Nucleotide and deduced amino acid sequence of the bovine adenovirus type 3 proteinase

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Adenoviruses code for a novel endoproteinase required for the maturation of infectious virions. The amino acid sequence is highly conserved among the human serotypes but has no homology to known proteinases. The enzyme is inhibited by agents specific for serine and for cysteine proteinase (1, 2). To determine the residues forming the active site we are sequencing the gene in different adenoviruses thereby identifying conserved residues as targets for site-specific mutagenesis. BAV-3 viral DNA restricted with HindIII was cloned into pBR322 and part of the HindIII-C fragment containing the proteinase was sequenced using primers (based on the hexon sequence published before), (3) and M13 vectors. 790 nucleotides of the viral 1-strand encoding the 204 residue proteinase is presented. 67% of the residues are identical with those of human adenovirus type 2.

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REFERENCES


ACGTTCCTGTTGAGGTGTTTGACGTGGCCCGCGTTCACCAGCCCCACAGAGGCGTGATCX5AAGTGGTGTA
CTTGAGAACCCCAATCTCGCCGCAACGCTACAACTGATAAGGCGCTACTGGGGCCAGATCTCTGCGCCAGCTT
GSREEELRFILHDLCNGVPYFLGT
TCGATAAACACCTTTCGGCCTGATCTCCAAGACCCGACATGCTGGCCATGACTGACACTGCCCCAGCC
FDKHFPGFISKDRMSCAIVNTAGR
CGAAACGGGGGCCGCTCAATTCGTCGCCAACATGCGCGCCAGACCTTTTACATGTGTTTGG
ETGCVHWMAMAWHPASQTFYMFD
CCTTTGCGTCTGCGAGATGAAAGCTAAGAAGAAGCTTACCAACTTTAGATACCGGCTCTAAAGGCGA
PPGFDSDQKKLQIYNFEYQGLLKR
GCCGCCGCACTCGTGACTGAGCCCTGAGCCCTTATTCAAAACACTCAACTGTCGAGCGAAGCG
SAULTSATDRCLTLIQSTQSVQGPN
CAGCCCGGGCTCCTGCGTCTTGCTCTGCACATTCTTCTCCACCCCGCTTTGGCCTGCGCCGCTTAGGGCCATG
560
SAAAGLCCFMHFLHAVFRWPLRAM
GACAAACATCCCAACATGACTCATTACCGCCGATTTCCCAAAACACATTTTAGAGACCGCCAGCTCCAAA
630
DNNPTMNLIHGVVPNMMLESPOQ
ATGCTTTGAGAACCCGAGAATCTGACTCATTCTAACCGCCGACTCCCGCTATTTGGTAAAGCA
700
NVLFLRNNQNLYRFVRHRSHPSHFV
TGCGCCGCAATTTGAGCTGAGCCGCCCGCTTTGATAAAATGTAAACAAATTAGACCGGCTGACCATGATTGC
770
AAQIEADTAFAKDMLTN
AGAAGGCACTCTCATTTTTTT

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