

Table 3. A-motif: AAG sites in 16 S and 23 S rRNA ^a.

Position ^b	Percent AA ^c	Percent AAG ^c	Predicted Structure Motifs ^d	Loop ^e	Position	Percent AA	Percent AAG	Predicted Structure Motifs
Hairpin Loops					Multi-Stem Loops			
16S rRNA					16S rRNA			
383	98	70	A	GNRA	60	98	98	A, GA
901	100	97	A, U	GNRA	197	99	93	A
23S rRNA					23 S rRNA			
311	91	84	U	6	499	99	98	
633	100	77	U	GNRA	574	99	98	
1226	62	52	A, U	GNRA	768	97	96	EL
1810	95	88	A	GNRA	873	100	89	
1872	70	65		GNRA	915	100	85	
1928	100	100	U	3	938	100	99	
2361	62	55		6	23 S rRNA			
Internal Loops					423	100	93	
16S rRNA					472	94	94	
1333	100	99	A		603	53	53	A, GA
1434	98	94			1010	100	53	
1469	54	54			1029	100	65	A, GA
1493	99	99	A		1308	99	99	
1503	100	100			1641	86	85	A
23S rRNA					2336	100	99	
609	100	68	A		2378	100	96	A, U
1001	99	99	A, GA		2412	93	85	
1156	98	85			2566	100	100	A
1354	100	99	A, GA, U		Bulge Loops			
1572	92	83	A, GA, U		23S rRNA			
1580	88	86	GA		1848	100	96	
1701	100	99	A, EL		23S rRNA			
2469	96	96	A, GA		23S rRNA			
2810	83	83	A		23S rRNA			

^arRNA positions listed have an AAG motif in more than 50% of the bacterial sequences and are indicated in green on Figure 5. ^bThe position number is the nucleotide at the 3' loop end, at the loop-helix junction. ^cMore detailed information is available at <http://www.ma.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 (in nucleotides) 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.