

A survey of the genomic distribution of alpha satellite DNA on all the human chromosomes, and derivation of a new consensus sequence

by K.H.Choo, B.Vissel, A.Nagy, E.Earle and P.Kalitsis

Nucleic Acids Research, **19**, pp. 1179–1182 (1991)

It should be noted that the accession number accompanying the above article has been deleted by EMBL Data Library. However, the sequence data reported is available on the EMBL netserver under the reference DS6053.

Errata

The self-cleaving domain from the genomic RNA of hepatitis delta virus: sequence requirements and the effects of denaturant

by A.T.Perrotta and M.D.Been

Nucleic Acids Research, **18**, pp. 6821–6827 (1990)

The publishers wish to apologize for an error which occurred during printing of this article. Some text was inadvertently omitted from the legend to figure 1 during translation. The correct legend is published below.

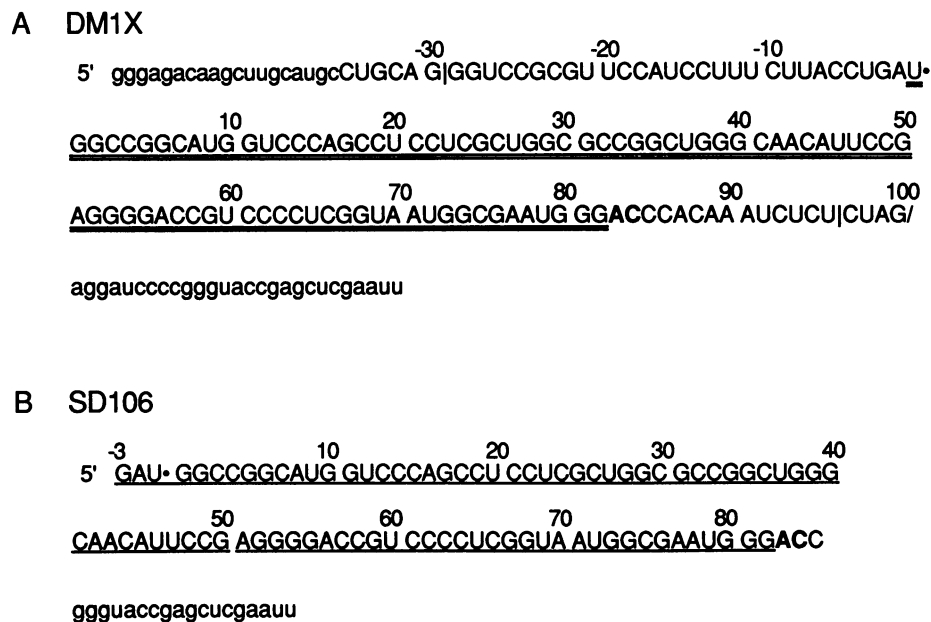


Figure 1. Sequences of the Transcripts Made from Plasmids pDM1X and pSD106. Upper case letters are HDV sequence; lower case are vector sequences; the heavy dot marks the break site and numbering is from this position. The double underlined DM1X sequence (A) is the minimal HDV sequence required for self-cleavage as determined using 5' and 3' deletions generated independently. The underlined SD106 sequence (B) was the shortest sequence actually shown to cleave in a single experiment. For both transcripts, bold face identifies the additional nucleotides required for efficient cleavage in 50% formamide. Vertical lines in the DM1X sequence mark the approximate position where inhibition of cleavage by flanking sequence is observed to start. The sequences shown are for transcripts made from EcoRI cut plasmid DNA, the diagonal slash indicates the end of the transcript made from XbaI cut pDM1X DNA.