

Table 6. A-motif: A sites in 16 S and 23 S rRNA ^a.

Position ^b	Percent A ^c	Predicted Structure Motifs ^d	Loop ^e	Position	Percent A	Predicted Structure Motifs
Hairpin Loops			Internal Loops			
16 S rRNA			16 S rRNA			
845	61		5	151	100	
1016	94	A, U	GNRA	174	94	A, GA
1453	52		UNCG	282	100	A
23 S rRNA			23 S rRNA			
199	100		4	389 +	100	A
548	59		4	482	98	A, GA
574	76	U	8	487	99	A, GA, E
616	75		5*	535	100	
1176	62		4	715	100	A, GA
1918	93		7	1306	100	A, GA
2478	100	A	7*	1408	99	A
2705	99		4*	1483	99	A, GA
2757	100	A	11*	1499	100	
2799	56		3	23 S rRNA		
2826	100		7	63 +	56	
2860	96	A, U	GNRA	91 +	89	
Multi-Stem Loops			Bulge Loops			
16 S rRNA			16 S rRNA			
16	100	A		103	99	A
315 +	100	A		207	99	A, GA, E
338 +	99	A		1050	100	
366	65			1419	95	A, GA
495	99			1664 +	100	
546 +	51			1689	100	A, GA, EL
864	100	U		1723	62	
983	100	A		1745	53	
994	100			1802	100	A, GA
1101	100			1885 +	98	
1157	100	A, GA		2005 +	85	A
1191	100			2327 +	100	A
1339	100			2614	100	
1349	100	A, GA, E		2657 #	100	A, GA, E
1398	100	A		2690	68	
23 S rRNA			23 S rRNA			
52	99	A, GA		16 S rRNA		
73	100			55 +	100	
94	81			65	94	
149 +	95	A		130 +	100	
233	100	GA		205	83	
270	92			397 +	100	
340	99	A, GA, EL		595 +	79	BT
412	98			1042 +	55	
432	100			1055	100	
460	99	A, GA, E		1196 +	99	
670	100			1227 +	100	
990	100			1394 +	100	
1103 +	100	A		23 S rRNA		
1384	100			443 +	100	
1603	99			739 +	61	BT
1829	100			896 +	99	
2042	84			927 +	89	
2062	100			1819	100	
2171 +	100	U		1981 +	99	
2173 +	100	A, GA, U		2051 +	61	
2346	100	A, GA		2873 +	100	
2358	98	A		2879 +	98	
2835	100	A				

^a rRNA positions have an A motif in more than 50% of the bacterial sequences and are indicated in yellow 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; BT, base triple; E, E loop; EL, E-like loop; GA, tandem G:A; PK, pseudoknot; 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.