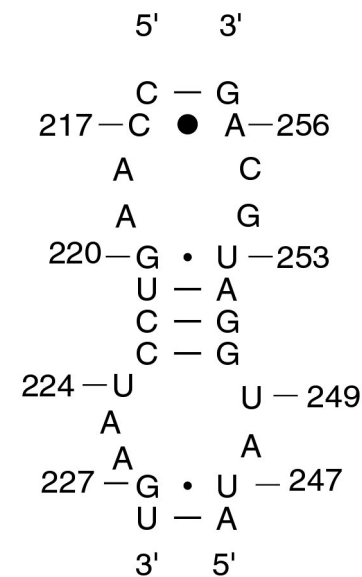


**Table 7.** Base Composition of Adenosine Platforms in Group IC1 Introns.

	Percentage <sup>a</sup>				Pairing <sup>b</sup>					
	A	C	G	U	A	C	G	U		
<u>219: 110 sequences</u>										
217 C <sup>c</sup>	-	85	15	-	256 A	49	19	22	10	GU 57%, CG 12%, AU 11%, GC 10%
218 A	<b>98</b>	-	-	-	255 C	8	62	28	2	
219 A	<b>98</b>	-	-	-	254 G	18	14	68	-	
220 G	11	15	<b>72</b>	2	253 U	7	10	13	<b>70</b>	
<u>226: 139 sequences</u>										
					249 U	7	23	5	65	UA 76%, UU 9%
224 U	4	4	5	87	248 A	81	2	7	10	
225 A	<b>83</b>	2	7	8						
226 A	<b>61</b>	26	4	9						
227 G	18	12	<b>65</b>	5	247 U	8	9	7	<b>76</b>	
										GU 62%, AU 12%, AC 5%, CG 5%



<sup>a</sup> Percentages were determined as described in text. Only percentages greater than 1% are shown. <sup>b</sup> Base pairing occurring more than 5%. <sup>c</sup> Indicates base present in P4-P6 subdomain of *Tetrahymena*.