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 [e]
		Hairpin Loops		
16S rRNA				
300	100	100	A, U	GNRA
1080	100	90	A, U	GNRA
1269	100	72	A, U	GNRA
23S rRNA				
167	100	99		9*
251	100	98	A	5*
322	100	71		3
466	100	79	A, U	GNRA
492	99	75		5*
646	87	86		5*
1073	100	100	U	9
1098	99	99	A, U	6*
1618	98	95	A	6*
1755	100	73		3
2147	95	95		4*
2534	54	53		6
2598	100	100	A, U	GNRA
2662 #	100	100	A, U	GNRA
		Multi-Stem Loops		
16S rRNA				
8	98	98		
26 +	100	99	A	
288	100	92		
353	98	98	A	
523 +	100	99		
828	80	71		
860	96	88	A	
1046 +	100	99		
1067	100	100	A, U	
23S rRNA				
177 +	59	58	A	
324 +	73	55		
332	100	88		
374	100	67	A, GA, E	
532 +	65	61		
627	99	98	A, GA	
655	98	98	A, GA	
699 +	99	95	A	
945	99	76	A	
975	99	99	A	
1189	100	99	A, GA, E	
1342	100	100	U	
1791	100	98	A	
1932	100	100	A, GA, EL	
2119	100	100		
2587	100	83	A, U	
2629	63	57		

Position	Percent A	Percent AG	Predicted Structure Motifs
	Internal Loops		
16S rRNA			
246 +	100	100	A
520	100	100	A
665	70	67	
687	100	97	A
802	100	99	A, EL
1252	72	68	
1275	93	92	
1418	100	98	A, GA
1456 +	82	73	
23S rRNA			
84	100	98	
244	100	99	A, GA, E
294 +	100	88	A
861	100	96	A, GA, E
878	86	73	
1111	100	100	
1237	100	82	
1268	100	65	A, GA, E
1373 +	100	91	EL
1434	78	58	
1439	90	56	
1477	92	88	A, GA, EL
1866	99	90	A, GA
2126	100	100	A, GA
2158	100	99	
2298 +	91	67	
2320	60	51	
2388 +	100	100	
2639	100	78	A, GA
	Bulge Loops		
16S rRNA			
583 +	100	100	
777	100	96	
23S rRNA			
213 +	100	100	
764 +	100	60	
941 +	100	99	
1205 +	76	67	
1490 +	97	96	
1586	90	79	
2602 +	100	100	

[a] rRNA positions have an AG motif in more than 50% of the bacterial sequences and are indicated in blue on Figure 5. [b] The 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. [c] More detailed information is available at http://www.rna.icmb.utexas.edu/ANALYSIS/A-STORY/. [d] **A**, AA.AG@helix.ends; **E**, E loop; **EL**, E-like loop; **GA**, tandem G:A; **U**, U-turn (see discussion). [e] Hairpin 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.