

cDNA sequences of two β -globin genes in a Sprague-Dawley rat

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In the attempts to understand the regulatory controls underlying the complex pattern of globin gene expression in the rat (1) we proceeded to clone the globin gene(s). We report here the nucleotide sequences and the predicted amino acid sequences from two differing beta-globin genes, isolated from our cDNA library of the Sprague Dawley rat. The nucleotide sequences were determined by the M13 dideoxy-sequencing method. The sequences, RBGM1 and RBGM2 showed extensive homology with other beta-globin like sequences. RBGM1 is almost identical to that of Prbg21 (2), except for two nucleotides which are at variant, and that the former sequence extends for another 43 bases in the 5' end. On the otherhand, RBGM2 differs significantly from RBGM1, both within the coding and the 5' flanking sequences. The first 442 bases of RBGM2 are identical to one of our genomic clones with only one nucleotide different up to the termination codon (3). However, within the 3' untranslated region, RBGM2 has only 70% homology with the genomic clone.

RBGM1

1	TGCTTCTGAC	ATAGTTGTGT	TGACTCACAA	ACTCAGAAAC	AGACACCATG
51	GTGCACCTGA	CTGATGCTGA	GAAGGCTGCT	GTTAATGGCC	TGTGGGGAAA
101	GGTGAACCCCT	GATGATGTTG	GTGGCGAGGC	CCTGGGCAGG	CTGCTGGTTG
151	TCTACCCCTTG	GACCCAGAGG	TACTTTGATA	GCTTTGGGGA	CTGTCTCTCT
201	GCCCTTGCTA	TCATGGGTAA	CCCTAAGGTG	AAGGCCCATG	GCAAGAAGGT
251	GATAAACGCC	TTCAATGATG	GCCTGAAACA	CTTGGACAAC	CTCAAGGGCA
301	CCTTTGCTCA	TCTGAGTGAA	CTCCACTGTG	ACAAGCTGCA	TGTGAGTCCCT
351	GAGAACTTCA	GGCTCCTGGG	CAATATGATT	GTGATTGTGT	TGGGCCACCA
401	CCTGGGCAAG	GAATTCACCC	CCTGTGCACA	GGCTGCCTTC	CAGAAGGTGG
451	TGGCTGGAGT	GGCCAGTGCC	CTGGCTCACA	AGTACCACCTA	AACCTCTTTT
501	CCTGCTCTTG	TCTTTGTGCA	ATGGTCAATT	GTTCCCAAGA	GAGCATCTGT
551	CAGTTGTTGT	CAAAATGACA	AAGACCTTTG	AAAATCTGTC	CTACTAATAA
601	AAGGCATTTA	CTTTCCTGTC	poly A-tail		

RBGM2

1	CCTCAGGAAC	AGACACCATG	GTGCACCTAA	CTGATGCTGA	GAAGGCTACT
51	GTTAGTGGCC	TGTGGGGAAA	GGTGAACCCT	GATAATGTTG	GCGCTGAGGC
101	CCTGGGCAGG	CTGCTGGTTG	TCTACCCTTG	GACCCAGAGG	TACTTTTCTA
151	AATTTGGGGA	CCTGTCTCTCT	GCCTCTGCTA	TTATGGGTAA	CCCCCAGTTG
201	AAGGCCCATG	GCAAGAAGGT	GATAAATGCC	TTCAATGATG	GCCTGAAACA
251	CTTGACAAC	CTCAAGGGCA	CCTTTGCTCA	TCTGAGTGAA	CTCCACTGTG
301	ACAAGCTGCA	TGTGGATCCT	GAGAACTTCA	GGCTCCTGGG	CAATATGATT
351	GTGATTGTGT	TGGGCCACCA	CCTGGGCAAG	GAATTCACCC	CCTGTGCACA
401	GGCTGCCTTC	CAGAAGGTGG	TAGCTGGAGT	GGCCAGTGCC	CTGGCTCACA
451	AGTACCACCTA	AACCTCTTTT	CCTGCTCTTG	TCTTTGTGCA	ATGGTCAATT
501	GTTCCCAAGA	GAGCATCTGT	CAGTTGTTGT	CAAAATGACA	AAGACCTTTG
551	AAAATCTGTC	CTACTAATAA	AAGGCATTTA	CTTTCCTGTC	poly A-tail

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REFERENCES

1. J.W.O. Tam, C.C.Hui, C. Woo and V.M.S. Lam (1987), In Fucharoen, S. et al (eds). Birth Defects: Original Article Series, Alan R. Liss, Inc., New York, 23 (5A), 133-137.
2. H. Satoh, H. Fujii and T. Okazaki (1987), In Biochemical and Biophysical Research Communications, 146 (2), 618-624.
3. W.M. Wong, V.M.S. Lam, L.Y.L. Cheng and J.W.O. Tam (1988), Nucleic Acid Research 16 (5), 2342.