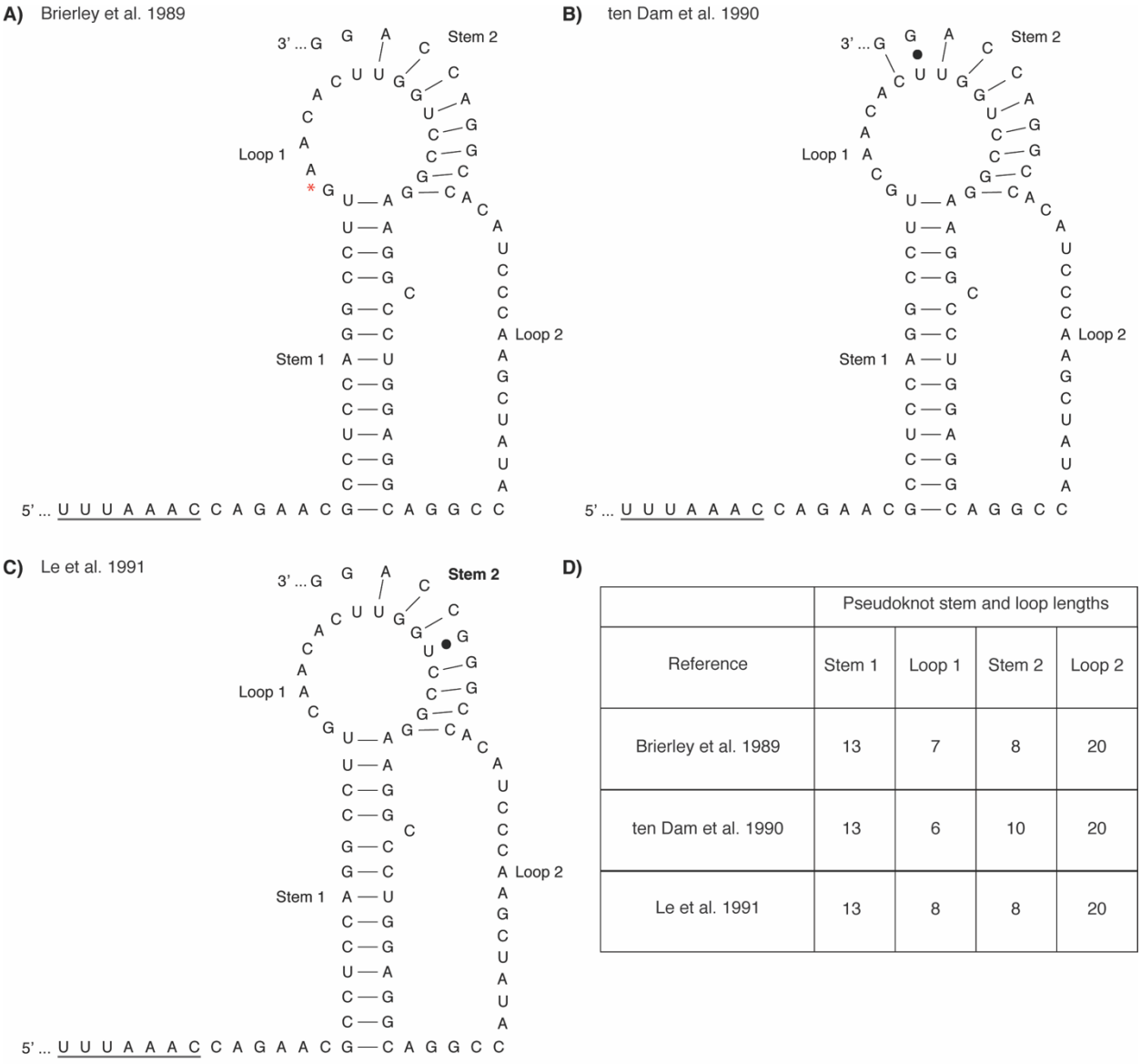

D)

	Pseudoknot stem and loop lengths			
Reference	Stem 1	Loop 1	Stem 2	Loop 2
Brierley et al. 1989	13	7	8	20
ten Dam et al. 1990	13	6	10	20
Le et al. 1991	13	8	8	20

Supplemental Figure S1. The HTLV-1 *pro-pol* frameshift site structure was previously proposed to be an H-type pseudoknot. The structures in A) and B) were proposed using a different HTLV-1 sequence than the sequence used in this manuscript (NC_001436.1). A) Brierley et al. used an HTLV-1 sequence that was taken from references cited in Jacks et al. (Jacks et al. 1988; Brierley et al. 1989). To the best of our knowledge, the HTLV-1 sequence referenced in the Jacks et al. is X04800.1 (Hiramatsu et al. 1987). However, there is a discrepancy between the sequence shown in Figure 7 of Brierley et al. (Brierley et al. 1989) and the X04800.1 sequence. The X04800.1 sequence includes a “C” that is missing from the Brierley et al. publication. The

location of this “C” is indicated by a red asterisk in the model here. B) ten Dam et al. used the same sequence as Brierly et al. (GenBank X04800.1), but proposed that pseudoknot stem 2 was extended by two additional base-pairs (ten Dam et al. 1990). C) Le et al. used an HTLV-1 sequence from *Human Retroviruses and AIDS* (Myers et al. 1989; Le et al. 1991). The HTLV-1 frameshift site sequence shown in their publication is consistent with the frameshift site sequence used here (NC_001436.1). D) In these models, the lengths of stem 1 (13 base-pairs) and loop 2 (20 nucleotides) were consistent, but the lengths of loop 1 (6-8 nucleotides) and stem 2 (8 or 10 base-pairs) varied.

Supplemental References

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