

**Table 2.** A motif: AAG:U sites in 16 S and 23 S rRNA <sup>a</sup>.

Position <sup>b</sup>	Percent AA <sup>c</sup>	Percent AAG <sup>c</sup>	Percent <u>G:U</u> <sup>c</sup>	Predicted Structure Motifs <sup>d</sup>
Multi-Stem Loops				
<b>23S rRNA</b>				
14	99	99	98	P
Internal Loops				
<b>16S rRNA</b>				
415	76	75	59	EL, P
432	100	55	45	GA, P
1289	100	55	55	A, P
<b>23S rRNA</b>				
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 <sup>e</sup>	86	48	46	P
Bulge Loops				
<b>23S rRNA</b>				
2542	100	100	99	P
2851	93	91	91	P

<sup>a</sup>rRNA positions have an AAG:U motif in more than 33% of the bacterial sequences and are indicated in red 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> **A**, AA.AG@helix.ends, **EL**, E-like Loop; **GA**, Tandem G:A pairings; **P**, adenosine platform (see Discussion). <sup>e</sup> 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.