

## Complete cDNA sequence of human foetal liver peroxisomal 3-oxoacyl-CoA thiolase

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Recently, Bout *et al* published a partial cDNA sequence encoding the human liver peroxisomal 3-oxoacyl-CoA thiolase (1). We present here a full cDNA sequence for human foetal liver peroxisomal thiolase. This differs from that of Bout *et al* in extending from 30 bases upstream of their cDNA start to the poly A tail, 221 bases downstream of the end of their cDNA and includes the unusual putative polyadenylation signal, AGTAAA, which is also found in the rat cDNA (2). We observe three further differences between our sequence and theirs; one is a conservative substitution at nucleotide 405 or 375 in our and their sequence respectively; one a base insertion at nucleotide 1321 in our sequence; the other may be a reverse transcriptase error in the Bout sequence, since our sequence almost exactly matches the rat cDNA sequence at this point (890-897 or 860-867 in our and their sequence respectively).

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M Q R L Q V V L G H L R G P A D S G W M P Q A A P C L S
1  CGGACTGGTGGCTGGTCTGCAGGGTTGACCTGGCGAATGCAGAGGCTCAGAGTGTGCTGGCCACTGAGGGTCCGGCCGATCCGGCTGGATGCCGAGGCCGCCCTTGCCTGAGC
GGTCCCCCGAGGCTCGGCCCGGAGCTGGTGGTGCACGGGGGGCGACGGCCATCTCGCGGGGGGGCGGGCGGCTCAAGGACACCCCGAGCGAGCTTCTCTCGGCGAGTC
21  G A P Q A S A A D V V V V H G R R T A I C R A G R G G F K D T T P D E L L S A V
M T A V L K D V N L R P E Q L G D I C V G N V L Q P G A G A I M A R I A Q F L S
241  M T A V L K D V N L R P E Q L G D I C V G N V L Q P G A G A I M A R I A Q F L S
ATGACCGGGTTCGAAGGAGCTGAATCGAGGCCGAACAGCTGGGGGACATCTGTGTGGAAATGTGCTGCAGCCTGGGGCCGGGGCAATCATGGCCGAATCGCCAGTTTCTCGAGT
361  D I P E T V P L S T V N R Q C S S G L Q A V A S I A G G I R N G S Y D I G M A C
GACATCCCGGAGACTGTGCTTTGTCCACTGTCAATAGACAGTGTTCGTGGGGCTACAGGAGTGGCCAGCATAGCAGGTGGCATCAGAAATGGGTCTTATGACATTGGCATGGCCGT
481  G V E S H S L A D R G N P G N I T S R L M E K E K A R D C L I P H G I T S E N V
GGGTGGAGTCCATGCTCCCTGGCTGACAGAGGGAACCCCTGGAATATTACTTCGGCTTGATGGAGAAGGAGAAGGCCAGAGATTCCCTGATTCATGGGGAATACCTCGAGAATGTG
601  A E R F G I S R E K Q D T F A L A S Q Q K A A R A Q S K G C F Q A E I V P V T T
GCTGAGCGGTTGGCATTTCCAGGGAGAACGGATACCTTTGCCCTGGCTCCACGACAGAAGCAGGAAGGCCAGAGCAAGGGCTGTTTCCAACTGAGATTGTGCCCTGTGACCC
721  T V H D D K G T K R S I T V T Q D E G I R P S T T M E G L A K L K P A F K K D G
ACGGTCCATGATGACAAGGGACCAAGAGGAGCATCACTGTGACCCAGGATGAGGGTATCCGGCCCCAGCCACCATGGAGGGCTGGCCAACTGAAGGCTGCCCTCAAGAAAGATGTT
S P A Bout
V L L rat
841  S T T A G N S S Q V S D G A A A T L L A R S K A E E L G L P I L G V L R S Y A
TCTACCACAGCTGAAACTCTAGCCAGGTGAGTGTGGGGAGCTGCCATCTGCTGGCCGGAGGCTCAAGGAGAAGATTGGGCCCTCCCATCTTGGGGTCTGAGGTCTTATGCA
CGTCTGCT rat
CAGTCTGC Bout
V V G V P P D I M G I G P A Y A I P V A L Q K A G L T V S D V D I F E I N E A F
961  GTGGTTGGGGTCCACCTGACATCATGGGCAATTGGACCTGGCTATGCCATCCAGTAGCTTTGCAAAAAGCAGGGCTGACAGTGAGTGACGTGGACATCTTGAGATCAATGAGGCCTTT
GCAAGCCAGGCTGCTACTGTGTGGAGAAGCTACGACTCCCCCTGAGAAGGTGAACCCCTGGGGGGTGCAGTGGCTTAGGCCATAGGCCACCCACTGGGCTGCATGGGGACGACAGGTCATC
1081  A S Q A A Y C V E K L R L P P E K A V N P L G G A V A L G H P L G C T G A R Q V I
GCAAGCCAGGCTGCTACTGTGTGGAGAAGCTACGACTCCCCCTGAGAAGGTGAACCCCTGGGGGGTGCAGTGGCTTAGGCCATAGGCCACCCACTGGGCTGCATGGGGACGACAGGTCATC
1201  T L L N E L K R R G K R A Y G V V S M C I G T G H G A A A V F E Y P G N *
ACGCTGCTCAATGAGCTGAAGCCCGTGGGAAGAGGGCATACGGAGTGGTGTCCATGTGCATCGGACTGGAATGGAGCCGCTGGCTTGTGAATACCTGGGAATGAGTGGAGTGC
1321  CAGGCTGGAGGGCTACGGAGACAGTCTGCTGCTTACGACGCAAGGCGAGTAAACCCACAAAGAACCCACATGGGAAACTAGCAGCTGGTGGTGGGAGTGGACGATCAAGCC
1441  ACTTCAACTCATTTGGAAAATGTGAACACTGATGACATGGTATAGGAGTGGTGGGGTGTGAGCCACCCATAGACCCCTCTTAGCTGCGAAGATAAAAAGCAGCTGGGTACCCAGG
1561  CCACAAGGCATGGTAAATCTTAAGCAAGGCAATCGATGGATGAGAAGTGAATGGGCATAGTAAAAGTGCATGAATTA (n)

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