Nucleotide sequence of a rat liver cDNA encoding the cytosolic 3-hydroxy-3-methylglutaryl coenzyme A synthase

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The screening of a rat liver cDNA library with a hamster probe that encompasses the nucleotides coding for the hamster enzyme (1), yielded a cDNA encoding the rat cytosolic 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) synthase. The cDNA spans 3275 bp and the only open reading frame codes for a protein of 520 amino acids, that is 97% homologous to the hamster cytosolic HMG-CoA synthase.

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REFERENCE

1. Gil,G., Goldstein,J.L., Slaughter,C.A. and Brown,M.S. (1986) *J. Biol. Chem.* **261**, 3710–3716.

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                    -91    CCCAGGGTCCGATCGCGTTTGGTGCCTGAAGGAGGAACCGGTGACAGACCTGGAGACTACAGTTCTCTGTCCTTCACACAGCTCTTTCACC

   1  ATGCCTGGGTCACTTCCTTTGAATGCAGAGGCTTGCTGGCCAAAAGATGTGGGAATCGTTGCCCTTGAAATCTACTTTCCTTCTCAGTATGTTGATCAAGCTGAGTTGGAAAAATACGAT
       M  P  G  S  L  P  L  N  A  E  A  C  W  P  K  D  V  G  I  V  A  L  E  I  Y  F  P  S  Q  Y  V  D  Q  A  E  L  E  K  Y  D
 121  GGTGTAGATGCTGGAAAGTATACCATTGGCCTGGGCCAGGCCAGGATGGGCTTCTGCACGGATCGCGAAGACATCAACTCTCTCTGCCTGACTGTGGTTCAGAAACTGATGGAGAGAAAT
       G  V  D  A  G  K  Y  T  I  G  L  G  Q  A  R  M  G  F  C  T  D  R  E  D  I  N  S  L  C  L  T  V  V  Q  K  L  M  E  R  N
 241  AGCCTTTCCTATGACTGCATTGGGCGGCTGGAAGTCGGGACAGAGACAATCATCGACAAATCAAAATCCGTGAAGTCTAATTTGATGCAGCTGTTTGAGGAGTCTGGGAATACAGATATA
       S  L  S  Y  D  C  I  G  R  L  E  V  G  T  E  T  I  I  D  K  S  K  S  V  K  S  N  L  M  Q  L  F  E  E  S  G  N  T  D  I
 361  GAAGGAATAGATACAACTAATGCATGCTATGGGGGCACAGCCGCAGTCTTCAATGCTGTGAACTGGATCGAATCCAGCTCTTGGGATGGACGATACGCTTTGGTAGTTGCAGGAGACATC
       E  G  I  D  T  T  N  A  C  Y  G  G  T  A  A  V  F  N  A  V  N  W  I  E  S  S  S  W  D  G  R  Y  A  L  V  V  A  G  D  I
 481  GCTATATATGCCTCAGGAAACGCCAGGCCTACAGGTGGAGTTGGAGCTGTGGCTCTGCTAATTGGGCCAAATGCTCCTGTAATTTTTGACCGAGGGCTTCGTGGGACACACATGCAGCAT
       A  I  Y  A  S  G  N  A  R  P  T  G  G  V  G  A  V  A  L  L  I  G  P  N  A  P  V  I  F  D  R  G  L  R  G  T  H  M  Q  H
 601  GCCTACGACTTTTACAAGCCTGACATGCTCTCTGAATACCCTGTGGTAGATGGAAAACTCTCCATACAGTGCTACCTCAGCGCATTGGACCGCTGCTATTCTGTCTACCGCAAAAAGATC
       A  Y  D  F  Y  K  P  D  M  L  S  E  Y  P  V  V  D  G  K  L  S  I  Q  C  Y  L  S  A  L  D  R  C  Y  S  V  Y  R  K  K  I
 721  CGGGCCCAGTGGCAGAAAGAGGGAAAGGATAAAGATTTTACCCTGAATGATTTTGGCTTCATGATCTTTCACTCGCCATACTGTAAACTGGTGCAGAAATCTCTAGCTAGGATGTTCCTG
       R  A  Q  W  Q  K  E  G  K  D  K  D  F  T  L  N  D  F  G  F  M  I  F  H  S  P  Y  C  K  L  V  Q  K  S  L  A  R  M  F  L
 841  AATGACTTTCTTAACGATCAAAACAGAGACAAAAACAGTATTTACAGTGGGCTGGAAGCCTTTGGGGATGTGAAATTAGAAGATACTTACTTCGACAGAGATGTGGAAAAGGCATTTATG
       N  D  F  L  N  D  Q  N  R  D  K  N  S  I  Y  S  G  L  E  A  F  G  D  V  K  L  E  D  T  Y  F  D  R  D  V  E  K  A  F  M
 961  AAGGCTAGTGCTGAGCTATTCAACCAGAAAACAAAGGCATCTTTGCTTGTATCGAATCAAAATGGAAACATGTACACATCCTCTGTATACGGTTCCCTTGCTTCTGTTCTGGCACAGTAC
       K  A  S  A  E  L  F  N  Q  K  T  K  A  S  L  L  V  S  N  Q  N  G  N  M  Y  T  S  S  V  Y  G  S  L  A  S  V  L  A  Q  Y
1081  TCACCTCAACAGTTGGCCGGGAAGAGGATTGGAGTGTTCTCTTACGGTTCTGGCTTGGCTGCCACACTCTACTCCCTTAAAGTCACACAAGATGCCACACCAGGATCTGCTCTTGACAAA
       S  P  Q  Q  L  A  G  K  R  I  G  V  F  S  Y  G  S  G  L  A  A  T  L  Y  S  L  K  V  T  Q  D  A  T  P  G  S  A  L  D  K
1201  ATAACAGCAAGTTTATGTGACCTTAAGTCAAGGCTTGACTCAAGAACGTGTGTGGCACCAGACGTCTTTGCTGAAAACATGAAGCTCAGAGAGGACACACATCACTTAGCCAACTATATT
       I  T  A  S  L  C  D  L  K  S  R  L  D  S  R  T  C  V  A  P  D  V  F  A  E  N  M  K  L  R  E  D  T  H  H  L  A  N  Y  I
1321  CCCCAGTGTTCAATAGATTCACTCTTCGAAGGAACATGGTATCTAGTCAGAGTGGATGAAAAGCACAGAAGAACTTACGCCCGGCGTCCCTCCACAAATGACCACAGTTTGGATGAAGGA
       P  Q  C  S  I  D  S  L  F  E  G  T  W  Y  L  V  R  V  D  E  K  H  R  R  T  Y  A  R  R  P  S  T  N  D  H  S  L  D  E  G
1441  GTGGGACTTGTGCATTCAAACACAGCTACAGAGCATATTCCAAGCCCGGCTAAGAAAGTGCCAAGACTTCCTGCGACCTCGGGCGAACCTGAGTCGGCTGTCATCAGTAACGGGGAGCAC
       V  G  L  V  H  S  N  T  A  T  E  H  I  P  S  P  A  K  K  V  P  R  L  P  A  T  S  G  E  P  E  S  A  V  I  S  N  G  E  H
1561  TGAGAGCCGTGGCCTTCACAGAGGCTCGGGGCTGGATGGGGTATGGGAAACGTTAGAGGAATGGATGTCTTGGGACAATTTTACAGATTACGTGTTGCTTAAAAATGTAATGTAACTGAC
1681  ACAGAGCCCAGAAAACTGTTGTGTTTTTGGAGAAGTCTCGCTGAGCTCCTAACACACTTCCTGCTGTGGGCTGGCCAATGGTGAATGTACTGCGATGGTGTTAAGGGCTCTGCAGAACGT
1801  CATACCTCGCTGCATGTTTACACGCATGCGGGTTAGGCTTCAAACTCGGTCTGAACTGAGTGCTTCTGACTGCAAAGGCAGAGGTACTGCTGTCCAGTTTAAAAAATTGTTTTTTTTTTT
1921  TTTAATGTGTAAGAATTTTTATACTTAAATAAAAAAAAGTACCTGTAGCTTTTGGGGGAAAAAAAAAAACCTTTTTCTAGGTTGGGGATTGTGGAATTTAAATGTTACACATAAACTCTG
2041  CTTAATGGCAAGGCAAACATTTATCTTTTTCGAAGATTTATAAATCCTGAAGAGAAAAAAAGAGGGTATGGTTCTAGGATCTGGATGAACCATCAGTGAGAAAGGTTAGTCATAATCAAG
2161  TGAGCAGAAGGATGCTGGCGTTGAGCAGGCCTCTGTCACAGCAACCAGGGCTCTGTGGGCACAGCTGAGGGAACTTTCTGGCCAGGTGCCCGTGACTGCTGCTCAGCTGCACTGAGATGC
2281  AGTGGAGCTGCTGCACGGAAGCTTGCTGTGGTGCTGAACGCCTTACCTGCGGATAAAGTGTAAAGTAGGAGGGATGGGCAGGGCACTATTAGGTTACAGTGTTACAGACCCAGGTTATAG
2401  ACTTGACAGCTCAAACTCACCAGACACCTTTTTCCCTTTGTGGTTTGTGTATTTTTTGTGTTTTGTTTGTTTTTTTTTATATTGTTCAATTTAAAAAATTTAGAAAATTTTAACCTTACG
2521  TTTTCACATAGTGTGATTAGCCAAAAGGAATTTCACTTCAAGATCTAGAAATAGAATTCATAACATTTTTTCCTAAACTTTGACTTTTAAAACAACGAAAATTACCACATGAGATGAACA
2641  AGAAAATTCATTAGAAAGTTCTCTGGGTGATTTTTGGTGCTGAACTGACATGAGCCTCATAGACTGTAAAACAGAGGTAGTTGAAACTAATGTACAGAACTACATTTTTTAATTTTATTT
2761  GCATTTAATTCTGTGAAGTTTCAGTTATCTAAAATAAACACATAAACGTGTAATGTTTCAGATTGCAAGGTGAGATGTAATGTAGCATTTGTAAGATATTCTTGTCAATATTAACTGGTA
2881  GGATTTTGATTTGTACAGTTTTAATTGGTTAAAATGATCTCATTTTAACATCCACTGCTATAGATGAATGATGTAAGCTCAGATTTAATGAATGGTGGGGAAATGGTGCATGTAATTTTT
3001  TCGCAAGTATCGAGAGTTCTGTATGTTTTGAAAAGAATAATTTAACGTTTGGGTTGCCAGGAAGGGGGCTTTCCCAGAGTCCATTGCCAGGCGTTGGGCAAGCCTCGCAATGTTGGCACG
3121  GAGCGTTAACCACACCTTACTAATAGCAAGGGGAATAACTTTGAAATAAAGTTTTAGACAAAT(A)n
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