Table 1. Characterization of nucleotides at loop-helix junctions for loops with unpaired 5' nucleotides in 16 S and 23 S rRNA.

Loop Type		Total	A	AA	AG	AAG	AAG:U
Total	Measured	527	294 (56%)	113 (21%)	136 (26%)	56 (11%)	13 (2%)
	Predicted	---	135 (26%)	35 (7%)	43 (8%)	11 (2%)	2 (0.4%)
Hairpin	Measured	91	53 (58%)	21 (23%)	26 (29%)	9 (10%)	0 (--)
	Predicted	---	24 (25%)	6 (6%)	8 (8%)	2 (2%)	0 (--)
Multi-Stem	Measured	202	110 (54%)	45 (22%)	48 (24%)	20 (10%)	1 (1%)
	Predicted	---	51 (26%)	13 (7%)	16 (8%)	4 (2%)	1 (1%)
Internal	Measured	163	95 (58%)	40 (25%)	50 (31%)	24 (15%)	10 (6%)
	Predicted	---	42 (26%)	11 (7%)	13 (8%)	3 (2%)	1 (1%)
Bulge	Measured	71	36 (51%)	7 (10%)	12 (17%)	3 (4%)	2 (3%)
	Predicted	---	18 (25%)	5 (7%)	6 (8%)	1 (1%)	0 (--)

Junctions were counted if an A-motif occurred in greater than 50% (33% for AAG:U) of the sequences in the bacterial 16 S and 23 S rRNA alignments (http://www.rna.icmb.utexas.edu/). Predicted values were calculated with nucleotide frequencies: A (25.7%), G (31.4%), and U (20.5%); values are rounded to the nearest whole number. Percentages are calculated with respect to the total number of positions for that loop type; values are rounded to the nearest whole number, with -- used to represent zero.