

# Cloning of cDNA encoding the complete precursor for bovine seminal ribonuclease

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Palmieri *et al.* (1) cloned and sequenced a cDNA fragment encoding bovine seminal ribonuclease (RNase BS1) from amino acid residue 47 up to the C-terminal residue. The characterized clone p17G3 in addition to the partial coding sequence contained the complete 3'-untranslated region. On screening a cDNA library from bovine seminal vesicle tissue by colony hybridisation employing synthetic primers a number of RNase BS1-specific clones were identified. cDNA clone pBSV5 displays an open reading frame encoding a hydrophobic leader peptide consisting of 26 aa and the mature RNase BS1 of 124 aa. pBSV5 comprises the full 3'-untranslated region. The DNA sequence of pBSV5 from position 240–808 differs from the reported sequence (1)

in positions 621 and 647 within the 3'-untranslated region. A surprisingly high degree of identity (92%) was found between the signal peptides of RNase BS1 and bovine pancreatic ribonuclease (2).

## REFERENCES

1. M. Palmieri, A. Carsana, A. Furia and M. Libonati (1985) *Eur. J. Biochem.* **125**, 275–277.
2. A. Carsana, F. Confalone, M. Palmieri, M. Libonati and A. Furia (1988) *Nucl. Acids Res.* **16**, 5491–5502.

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TCCTCCAGTGGAGTGAGGTCATCATGGCTCTGAAGTCTCTAGTCGTGTTGCCACTGCTGGTCTGGTGCTGCTGCTGGTGCGGGTCCAGCCTTCCCTGGGCAAGGAATCTGCAGCTGCCA
M A L K S L V V L P L L V L V L L L V R V Q P S L G K E S A A A K
-1 +1
AGTTCGAGCGGCAGCACATGGACTCTGGCAACTCCCCAGCAGCAGCTCCAACCTACTGCAACCTGATGATGTGCTGCCGGAAGATGACCCAGGGGAAATGCAAGCCAGTGAACACCTTTG
F E R Q H M D S G N S P S S S S N Y C N L M M C C R K M T Q G K C K P V N T F V
TGCATGAGTCCCTGGCCGATGTTAAGCCGTGTGCTCCAGAAAGTCACTTGCAAGAATGGGCAGACCAACTGCTACCAGAGCAAATCCACCATGCCGATCACAGACTGCCCGGAGA
H E S L A D V K A V C S Q K K V T C K N G Q T N C Y Q S K S T M R I T D C R E T
CTGGCAGCTCCAAGTACCCCAACTGCGCCTACAAGACCACCCAGGTGGAGAAACACATCATAGTGGCTTTGTGGCGGTAAACCGTCCGTGCCAGTCCACTTCGATGCTTCAGTGTAGATCT
G S S K Y P N C A Y K T T Q V E K H I I V A C G G K P S V P V H F D A S V *
CCACCTGAGGCCAGAACAGTGAGATGCACCGCTTCATCACAAGGCATCTGCCTCTCCCTCTTGTTCCTTACCTGAGGGCAATAACTCAAGTTAGTTAAGGTTTTTATCCCTGCAACC
CCCACCACACACCCACCCACACACACCCATGTTTCCCTGGCATGAGGGCAATAACTCAAGCTAGTTAGGGCTCTTATCCAACATACACATGCTCCCTGGCCTGAGGCTTGCCC
CTGTGTAGTTTGGGAATTGAGAAGTGGGTTGTAATATGGGACCCATGTTAACCTAATCACTGCTACTTTCAATAAAACACACTTGCAA
    
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