

The nucleotide sequence of rat transition protein 2 (TP2) cDNA

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We screened a rat testis cDNA library with an oligonucleotide of 81 mer prepared according to a part of the published aminoacid sequence of the rat transition protein TP 2 (1). We have isolated 3 independent cDNA clones with the length of 507-540 bp containing the coding region of 348 bp for rat transition protein 2. Rat TP2 cDNA encodes a polypeptide of 116 aminoacids. The insert of the full length cDNA clone contains a 3'-noncoding region of 155 bp and the polyadenylation signal ATTAAA at position 468. The 5'-noncoding region is 36 bp long. The known 27 aminoacids of rat TP2 (1) match perfectly with a part of the deduced aminoacid sequence of our rat TP2 cDNA (underlined). There is a homology of 86% to mouse TP2 cDNA (2). Comparing the polypeptides of rat and mouse TP2, rat TP2 is altered in the aminoacid sequence in 21 positions and shows a gap of 3 aminoacids in position 31.

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-30      -20      -10      0      10      20      30      40      50      60
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:
CGATGAGTGGTGGGAAGGCTCTGCATCTTGGTGCC ATG GGA GGC CAC ACT CCG AGG GGC AGA GCT CCC ACC ACT CAT CCC CAC CCG CAC AGC TCC TCT
Met Gly Gly His Thr Arg Arg Gly Arg Ala Pro Thr Thr His Pro His Pro His Ser Ser
1
:
70      80      90      100      110      120      130      140      150
:
:
CGG CCT CAA AGT CAC ACC AAT AAC CAG TGT GCC TGC AGC CAC CAC TGC CCG AGC TGC AGC CAA GCA GGC CAC CCG AGC TCC AGT TCC AGC
Arg Pro Gln Ser His Thr Asn Asn Gln Cys Ala Cys Ser His His Cys Arg Ser Cys Ser Gln Ala Gly His Pro Ser Ser Ser Ser Ser
30
:
160      170      180      190      200      210      220      230      240
:
:
CCC AGC CCT GGC CCG CCG AGC AAG CAC CCC AAA ACA CCC ATG CAC TCT CGT TAC TCA CCT TCA AGA CCC AGC CAC CGC GGC AGC TGC CCC
Pro Ser Pro Gly Pro Pro Thr Lys His Pro Lys Thr Pro Met His Ser Arg Tyr Ser Pro Ser Arg Pro Ser His Arg Gly Ser Cys Pro
60
:
250      260      270      280      290      300      310      320      330
:
:
AAG AAC AGG AAG ACC TTG GAA GGA AAC GTG AGC AAG AGA AAG GCG GTC AGG AGG CCG AAG CCG ACT CAC AGA GCT AAG AGG CGT AGC TCA
Lys Asn Arg Lys Thr Leu Glu Gly Asn Val Ser Lys Arg Lys Ala Val Arg Arg Lys Arg Thr His Arg Ala Lys Arg Arg Ser Ser
90
:
340      350      360      370      380      390      400      410      420      430      440
:
:
GGA CGA AGA TAC AAG TGA CACACTCCAGGATGTTCCCTGTGTCCATTTGATCCCAAAGGAGATAGCCATCCTAGGGGAATGTTGGGATGACAGTACAGGAACATGTCACTGCA
Gly Arg Arg Tyr Lys ***
116
:
450      460      470      480      490      500
:
:
GCAATTTCATGCATCATGGAATTAAAGCTTGTACCCCTGGAAAAAATAAAAAAAAAA

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References

1. Kenneth D. Cole and Stephen Kistler (1987) Biochem. Biophys. Res. Commun. Vol 147, pp. 437-442
2. Kenneth C. Kleene and James F. Flynn (1987) J. Biol. Chem. Vol 262, No. 36, pp. 17272-17277