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# Primary structure of the human beta-adrenergic receptor gene

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A human genomic DNA library (1) was screened with two overlapping 60-mer oligonucleotide probes based on the hamster beta-adrenergic receptor (ßAR) sequence (nucleotides 547-606 and 583-642, respectively) (2). One clone, λhßAR17 was identified and a 12 kb *Eco*RI restriction fragment subcloned (phßAR3). 2305 bp of the hybridizing region was sequenced (Fig. 1). Analysis of the predicted 413 amino acid sequence revealed seven hydrophobic transmembrane domains, characteristic of guanine nucleotide-protein coupled receptors. The entire coding sequence is encoded on a single exon as is also seen in the hamster gene. While the promoter region of this gene is not obvious, the 200 bp 5' of the initiation codon are 77% conserved with the hamster ßAR cDNA sequence indicating that these sequences are most likely transcribed (by comparison, coding sequences are 87.5% conserved). The predicted human and hamster ßAR proteins are 88% homologous, while the turkey ßAR product (3) is 50% conserved with the human sequence.

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   1  GAATTCATGCCGCGTTTCTGTGTTGGACAGGGGTGACTTTGTGCCGGATGGCTTCTGTGTGAGAGCGCGCGCGAGTGTGCATGTCGGTGAGCTGGGAGGGTGTGTCTCAGTGTCTATG
 121  GCTGTGGTTCGGTATAAGTCTAAGCATGTCTGCCAGGGTGTATTTGTGCCTGTATGTGCGTGCCTCGGTGGGCACTCTCGTTTCCTTCCGAATGTGGGGCAGTGCCGGTGTGCTGCCCTC
 241  TGCCTTGAGACCTCAAGCCGCGCAGGCGCCCAGGGCAGGCAGGTAGCGGCCACAGAAGAGCCAAAAGCTCCCGGGTTGGCTGGTAAGCACACCACCTCCAGCTTTAGCCCCTCTGGGGCCA
 361  GCCAGGGTAGCCGGGAAGCAGTGGTGGCCCGCCCTCCAGGGAGCAGTTGGGCCCCGCCCGGGCCCAGCCTCAGGAGAAGGAGGGCGAGGGGAGGGGAGGGAAAGGGGAGGAGTGCCTCGCC
 481  CCTTCGCGGCTGCCGGCGTGCCATTGGCCGAAAGTTCCCGTACGTCACGGCGAGGGCAGTTCCCCTAAAGTCCTGTGCACATAACGGGCAGAACGCACTGCGAAGCGGCTTCTTCAGAGC
 601  ACGGGCTGGAACTGGCAGGCACCGCGAGCCCCTAGCACCCGACAAGCTGAGTGTGCAGGACGAGTCCCCACCACACACCCACACCAGCCGCTGAATGAGGCTTCCAGGCGTCCGCTCGCG
   1                                                                                                  M  G  Q  P  G  N  G  S  A  F  L  L  A  P  N
 721  GCCCGCAGAGCCCCGCCGTGGGTCCGCCTGCTGAGGCGCCCCCAGCCAGTGCGCTTACCTGCCAGACTGCGCGCCATGGGGCAACCCGGGAACGGCAGCGCCTTCTTGCTGGCACCCAAT
  16  R  S  H  A  P  D  H  D  V  T  Q  Q  R  D  E  V  W  V  V  G  M  G  I  V  M  S  L  I  V  L  A  I  V  F  G  N  V  L  V  I
 841  AGAAGCCATGCGCCGGACCACGACGTCACGCAGCAAAGGGACGAGGTGTGGGTGTGGGCATGGGCATCGTCATGTCTCTCATCGTCCTGGCCATCGTGTTTGGCAATGTGCTGGTCATC
  56  T  A  I  A  K  F  E  R  L  Q  T  V  T  N  Y  F  I  T  S  L  A  C  A  D  L  V  M  G  L  A  V  V  P  F  G  A  A  H  I  L
 961  ACAGCCATTGCCAAGTTCGAGCGTCTGCAGACGGTCACCAACTACTTCATCACTTCACTGGCCTGTGCTGATCTGGTCATGGGCCTGGCAGTGGTGCCCTTTGGGGCCGCCCATATTCTT
  96  M  K  N  W  T  F  G  N  F  W  C  E  F  W  T  S  I  D  V  L  C  V  T  A  S  I  E  T  L  C  V  I  A  V  D  R  Y  F  A  I
1081  ATGAAAATGTGGACTTTTGGCAACTTCTGGTGCGAGTTTTGGACTTCCATTGATGTGCTGTGCGTCACGGCCAGCATTGAGACCCTGTGCGTGATCGCAGTGGATCGCTACTTTGCCATT
 136  T  S  P  F  K  Y  Q  S  L  L  T  K  N  K  A  R  V  I  I  L  N  V  W  I  V  S  G  L  T  S  F  L  P  I  Q  M  H  W  Y  R
1201  ACTTCACCTTTCAAGTACCAGAGCCTGCTGACCAAGAATAAGGCCCGGGTGATCATTCTGATGGTGTGGATTGTGTCAGGCCTTACCTCCTTCTTGCCCATTCAGATGCACTGGTACCGG
 176  A  T  H  Q  E  A  I  N  C  Y  A  N  E  T  C  C  D  F  F  T  N  Q  A  Y  A  I  A  S  S  I  V  S  F  Y  V  P  L  V  I  M
1321  GCCACCCACCAGGAAGCCATCAACTGCTATGCCAATGAGACCTGCTGTGACTTCTTCACGAACCAAGCCTATGCCATTGCCTCTTCCATCGTGTCCTTCTACGTTCCCCTGGTGATCATG
 216  V  F  V  Y  S  R  V  F  Q  E  A  K  R  Q  L  Q  K  I  D  K  S  E  G  R  F  H  V  Q  N  L  S  Q  V  E  Q  D  G  R  T  G
1441  GTCTTCGTCTACTCCAGGGTCTTTCAGGAGGCCAAAAGGCAGCTCCAGAAGATTGACAAATCTGAGGGCCGCTTCCATGTCCAGAACCTTAGCCAGGTGGAGCAGGATGGGCGGACGGGG
 256  H  G  L  R  R  S  S  K  F  C  L  K  E  H  K  A  L  K  T  L  G  I  I  M  G  T  F  T  L  C  W  L  P  F  P  I  V  N  I  V
1561  CATGGACTCCGCAGATCTTCCAAGTTCTGCTTGAAGGAGCACAAAGCCCTCAAGACGTTAGGCATCATCATGGGCACTTTCACCCTCTGCTGGCTGCCCTTCTTCATCGTTAACATTGTG
 296  H  V  I  Q  D  W  L  I  R  K  E  V  Y  I  L  L  N  W  I  G  Y  V  W  S  G  F  W  P  L  I  Y  C  R  S  P  D  F  R  I  A
1681  CATGTGATCCAGGATAACCTCATCCGTAAGGAAGTTTACATCCTCCTAAATTGGATAGGCTATGTCAATTCTGGTTTCAATCCCCTTATCTACTGCCGGAGCCCAGATTTCAGGATTGCC
 336  F  Q  E  L  L  C  L  R  R  S  S  L  K  A  Y  G  W  G  Y  S  S  W  G  N  T  G  E  Q  S  G  Y  H  V  E  Q  E  K  E  W  K
1801  TTCCAGGAGCTTCTGTGCCTGCGCAGGTCTTCTTTGAAGGCCTATGGGAATGGCTACTCCAGCAACGGCAACACAGGGGAGCAGAGTGGATATCACGTGGAACAGGAGAAAGAAAATAAA
 376  L  L  C  E  D  L  P  G  T  E  D  F  V  G  H  Q  G  T  V  P  S  D  M  I  D  S  Q  G  R  M  C  S  T  W  D  S  L  L
1921  CTGCTGTGTGAAGACCTCCCAGGCACGGAAGACTTTGTGGGCCATCAAGGTACTGTGCCTAGCGATAACATTGATTCACAAGGGAGGAATTGTAGTACAAATGACTCACTGCTGTAAAGC
2041  AGTTTTTCTACTTTTAAAGACCCCCCCCCCCCAACAGAACACTAAACAGACTATTTAACTTGAGGGTAATAAACTTAGAATAAAATTGTAAAATTGTATAGAGATATGCAGAAGGAAGGGC
2161  ATCCTTCTGCCTTTTTTATTTTTTTAAGCTGTAAAAAGAGAGAAAACTTATTTGAGTGATTATTTGTTATTTGTACAGTTCAGTTCCTCTTTGCATGGAATTTGTAAGTTTATGTCTAAA
2281  GAGCTTTAGTCCTAGAGGACCTGAGTC
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