

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

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

<sup>a</sup> A single dominant A may be associated with 1-3 motifs.

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

<b># Motifs</b>	<b>16S rRNA</b>	<b>23S rRNA</b>	<b>Total</b>
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