

Simian rotavirus SA11 segment 11 contains overlapping reading frames

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Gene segment 11 of the Simian rotavirus SA11 codes for a 28kd polypeptide which may be a minor component of the capsid layer (1). This gene was subcloned into Bluescribe M13+ (Stratagene) and sequenced using denatured ds DNA template and primers flanking the insert (2). The gene of 667 nucleotides has one open reading frame of 597 bases (198 amino acids) and a second (+1) of 279 bases (92 amino acids) starting at base 80. This is also conserved in both Wa (3) and UK Bovine (4) rotavirus strains. In the latter strain the reading frame is extended by 6 amino acids. An overlapping reading frame has been previously described for the reovirus σ 1 protein (5), the prototype virus of the Reoviridae. We have been unable to detect any protein product translated from the overlapping reading frame *in vitro*.

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      M S L S I D V T S L P S I P S T I Y K N
GGCTTTTAAAGCGCTACAGTGTCTCTCAGTATTGACGTGACGAGTCTTCCTTCTATTCCCTCAATATATATAAGAA 80
      E S S S T T S T L S G K S I G R S E Q Y I S P D A E
TGAATCGTCTTCAACAACGTCACACTCTTCTGGAAAATCTTATGGTAGGAGTGAACAGTACATTTCCAGATGCAGAAG 160
M N R L Q Q R Q L F L E N L L V G V N S T F H Q M Q K
      A F N K Y M L S K S P E D I G P S D S A S N D P L T S
CATTCAATAAATACATGCTGTGCAAGTCTCCAGAGGATATTGGACCATCTGATTCTGCTTCAAACGATCACTCACCAGT 240
H S I N T C C R S L Q R I L D H L I L L Q T I H S P V
      F S I R S N A V K T N A D A G V S M D S S A Q S R P S
TTTTCGATTAGATCGAATGCAAGTAAAGACAAATGCAGACGCTGGCGTGTCTATGGATTTCATCAGCACAAATCAGACCTTC 320
F R L D R M Q L R Q M Q T L A C L W I H Q H N H D L
      S N V G C D Q V D F S L N K G L K V K A N L D S S I
AAGTAATCGGATCGATCAAGTGGATTCTCCTTAAATAAAGGCTTAAAGTAAAGCTAATTTGGACTCATCAATAT 400
Q V M S D A I K W I S P
      S I S T D T K K E K S K Q N H K S R K H Y P R I E A E
CAATATCTACGGATACTAAAAGGAGAATCAAAACAAAACCATAAAGTAGGAAGCACTACCCAAGAATTGAAGCAGAG 480
      S D S D D Y V L D D S D S D D G K C K N C K Y K K K Y
TCGATTGATGATTATGCTACTGGATGATTCAGATAGTATGATGTTAAATGTAAGAACTGTAATATAAAGAAGAAATA 560
      F A L R M R M K Q V A M Q L I E D L
CTTCGCATTAAGAAATGAGAATGAACAAGTCCGAATGCAATTGATTGAAGATTTGTAAGTCTGACCTGGGAACACACTAG 640
      GGAGCTCCCCACTCCAGTTATGTGACC 667

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The protein from the major open reading frame is shown above the sequence, the alternative protein is underlined.

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