

Table 4. A-motif: AG sites in 16 S and 23 S rRNA ^a

Position ^b	Percent A ^c	Percent AG ^c	Predicted Structure Motifs ^d	Loop ^c	Position	Percent A	Percent AG	Predicted Structure Motifs
Hairpin Loops				Internal Loops				
16S rRNA				16S rRNA				
300	100	100	A, U	GNRA	246 +	100	100	A
1080	100	90	A, U	GNRA	520	100	100	A
1269	100	72	A, U	GNRA	665	70	67	
					687	100	97	A
					802	100	99	A, EL
23S rRNA				23S rRNA				
167	100	99		9*	1252	72	68	
251	100	98	A	5*	1275	93	92	
322	100	71		3	1418	100	98	A, GA
466	100	79	A, U	GNRA	1456 +	82	73	
492	99	75		5*				
646	87	86		5*				
1073	100	100	U	9	84	100	98	
1098	99	99	A, U	6*	244	100	99	A, GA, E
1618	98	95	A	6*	294 +	100	88	A
1755	100	73		3	861	100	96	A, GA, E
2147	95	95		4*	878	86	73	
2534	54	53		6	1111	100	100	
2598	100	100	A, U	GNRA	1237	100	82	
2662 #	100	100	A, U	GNRA	1268	100	65	A, GA, E
					1373 +	100	91	EL
					1434	78	58	
					1439	90	56	
16S rRNA				16S rRNA				
8	98	98			1477	92	88	A, GA, EL
26 +	100	99	A		1866	99	90	A, GA
288	100	92			2126	100	100	A, GA
353	98	98	A		2158	100	99	
523 +	100	99			2298 +	91	67	
828	80	71			2320	60	51	
860	96	88	A		2388 +	100	100	
1046 +	100	99			2639	100	78	A, GA
1067	100	100	A, U					
Multi-Stem Loops				Bulge Loops				
16S rRNA				16S rRNA				
177 +	59	58	A		583 +	100	100	
324 +	73	55			777	100	96	
332	100	88						
374	100	67	A, GA, E					
532 +	65	61						
627	99	98	A, GA		213 +	100	100	
655	98	98	A, GA		764 +	100	60	
699 +	99	95	A		941 +	100	99	
945	99	76	A		1205 +	76	67	
975	99	99	A		1490 +	97	96	
1189	100	99	A, GA, E		1586	90	79	
1342	100	100	U		2602 +	100	100	
1791	100	98	A					
1932	100	100	A, GA, EL					
2119	100	100						
2587	100	83	A, U					
2629	63	57						

^arRNA positions have an AG motif in more than 50% of the bacterial sequences and are indicated in blue on Figure 5. ^bThe position number is the nucleotide at the 3' loop end, at the loop-helix junction; +, the nucleotide prior to this position is base-paired; #, Sarcin/Ricin loop. ^cMore detailed information is available at <http://www.rna.icmb.utexas.edu/ANALYSIS/A-STORY/>. ^dA, AA.AG@helix.ends; E, E loop; EL, E-like loop; GA, tandem G:A; U, U-turn (see discussion). ^eHairpin loop size and special characteristics: GNRA, tetraloops (Woese *et al.* 1990) occur in more than 70% of the bacterial rRNA sequences; *, unusually stable G:A or U:U first mismatch.