Table 8a. Summary of Dominant A's and Related Motifs (Based Upon Tables 1-6).

#	Category	16S rRNA	23S rRNA	Total
1	# of Adenosine Platforms	3 (3%)	10 (5%)	13 (4%)
2	# of E Loops	4 (4%)	8 (4%)	12 (4%)
3	# of E-like Loops	4 (4%)	7 (4%)	11 (4%)
4	# of AA,AG@helix.ends	44 (44%)	72 (37%)	116 (39%)
4a	# of AA,AG@helix.ends in GNRA tetraloops	8 (8%)	8 (4%)	16 (5%)
4b	# of other AA,AG@helix.ends	36 (36%)	64 (33%)	100 (34%)
5	# of Tandem GA's	13 (13%)	37 (19%)	50 (17%)
6	# of U-turns	11 (11%)	29 (15%)	40 (14%)
7	# of Single Bulges	9 (9%)	14 (7%)	23 (8%)
8	Total # of Dominant A's associated with motifs (1-6) [a]	51 (51%)	98 (51%)	149 (51%)
9	# of Dominant A's not associated with motifs (1-6)	49 (49%)	96 (49%)	145 (49%)
10	Total # of Dominant A's at 3' ends of loops (8 + 9)	100	194	294

[a] A single dominant A may be associated with 1-3 motifs.

Table 8b. Number of Motifs per Dominant A (not including Single Bulges).

# Motifs	16S rRNA	23S rRNA	Total
1	25 (49%)	51 (52%)	76 (51%)
2	24 (47%)	30 (31%)	54 (36%)
3	2 (4%)	17 (17%)	19 (13%)
Total # of Dominant A's	51	98	149
Total # of Associated Motifs	79	162	241
Average # of Associated Motifs per Dominant A Position with an Associated Motif	1.5	1.7	1.6