

**Table 5.** A-motif: AA sites in 16 S and 23 S rRNA <sup>a</sup>

Position <sup>b</sup>	Percent AA <sup>c</sup>	Sequence <sup>d</sup>	Predicted Structure Motifs <sup>e</sup>	Loop <sup>f</sup>	Position	Percent AA	Sequence	Predicted Structure Motifs
Hairpin Loops					Multi-Stem Loops			
<b>16 S rRNA</b>					<b>16 S rRNA</b>			
162	99	<u>AAC</u>	A, U	GNRA	120	99	<u>AAC</u>	U
622	99	<u>AAC</u>	U	5	510	99	<u>AAC</u>	
696	100	<u>AAU</u>	A, U	6*	959	100	<u>AAU</u>	A, GA
1170	97	<u>AAA</u>		5*	1005	51	<u>AAU</u>	
1519	97	<u>AAG</u>	A	GNRA				
<b>23 S rRNA</b>					<b>23 S rRNA</b>			
127	100	<u>AAC</u>	A	GNRA	182	56	<u>AAC</u>	A
390	72	<u>AAA</u>		7	218	61	<u>AAA</u>	
752	92	<u>AAA</u>	U	8*	223	94	<u>AAU</u>	A, GA, U
1085	100	<u>AAA</u>	U	3	300	99	<u>AAC</u>	EL
1367	66	<u>AAG</u>		GNRA	429	98	<u>AAA</u>	
1635	55	<u>AAU</u>	A	5*	483	58	<u>AAC</u>	A, U
2311	84	<u>AAU</u>		7	735	99	<u>AAC</u>	
					793	61	<u>AAA</u>	A, GA
					821	100	<u>AAU</u>	U
					1275	99	<u>AAA</u>	
					1302	68	<u>AAG</u>	
					1610	100	<u>AAC</u>	
					1786	100	<u>AAA</u>	
					1978	100	<u>AAC</u>	A
					2199	100	<u>AAC</u>	A, GA, U
					2287	65	<u>AAA</u>	A, GA
					2426	98	<u>AAC</u>	U
					2433	100	<u>AAA</u>	U
					2734	50	<u>AAG</u>	
Internal Loops					Bulge Loops			
<b>16 S rRNA</b>					<b>16 S rRNA</b>			
374	100	<u>AAU</u>	A		51	87	<u>AAC</u>	
449	52	<u>AAG</u>	E		72	58	<u>AGC</u>	
676	100	<u>AAU</u>	A, GA		642	51	<u>AAC</u>	
782	100	<u>AAC</u>	A, EL					
909	100	<u>AAC</u>	A, E					
1447	94	<u>AAC</u>						
<b>23 S rRNA</b>					<b>23 S rRNA</b>			
257	60	<u>AAG</u>	E		1900	89	<u>AAA</u>	
346	89	<u>AAA</u>						
515	100	<u>AAC</u>	U					
677	82	<u>AAC</u>						
901	60	<u>AAC</u>						
911	100	<u>AAC</u>						
1143	100	<u>AAA</u>						
1322	71	<u>AAG</u>						
1655	99	<u>AAC</u>	A					
2015	90	<u>AAU</u>						
2741	100	<u>AAC</u>	A, GA, U					

<sup>a</sup>rRNA positions have an AA motif in more than 50% of the bacterial sequences and are indicated in orange on Figure 5. <sup>b</sup>The position number is the nucleotide at the 3' loop end, at the loop-helix junction. <sup>c</sup>More detailed information is available at <http://www.rna.icmb.utexas.edu/ANALYSIS/A-STORY/>. <sup>d</sup>Most prevalent loop-helix sequence. <sup>e</sup>A, AA.AG@helix.ends; E, E loop; EL, E-like loop; GA, tandem G:A; U, U-turn (see discussion). <sup>f</sup>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.