Nucleotide and amino-acid sequence of human testis-derived *TCP1*

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TCP1 is the human homologue of the mouse t-complex gene Tcp-1 (Willison *et al.* 1987). cDNA clones have been isolated from a human testis cDNA library by cross-hybridization with a mouse subclone. The longest human cDNA inserts included an ATG codon at a position homologous to the mouse Tcp-1 initiation codon (Willison *et al.* 1986). The human cDNA clones were colinear to the mouse sequence except for a single base frameshift in the mouse sequence at amino acid 524 caused by a sequencing error by Willison *et al.* (1986). The corrected sequence of mouse bases 1630–1641 is ATCCTTCGGATT. Consequently the mouse open reading frame terminates at the same amino acid as human. The mouse and human TCP1 ORFs both encode polypeptides of 556 amino acids which are 95.5% homologous. One out of ten human testis cDNA clones contained the extended 3′ untranslated region described by Willison *et al.* 1987.

REFERENCES

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2. Willison,K.R., Kelly,A., Dudley,K., Goodfellow,P., Spurr,N., Groves,V., Gorman,P., Sheer,D. and Trowsdale,J. (1987) *EMBO J.* **6**, 1967–1974.

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                                                                     ACGTGTATCGCTGCCGTCAAG    21
ATGGAGGGGCCTTTGTCCGTGTTCGGTGACCGCAGCACTGGGGAAACGATCCGCTCCCAAAACGTTATGGCTGCAGCTTCGATTGCCAAT   111
 M  E  G  P  L  S  V  F  G  D  R  S  T  G  E  T  I  R  S  Q  N  V  M  A  A  A  S  I  A  N     30
ATTGTAAAAAGTTCTCTTGGTCCAGTTGGCTTGGATAAAATGTTGGTGGATGATATTGGTGATGTAACCATTACTAACGATGGTGCAACC   201
 I  V  K  S  S  L  G  P  V  G  L  D  K  M  L  V  D  D  I  G  D  V  T  I  T  N  D  G  A  T     60
ATCCTGAAGTTACTGGAGGTAGAACATCCTGCAGCTAAAGTTCTTTGTGAGCTGGCTGATCTGCAAGACAAAGAAGTTGGAGATGGAACT   291
 I  L  K  L  L  E  V  E  H  P  A  A  K  V  L  C  E  L  A  D  L  Q  D  K  E  V  G  D  G  T     90
ACTTCAGTGGTTATTATTGCAGCAGAACTCCTAAAAAATGCAGATGAATTAGTCAAACAGAAAATTCATCCCACATCAGTTATTAGTGGC   381
 T  S  V  V  I  I  A  A  E  L  L  K  N  A  D  E  L  V  K  Q  K  I  H  P  T  S  V  I  S  G    120
TATCGACTTGCTTGCAAGGAAGCAGTGCGTTATATCAATGAAAACCTAATTGTTAACACAGATGAACTGGGAAGAGATTGCCTGATTAAT   471
 Y  R  L  A  C  K  E  A  V  R  Y  I  N  E  N  L  I  V  N  T  D  E  L  G  R  D  C  L  I  N    150
GCTGCTAAGACATCCATGTCTTCCAAAATCATTGGGATAAATGGTGATTTCTTTGCTAACATGGTAGTAGATGCTGTACTTGCTATTAAA   561
 A  A  K  T  S  M  S  S  K  I  I  G  I  N  G  D  F  F  A  N  M  V  V  D  A  V  L  A  I  K    180
TACACAGACATAAGAGGCCAGCCACGCTATCCAGTCAACTCTGTTAATATTTTGAAAGCCCATGGGAGAAGTCAAATGGAGAGTATGCTC   651
 Y  T  D  I  R  G  Q  P  R  Y  P  V  N  S  V  N  I  L  K  A  H  G  R  S  Q  M  E  S  M  L    210
ATCAGTGGCTATGCACTCAACTGTGTGGTGGGATCCCAGGGCATGCCCAAGAGAATCGTAAATGCAAAAATTGCTTGCCTTGACTTCAGC   741
 I  S  G  Y  A  L  N  C  V  V  G  S  Q  G  M  P  K  R  I  V  N  A  K  I  A  C  L  D  F  S    240
CTGCAAAAAACAAAAATGAAGCTTGGTGTACAGGTGGTCATTACAGACCCTGAAAAACTGGACCAAATTAGACAGAGAGAATCAGATATC   831
 L  Q  K  T  K  M  K  L  G  V  Q  V  V  I  T  D  P  E  K  L  D  Q  I  R  Q  R  E  S  D  I    270
ACCAAGGAGAGAATTCAGAAGATCCTGGCAACTGGTGCCAATGTTATTCTAACCACTGGTGGAATTGATGATATGTGTCTGAAGTATTTT   921
 T  K  E  R  I  Q  K  I  L  A  T  G  A  N  V  I  L  T  T  G  G  I  D  D  M  C  L  K  Y  F    300
GTGGAGGCTGGTGCTATGGCAGTTAGAAGAGTTTTAAAAAGGGACCTTAAACGCATTGCCAAAGCTTCTGGAGCAACTATTCTGTCAACC  1011
 V  E  A  G  A  M  A  V  R  R  V  L  K  R  D  L  K  R  I  A  K  A  S  G  A  T  I  L  S  T    330
CTGGCCAATTTGGAAGGTGAAGAAACTTTTGAAGCTGCAATGTTGGGACAGGCAGAAGAAGTGGTACAGGAGAGAATTTGTGATGATGAG  1101
 L  A  N  L  E  G  E  E  T  F  E  A  A  M  L  G  Q  A  E  E  V  V  Q  E  R  I  C  D  D  E    360
CTGATCTTAATCAAAAATACTAAGGCTCGTACGTCTGCATCGATTATCTTACGTGGGGCAAATGATTTCATGTGTGATGAGATGGAGCGC  1191
 L  I  L  I  K  N  T  K  A  R  T  S  A  S  I  I  L  R  G  A  N  D  F  M  C  D  E  M  E  R    390
TCTTTACATGATGCACTTTGTGTAGTGAAGAGAGTTTTGGAGTCAAAATCTGTGGTTCCCGGTGGGGGTGCTGTAGAAGCAGCCCTTTCC  1281
 S  L  H  D  A  L  C  V  V  K  R  V  L  E  S  K  S  V  V  P  G  G  G  A  V  E  A  A  L  S    420
ATATACCTTGAAAACTATGCAACCAGCATGGGGTCTCGGGAACAGCTTGCGATTGCAGAGTTTGCAAGATCACTTCTTGTTATTCCCAAT  1371
 I  Y  L  E  N  Y  A  T  S  M  G  S  R  E  Q  L  A  I  A  E  F  A  R  S  L  L  V  I  P  N    450
ACACTAGCAGTTAATGCTGCCCAGGACTCCACAGATCTGGTTGCAAAATTAAGAGCTTTTCATAATGAGGCCCAGGTTAACCCAGAACGT  1461
 T  L  A  V  N  A  A  Q  D  S  T  D  L  V  A  K  L  R  A  F  H  N  E  A  Q  V  N  P  E  R    480
AAAAATCTAAAATGGATTGGTCTTGATTTGAGCAATGGTAAACCTCGAGACAACAAACAAGCAGGGGTGTTTGAACCAACCATAGTTAAA  1551
 K  N  L  K  W  I  G  L  D  L  S  N  G  K  P  R  D  N  K  Q  A  G  V  F  E  P  T  I  V  K    510
GTTAAGAGTTTGAAATTTGCAACAGAAGCTGCAATCACCATTCTTCGAATTGATGATCTTATTAAATTACATCCAGAAAGTAAAGATGAT  1641
 V  K  S  L  K  F  A  T  E  A  A  I  T  I  L  R  I  D  D  L  I  K  L  H  P  E  S  K  D  D    540
AAACATGGAAGTTATGAAGATGCTGTTCACTCTGGAGCCCTTAATGATTGATCTGATGTTCCTTTTATTTATAACAATGTTAAATGCAAT  1731
 K  H  G  S  Y  E  D  A  V  H  S  G  A  L  N  D  *                                             556
GTCTTGTACCTTGAGTTGAGTATTACACATTAAAGTAAAGTACAAGCTGT(A)n                                      1782
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