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Poster 11

Solution Structure of the SL1 RNA of the M1 Double-Stranded RNA Virus of *Saccharomyces cerevisiae*

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The structure of the 20-nucleotide SL1 VBS RNA, 5′-GGAGACGC[GAUUC]GCGCUCC (bulged A underlined and loop bases in square brackets), has been determined by NMR spectroscopy. This RNA fragment is known to play a crucial role in viral particle binding to the plus strand and packaging of the RNA. Structure calculations give a precisely defined structure with an average pairwise root mean square deviation (RMSD) of 1.28 Å for the entire molecule, 0.57 Å for the loop region (C8-G14), and 0.46 Å for the bulge region (G4-G7, C15-C17), respectively. Base stacking continues for three nucleotides on the 5′-side of the loop. The final structure contains a single hydrogen bond involving the guanine imino proton and the carbonyl O2 of the cytosine between the nucleotides on the 5′- and 3′-ends of the loop, although they do not form a Watson-Crick base pair. All three pyrimidine bases in the loop point to the direction of the major groove, which implies that Cap-Pol protein may recognize the major groove of the SL1 loop region. The bulged A5 residue is stacked in the stem, but there are NOEs suggesting that the bulged A5 spends part of the time as a bulged-out conformation. The rigid conformation of the upper stem and loop regions may allow the SL1 VBS RNA to interact with Cap-Pol protein without drastically changing its own conformation.