Nucleotide sequence of a hamster cDNA highly homologous to the Xenopus laevis S19 ribosomal protein

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We have previously described (1) the isolation of a cDNA clone differentially expressed in Syrian hamster embryo fibroblast (HEF) and HSV-2 transformed HEF. Northern blot hybridization with this insert detected a message of 0.75 kb in all cell lines and tissues tested. We used this probe to screen a cDNA library with mRNA prepared from HSV-2 transformed HEF. We isolated a near full-length cDNA clone which is highly homologous to the Xenopus laevis S19 ribosomal protein (2). The extent of identity of these two nucleotide sequences is 81%. Deduced amino acid sequences from these two clones are identical except that the 93rd residue is arginine in hamster but lysine in Xenopus laevis and the last three which are different in the two species. The cDNA contains a single open reading frame of 399 nucleotides and a poly-A+ stretch, and codes for a protein of 133 amino acids of 15.4 kD. The sequence of the 5’ untranslated region from nucleotide +1 to +15 was determined by primer-extension: as expected for ribosomal protein, it contains a high ratio of GC nucleotides. The putative encoded protein has an excess of basic (26.9%) over acidic (8.2%) residues and also has high content of hydrophobic amino acid (26.9%).

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REFERENCES

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