTC GGCCTTTTGG CTAAGATCAA GTGTAGTATC
Region II                                     U2 snRNA gene                                     +140
TGTTCTTATC AGTTAATAT CTGATACGTC CTCTATCCGA GGACAATATA TTAAATGGAT TTTTGGAAGT AGGAGTTGGA ATAGGAGCTT GCTCCGTCGA
+240
CTCCACGCAT CGACCTGGTA TTGCAGTACC TCCAGGAACG GTGCACCCTC TCTGGGGAGT AAAGTTGGTT TTAAAGTCAG AGCATGGTGA TTGTAGGGCA
+265                                     Region III
GTCCAACCTT TTTAATATG CTGTG

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