Table 2. A motif: AAG:U sites in 16 S and 23 S rRNA [a].

Position [b]	Percent AA [c]	Percent AAG [c]	Percent G:U [c]	Predicted Structure Motifs [d]
		Multi-Stem Loops		
23S rRNA				
14	99	99	98	P
		Internal Loops		
16S rRNA				
415	76	75	59	EL, P
432	100	55	45	GA, P
1289	100	55	55	A, P
23S rRNA				
706	100	94	94	A, P
1214	97	97	97	A, P
1470	86	81	76	GA, P
1854	100	54	39	GA, P
1877	98	98	98	P
1890	100	100	100	P
2135 [e]	86	48	46	P
		Bulge Loops		
23S rRNA				
2542	100	100	99	P
2851	93	91	91	P

[a] rRNA positions have an AAG:U motif in more than 33% of the bacterial sequences and are indicated in red on Figure 5. [b] The position number is the nucleotide at the 3' loop end, at the loop-helix junction. [c] More detailed information is available at http://www.rna.icmb.utexas.edu/ANALYSIS/A-STORY/. [d] **A**, AA.AG@helix.ends, **EL**, E-like Loop; **GA**, Tandem G:A pairings; **P**, adenosine platform (see Discussion). [e] Although this site contains less than 50% AAG, it was included because it contains more than 33% G:U and narrowly missed the required minimum for AAG.