

Nucleotide sequence of a full length cDNA clone encoding the deoxyribonuclease I from the rat parotid gland

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Monomeric actin interacts with bovine pancreatic DNaseI with high affinity ($K_b=5 \times 10^8 \text{ M}^{-1}$) thus forming a stoichiometric 1:1 complex (1). The parotid DNaseI has a lower affinity to actin ($5.5 \times 10^6 \text{ M}^{-1}$) and exhibits no immunologic crossreactivity with the bovine enzyme (2). A parotid specific λ gt11 cDNA library has been constructed and screened with a synthetic oligonucleotide sequence deduced from the amino acid sequence of the bovine pancreatic DNaseI kindly supplied by Dr. D.Suck (EMBL, Heidelberg). 8 cDNA clones were isolated and the sequence of a full-length clone is shown below. The translated protein is 284 amino acids long with a signal peptide of 22 residues and an extension of the C-terminus of two amino acids compared to chemically analysed amino acid sequence of the bovine DNaseI. At the amino acid level the proteins share a homology of 77%. Northern blot hybridisation indicates that the analysed sequence is a single copy gene. Interestingly, exchanges at position 13 and 67 exist between the DNaseI of the bovine and rat sources (13 Asp versus Glu and 67 Ile versus Val) which are known to participate in the DNaseI-actin contact (3) and might thus explain the observed differences of their affinity to actin (2).

REFERENCES

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CGGAGACATCTCTGTGTCAGCGGTGAATGAGCTCCCTTGTTCATCGACAGTCCAGAG
60 CAGACTCGGGGCTCATCATACCAACAGAGCAGGTCGTGTTCTGGCTACTGCAGCCATCTGA
120 GTGGCTTTCAGGATGAGGTACACAGGGCTGATGGGAATACTGCTCACCCTGGTCAACCTG
    M R Y T G L M G I L L T L V N L
180 CTGCAGCTGGCTGCGACTCTGAGAATTGCAGCCTCAACATCCGGACTTTTGGGGATACT
    L Q L A A T L R I A A F N I R T F G D T
240 AAGATGTCTAATGCCACCTCTCTAGCTACATTGTGAAAATCCCTGAGTCGCTATGACATT
    K M S N A T L S S Y I V K I L S R Y D I
300 GCTGTGGTCCAAGAGGTCAGAGCACTCACCTGGTTGCTGTTGGGAAGCTACTGGATGAA
    A V V Q E V R D T H L V A V G K L L D E
360 CTCATCGGGACATCCCTGACAACATATCGCTATATAATCAGTGAGCCGCTGGGCCGCAAA
    L N R D I P D N Y R Y I I S E P L G R K
420 AGCTACAAGGAACAGTACCTTTTGTGTACAGGCCAGCCAGGTGCTGTTTGGATAGC
    S Y K E Q Y L F V Y R P S Q V S V L D S
480 TATCATTATGACGATGGCTGTGAACCTGTGAAATGACACCTTCAGCCGAGAGCCAGCC
    Y H Y D D G C E P C G N D T F S R E P A
540 ATTGTCAAGTCTTTTCCCATCACTGAGGTCGAGAGTTTGGCATGTGCCCTTGAC
    I V K F F S P Y T E V R E F A I V P L H
600 TCAGCCCCAACAGAGGCTGTGAGTGAGATCGATGCCCTCTACGATGTTTATCTAGATGC
    S A P T E A V S E I D A L Y D V Y L D V
660 CGCCAAAAGTGGGGCCTGGAGGACATCATGTTTCATGGGAGATTCAATGCTGGCTGCAGC
    R Q K W G L E D I M F M G D F N A G C S
720 TACGTCACCTCCTCCCAATGGTCTCCATTGCGCCTCGGCAAGCCCCATCTCCAGTGG
    Y V T S S Q W S S I R L R T S P I F R W
780 CTGATCCCTGACAGTGGGACACCACAGCCACATCCACACACTGTGCTTATGACAGGATT
    L I P D S A D T T A T S T H C A Y D R I
840 GTGGTTGCTGGAGCTGCTCCAGGCTGCTGTTGTTCCAGCTCGGCTGTCCCTTTGAC
    V V A G A L L Q A A V V P S S A V P F D
900 TTCCAAGCAGAATACAGACTTACCAACAGATGGCTGAAGCCATCAGTGACCATTACCCA
    F Q A E Y R L T N Q M A E A I S D H Y P
960 GTGGAGGTGACACTCAGAAAGCACTAATGTCATTGAGTTCAGCCACACTGCTCCGGTGA
    V E V T L R K T *
1020 GGAAGAGTCCACCTCACCTATGTGTGGTACTGCGGCAITCCAACACCTCGGCACAGGGAA
1080 TGTCTACCACGCGGACTTAGAAATCTGTTTAAATGGAGTAAATAAAGCTGAGCCTGAGC
1140 AGGTAAAAAAAAAAAAA

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